

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 118926

TO: James Schultz

Location: REM/2D18/2C18

Art Unit: 1635

Wednesday, April 07, 2004

Case Serial Number: 10/006911

From: David Schreiber

Location: Biotech-Chem Library

Remsen E01A61 Phone: 272-2526

david.schreiber@uspto.gov

Search Notes	The state of the s	
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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor Remsen Bldg. 01 D86 571-272-2507

/ 0	luntary Results Feedback Folin
A	I am an examiner in Workgroup: Example: 1610
>	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	☐ Foreign Patent(s)
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
۲	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention.
Cor	mments:

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bldg.



ACCESSION: AX423055 ACCESSION: AX432323 ACCESSION: AX499823 ACCESSION: AX499825 ACCESSION: AX499825 ACCESSION: AX724377 ACCESSION: AX724377 ACCESSION: AX724377 ACCESSION: AX731325 ACCESSION: AX731323 ACCESSION: AX731323	ACCESSION: AX75976 ACCESSION: AX75976 ACCESSION: AX759613 ACCESSION: AX756013 ACCESSION: AX746014 ACCESSION: BD25520 ACCESSION: BD25520 ACCESSION: BD25520 ACCESSION: BD25520	ACCESSION: AX499826 ACCESSION: AX499827 ACCESSION: AX736520 ACCESSION: AX736520 ACCESSION: AX7365858 ACCESSION: AX758393 ACCESSION: AX7686844 ACCESSION: BD268284 ACCESSION: BD268284 ACCESSION: BD268284	ACCESSION: AR13000 ACCESSION: AR325045 ACCESSION: AR32511 ACCESSION: AX211870 ACCESSION: AX211780 ACCESSION: AX422844 ACCESSION: AX422844 ACCESSION: AX422844	ACCESSION - AK67229 ACCESSION - AK67229 ACCESSION - AK72263 ACCESSION - AK72263 ACCESSION - AK72209 ACCESSION - AK73209 ACCESSION - AK73209 ACCESSION - AK73209 ACCESSION - AK73673 ACCESSION - AK73673 ACCESSION - AK73673 ACCESSION - AK756410 ACCESSION - AK75600 ACCESSION - AK75600 ACCESSION - AK75600 ACCESSION - AK75600 ACCESSION - AK76200 ACCESSION - AK76200 ACCESSION - BD253926 ACCESSION - BD253926 ACCESSION - BD253929 ACCESSION - AK180199 ACCESSION - AK1825342
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ORGANISM Unknown. Unclassified. Unclassified. Unclassified. Unclassified. 1 (bases 1 to 20) AuthORS Condon,T.P. and Flournoy,S.Cheng. TITLE Antisense modulation of ADAM10 expression JOURNAL Patent: US 6228648-A 21 08-WAY-2001; FEATURES 120 /organism="unknown" /mol_type="unassigned DNA" Query Match 11.7%; Score 15.2; DB 1; Length 20; Best Local Similarity 85.0%; Pred. No. 12; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps Qy 1424 TCGTTCATGCAGACATATA 1443 Db 20 TTGTTATATGCAGACATATA 1		synthetic artificial Barany,F., Method of sequence CORNELL RE	Query Match Destruct " Query Match District No. 12; Dest Local Similarity 85.0%; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	Oy 1364 CCACGCATCACGAGCCATCG 1383 Db		JOURNAL Patent: US 5598810-A 3 23-NOV-1999; FEATURES Location/Qualifiers source 120 /organism="unknown" /mol_type="unassigned DNA" Query Match 11.4%; Score 14.8; DB 1; Length 20; Best Local Similarity 88.9%; Pred. No. 15;
ACCESSION: AJ587409 ACCESSION: A64290 ACCESSION: A88590 ACCESSION: A88639 ACCESSION: A90557 ACCESSION: A90657 ACCESSION: A90656 ACCESSION: AR093390 ACCESSION: AR102589 ACCESSION: AR141985 ACCESSION: AR141985 ACCESSION: AR141985 ACCESSION: BD271882 ACCESSION: B5874 ACCESSION: 158674 ACCESSION: 158674 ACCESSION: AR26292 ACCESSION: AR363706 ACCESSION: AR363707 ACCESSION: AR468930 ACCESSION: AR468930 ACCESSION: AR468930 ACCESSION: AR468930	ACCESSION: AX572321 ACCESSION: AX572338 ACCESSION: BD066103 ACCESSION: BD066152 ACCESSION: AX017787 ACCESSION: AX174279 ACCESSION: AX336	linear PAT 07-SEP-2000	<pre>mbryophyta; Tracheophyta; Poales; Poaceae; n,J.S. and Thomas,W.T. ttion of cereals</pre>	RESEARCH INST (GB); POWELL GOHN STUART (GB); THOMAS	Length 22; ; Indels 0; Gaps 0;	linear PAT 08-AUG-2001
7.5 13 1 AJS87409 7.5 14 1 A86290 7.5 14 1 A86390 7.5 14 1 A90666 7.5 14 1 A90666 7.5 14 1 AR093390 7.5 14 1 AR102589 7.5 14 1 AR142995 7.5 14 1 AR142990 7.5 14 1 AR2471882 7.5 14 1 AR247188 7.5 14 1 AR247188 7.5 14 1 AR24718 7.5 14 1 AR24718 7.5 14 1 AR24718 7.5 14 1 AR363706 8 7.5 14 1 AR363706 8 7.5 14 1 AR36873706	7.5 14 17 7.5 14 17 7.5 14 17 7.5 14 17 7.5 14 17 7.5 16 7.9 16 7.9 17 7	ALIGNMENTS AX017787 22 bp DNA AX017787 AX017787 AX017787 AX017787 AX017787	Hordeum vulgare Hordeum vulgare Hordeum vulgare Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Traci Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae Pooideae; Triticaee; Hordeum. Tamsey,L.D., Powell,W., Waugh,R., Swanston,J.S. and Thoma Dna sequences and their use for the selection of cereals	Patent: Wo 9946404-A 16 16-SEP-1999; RAMSEY LUXE DOUGLAS (GB); SCOTTISH CROP RESEARW WAYNE (GB); WANCH ROBERT (GB); SWANSTON JOHN ST WILLIAM THEODORE BLAYNE (GB) Location/Qualifiers 122 /organism="Hordeum vulgare" /mol_type="unassigned DNA" /db_xref="taxon:4513"	12.0%; Score 15.6; DB 1; imilarity 81.8%; Pred. No. 11; conservative 0; Mismatches 4 TCTATGCAGACATATACATGGA 1449 TCTATGCACACATCATGGA 1 TCTATGCACACATCATGGA 1	AR150534 20 bp DNA Sequence 21 from patent US 6228648. AR150534 AR150534.1 GI:15115125 Ünknown.
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Matches

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

I (bases 1 to 20)

Galibert,F. and Andre,C.

Total genome radiation hybrid map of canine genome and its use for identification of interesting genes

AL Patent: JP 2002330091-A58 17-SEP-2002;

CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE

OS Canis familiaris (dog)

PP 17-SEP-2002

PP 15-NOV-1999 UP 2000582596

PP 15-NOV-1999 UP 2000582596

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Crabtree, G.R., Northrop, J.P., Ho,S.N. and Flanagan, W.M.
Crabtree, G.R., Northrop, J.P., Ho,S.N. and Flanagan, W.M.
NF-AT polypeptides and polynucleotides and screening methods for immunosuppressive agents
Patent: US 635230-A 54 05-MAR-2002;
Location/Qualifiers
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptoesis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 03022177-A 2839 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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llarity 93.8%; Pred. No. 16;
Conservative 0; Mismatches 1; Indels
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          2; Indels
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Sequence 5021 from Patent WO03040369.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 54 from patent US 6352830.
AR198318
          Mismatches
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                                                              1394 AAAGGAGGTAAATTGTT 1411
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Homo sapiens
             Conservative
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Unclassified.
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Matches 15; Conserv
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AR198318
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AX737249/c
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AUTHORS TITLE

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FEATURES

RESULT 7

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Gaps

JOURNAL

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method and reagent for the inhibition of erg
Patent: WO 0188124-A 555 22-NOV-2001;
RIBOZYME PRRAMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Sequence 1131 from Patent EP1229046.
                                                                                                                                                                                                                                                                                                               Unclassified.

1 (bases 1 to 18)

1 (bases 1 to 18)

Locb, L.A. and Black, M.E.

Thymidine kinase mutants

Patent: US 6451571-A 31 17-SEP-2002;

Location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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Sequence 555 from Patent WO0188124.
AX422219
                                                                                                                                    AR230217 18 bp Sequence 31 from patent US 6451571. AR230217
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/organism="unknown"
/wol_type="genomic DNA"
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AX499824.1 GI:23382117
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1409 GTTAATGATGACCA 1422
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                        GTTAATGATGACCA 14
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Best Local Similarity
Matches 15; Conserv
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AX499824/c
LOCUS
DEFINITION
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KEYWORDS
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JOURNAL
FEATURES
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JOURNAL
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AX422219
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Thymidine kinase mutants and fusion proteins having thymidine kinase and guanylate kinase activities.
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Thymidine kinase mutants and fusion proteins having thymidine
kinase and
                                                                                                                                                                                              Unclassified.

Unclassified.

(Mases 1 to 20)

Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B and Pletcher,L.D.
Sankaran,B and Pletcher,L.D.
Chlamydia pneumoniae polymucleotides and uses thereof
Patent: US 6559294-A 3773 06-MAY-2003;

Location/Qualifiers
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C12N15/09,A61K31/711,A61K35/76,A61K38/45,A61K48/00,A61K49/00,
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A61P35/00,C12N5/10,C12N9/12,C12N15/00,A61K37/52,C12N5/00 CC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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Key Location/Qualifiers
source 1..18
                                                20 bp DN/
Sequence 3773 from patent US 6559294.

    .18
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

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JP 2002516061-A/25
04-JUN-2002
14-OCT-1998 JP 2000516019
14-OCT-1997 US 60/061812
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JP 2002516061-A/25.
unidentified
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PN JP 2002516061-A/25
PP JP 2002516061-A/25
PF 14-OCT-1998 JP 2000
PP 14-OCT-1997 US
PP MARGARET E BLACK
PC C12N15/09, AGIN31/77
PC A61P35/00, C12N5/10
PC A61P35/00, C12N5/10
Strandedness: Single;
CC Topology: Linear;
CT Topology: Linear;
CT Topology: Linear;
CT Topology: Linear;
CC Topology: Linear;
CC Topology: Linear;
CT Top
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Black, M.E.
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BD234621
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PAT 15-MAY-2001

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                        Robbins, J.M. and Tritz, R. Ribozyme therapy for the treatment of proliferative skin and eye
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Method and reagent for the inhibition of erg
Patent: WO 0188124-A 554 22-NOV-2011,
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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WO0130362.
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Sequence 554 from Patent WO0188124.
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"
                                                    10.6%; Score 13.8; Dilarity 88.2%; Pred. No. 24; Conservative 0; Mismatches
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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88.2%; Pred. No. 24
/organism="unknown"
/mol_type="genomic DNA"
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Location/Qualifiers
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Seguence 3027 from Patent
AX131809
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                                                                                                                            1354 GAAAATATTCCACGCA 1370
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Best Local Similarity 93.33
Matches 14; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
         Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptoesis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 3032177-A. 2581 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density disequilibrium map of the human genome Patent: US 6377751-A 5909 25-MAR-2003;
Location/Qualifiers
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Patent: EP 1229046-A 1131 07-AUG-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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Pred. No. 22;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                    Query Match 10.6%; Score 13.8; Dest Local Similarity 88.2%; Pred. No. 22; Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                 /mol_type="unassigned DNA"
/db_xref="taxon:9606"
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organism="Homo sapiens"
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AR294174
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Best Local Similarity 88.2%;
Matches 15; Conservative
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                                                                            Zhan, J.
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AR294174/c
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PAT 17-JUL-2003
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                                                                                                                             de Smet,K. and Stuyver,L.
Method for detection of drug-induced mutations in the hiv reverse transcriptase gene
Patent: WO 020555741-A 358 18-JUL-2002;
INNOGENETICS N.V. (BE)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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A method for identifying and characterizing cells and tissues Patent: WO 9934016-A 254 08-JUL-1999;
GENENA LTD (IL); VIDER BEN ZION (IL)
Location/Qualifiers
                                                     Human immunodeficiencý virus
Viruses, Retroid viruses, Retroviridae, Lentivirus, Primate
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Batt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 3070 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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/mol_type="unassigned DNA"
/db_xref="taxon:12721"
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ilarity 93.3%; Pred. No. 29;
Conservative 0; Mismatches 1;
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Sequence 254 from Patent W09934016.
AX020754
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                     Human immunodeficiency virus
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JP 2002541795-A/3070.
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 AX572318.1 GI:26004408
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Best Local Similarity 83.3%;
Matches 15; Conservative 0
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Method for detection of drug-induced mutations in the hiv reverse transcriptase gene
Patent: WO 02055741-A 359 18-JUL-2002;
                                                                                                                                                                                                                                                                                                       de Smet,K. and Stuyver,L.
Method for detection of drug-induced mutations in the hiv reverse
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Human immunodeficiency virus
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
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Human immunodeficiency virus
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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/mol type="unassigned DNA"
/db_xref="taxon:12721"
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/mol_type="unassigned DNA"
/db_xref="taxon:12721"
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10.3%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 27;
Matches 14; Conservative 0; Mismatches 1;
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Patent: WO 02055741-A 357 18-JUL-2002;
INNOGENETICS N.V. (BE)
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Sequence 358 from Patent W002055741.
AX572318
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Sequence 359 from Patent W002055741.
AX572319 1GI:26004409
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Sequence 357 from Patent WO02055741.
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10.3%; Score 13.4; D
Best Local Similarity 93.3%; Pred. No. 27;
Matches 14; Conservative 0; Mismatches
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Regulation of repressor genes using nucleic acid molecules.
BD255280
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A61K37/02,
(C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH
Location/Qualifiers
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PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N15/09, AG1K38/00, AG1K48/00, AG1P43/00, C12N5/10, PC C12P21/02,
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C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02,
C12R1:91),
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Regulation of repressor genes using nucleic acid molecules.
BD255279
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Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Bogulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 3072 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 3073 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
OS ENWEATYORE
PN JP 200757-
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Location/Qualifiers
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100.0%; Pred. No. 34;
rative 0; Mismatches
                   Pred. No. 34;
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    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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JP 2002541795-A/3072.
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JP 2002541795-A/3073.
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BD255279/c
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Regulation of repressor genes using nucleic acid molecules.
BD255278
        OS Eukaryote
PN JP 2002441795-A/3070
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PF 12-APR-1999 US 60/129390
PI LAMRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC C12P21/02, C12P21/02, A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC C12P21/02, A61K31/711, C12N5/10, C12R1:91), (C12P21/02, PC C12P21/02, 
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(C12NS/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH
Location/Qualifiers
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(C12P21/02,C12R1:91), (C12P21/02,C12R1:91),C12N15/00,C12N5/00,
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Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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JP 2002541795-A/3071.
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Best Local Similarity 100.08
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        OS Eukaryote
PN JP 2002541795-A/3076
PD 10-DEC-2002
PF 11-ARR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK, PAWELA PAVCO, JAMES MCSWIGGEN GI2N15/09, AGIK38/00, AGIK48/00, AG1P43/00, C12N5/10, PC
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Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002941795-A 3076 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Location/Qualifiers
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Patent: WO 03004526-A 173 16-JAN-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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/organism="unidentified"
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/db_xref="taxon:32644"
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(C12N5/00, C12R1:91)
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JP 2002541795-A/3076.
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(C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH
Location/Qualifiers
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(C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH
Location/Qualifiers
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                                                                                                                                                               C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
                                                                                                                                                                                              (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
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PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PP 12-APR-1999 US 60/129390
PP 12-APRENCE BLATT, MICHARL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN |
C12N15/09, A61X38/00, A61X48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
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N JP 2002541795-A/3074
PD 10-DEC-2002
PP 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/1229390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61K28/10, PC
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unclassified.
1 (bass 1 to 17)
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Paptlation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 3074 10-DEC-2002;
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organism='Eukaryote'
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JP 2002541795-A/3074.
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PC (C12P)
PC A61K3
PC (C12N)
CC Regul:
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(C12P21/02,C12R1:91), (C12P21/02,C12R1:91),C12N15/00,C12N5/00, A61R37/02, (C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="unassigned DNA"
/mol_type="unassigned DNA"
/db_xref="texon:32630"
/note="Primer zur Klassifizierung von Enterobakterien"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genotypic classification method
Patent: WO 0061796-A 103 19-0CT-2000;
HEISIG PETER (DE); MERLIN GES FUER MIKROBIOLOGISC (DE); FUCHS
GOMEZ YOLANDA (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. a Randi,A.M.
Method and reagent for the inhibition of erg
Patent: WO 0188124-A 36 22-NOV-2001;
RIBOZYME PHRAMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Location/Qualifiers
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9.8%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 37;
Matches 14; Conservative 0; Mismatches 2;
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Best Local Similarity 87.5%; Pred. No. 37;
Matches 14; Conservative 0; Mismatches
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Sequence 103 from Patent W00061796.
AX039033
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Sequence 36 from Patent WO0188124.
AX421700

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/mol_type="genomic DNA"
/db_xref="taxon:32644"

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synthetic construct
artificial sequences.
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AX039033/c
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AX421700
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B 1 (bases 1 to 17)
S Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
S Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Resulation of repressor genes using nucleic acid molecules
B 2002541795-A 3148 10-DEC-2002;
D BLOECYNE PHARMACEUTICALS INC
OS EUKaryote
D 10-DEC-2002
PP 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PR 12-APR-1999 US 60/129390
PR 12-APR-1999 US 60/129390
PR 12-APR-1999 US COORDES ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC CI2NIS/09,A6IX38/00,A6IX48/00,A6IP43/00,CI2NIS/10,PC CI2P21/02,CI2P21/02,CI2P21/02,CI2P21/02,PC CI2P21/02,PC CI2P2/02,PC CI2P2/
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Telerman,A., Amson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptoesis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 3022177-A 4898 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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100.0%; Pred. No. ...
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BD255355.1 GI:33065125
JP 2002541795-A/3148.
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Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                  Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Mclaughlin, F.G. a. Randi, A.M. Method and reagent for the inhibition of erg Patent: WO 0188124-A 1575 22-NOV-2001, RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
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                                                                                                           linear
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Sequence 1575 from Patent W00188124.
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9.8%; Score 12.8; D.
Best Local Similarity 87.5%; Pred. No. 37;
Matches 14; Conservative 0; Mismatches

    .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX423239.1 GI:21526621
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Homo sapiens
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AX499823/c
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Randi,A.M.
Method and reagent for the inhibition of erg
Patent: WO 0188124-A 1390 22-NOV-2001,
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Sequence 1390 from Patent WO0188124..
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Sequence 1391 from Patent W00188124.
AX423055
AX423055.1 GI:21526437
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9.8%; Score 12.8; D
Best Local Similarity 87.5%; Pred. No. 37;
Matches 14; Conservative 0; Mismatches
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Best Local Similarity 87.5
Matches 14; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Telerman, A., Amson, R. and Tuijnder, M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as
                                                                                                                                                                 Length 17;
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medicines
Patent: WO 03025176-A 2064 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Mismatches
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/mol_type="unassigned DNA"
/db_xref="taxon:10090"
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/wol_type="unassigned DNA"
                                                                                             /organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
                                                                                                                                                               ch 9.8%; Score 12.8; 1 Similarity 87.5%; Pred. No. 37 14; Conservative 0; Mismatches
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                             Human testis expressed patched like protein Patent: EP 1229646-A 1132 07-AUG-2002; Aeomica, Inc. (US) Location/Qualifiers
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Sequence 2064 from Patent WO03025176.
AX724377.1 GI:30503720
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Patent: WO 03004526-A 2007 16-JAN-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                      Homo sapiens (human)
Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                  Telerman, A., Amson, R. and Tuijnder, M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 03025177-A 3953 27-MAR-2003;
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 03025177-A 5356 27-MAR-2003;
Molecular Engines Laboratories (FR)
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9.8%; Score 12.8; Dest Local Similarity 87.5%; Pred. No. 37;
Matches 14; Conservative 0; Mismatches
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Best Local Similarity 87.5%; Pred. No. 37;
Matches 14; Conservative 0; Mismatches
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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tive 0; Mismatches 2; Indels
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Molecular Engines Laboratories (FR)
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Sequence 2996 from Patent WO03025175.
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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es 14; Conservative 0; Mismatches
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Query Match

AX732711/c LOCUS DEFINITION

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Camble, R. and Edge, M.D.
Analogous interferon polypeptides, process for their preparation and pharmaceutical compositions containing them
Patent: EP 0194006-A 30 10.5EP-1986;
IMPERIAL CHEMICAL INDUSTRIES PLC
                                  Telerman, A., Amson, R. and Tuijnder, M. Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
Patent: WO 03040369-A 2994 15-MAY-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          van Herpen, M.M., Hulzink, J.M. and Croes, A.F.
Regulation of translation of heterologously expressed genes
Patent: WO 03031613.A 2 17-ARR-2003;
KATHOLIEKE UNIVERSITEIT NIJMEGEN (NL)
       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                               Length 17;
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Best Local Similarity 87.5%; Pred. No. 37;
Matches 14; Conservative 0; Mismatches
                                                                                                                                                                                                        /mol_type="unassigned DNA"
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37.5%; Pred. No. 39;
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Location/Qualifiers
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Sequence 2 from Patent WO03031613.
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/organism="Homo sapiens"
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Primer"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 03040369-A 2842 15-MAY-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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   Sequence 2842 from Patent W003040369.
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                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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AX759630.1 GI:32254246
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C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
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ec (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
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PR 12-APR-1999 US 60/129390
PR 12-APR-1999 US 60/129390
FI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC C12P21/02,
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JP 2002541795-A/3003.
unidentified
unidentified
unclassified.
1 (bases 1 to 17)
Blatt, L., Zwick, W., Pavco, P. and Mcswiggen, J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 3003 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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ilarity 92.9%; Pred. No. 46;
Conservative 0; Mismatches 1;
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/db_xref="taxon:32644"
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JP 2002541795-A/4283.
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Regulation of repressor genes using nucleic acid molecules.
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(C12NS/00,C12R1.91)
Regulation of repressor genes using nucleic acid molecules FH
Location/Qualifiers
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OS BUKATYOTE
PN JP 2002541795-A/3002
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PF LARRINGE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N15/09, A61K38/00, A61R48/00, A61P43/00, C12N5/10, PC C12P21/02,
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oc (CI2P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 3002 10-DEC-2002;
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Vogelstein, B., Kinzler, K.W., Zhang, L. and Zhou, W. Gene expression profiles in normal and cancer cells Patent: US 6333152-A 628 25-DEC-2001;
Location/Qualifiers
                                                                                 1; Indels
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                                                  DB 1;
                                      9.5%; Scor.
92.9%; Pred. No. 41.
                                                                                                                                                                                                                            Sequence 628 from patent US 6333152.
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Pred. No. 41;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="unknown"
/wol_type="unassigned DNA"
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JP 2002541795-A/3002.
unidentified
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Best Local Similarity 92.9%;
Matches 13; Conservative (
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: EP 1229046-A 1133 07-AUG-2002;
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Sequence 1134 from Patent EP1229046.
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Best Local Similarity 92.9%; Pred. No. 46;
Matches 13; Conservative 0; Mismatches
                                                                          9.5%; Score 12.4; D
92.9%; Pred. No. 46;
ative 0; Mismatches
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
 /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Location/Qualifiers
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AX499827/c
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Regulation of repressor genes using nucleic acid molecules.
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CC12R1:91),

PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,

PC A61N3/02,

PC (C12N5/00,C12R1:91)

CC Regulation of repressor genes using nucleic acid molecules FH Location/Qualifiers
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1 (bases 1 to 17)
Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Regulation of repus using nucleic acid molecules
Patent: JP 2002541795-A 4283 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
S BUKARYOTE
PN JP 2002541795-A/4283
PD 10-DEC-2002
PP 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHARL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC CLENES, O., ACINES, 10, PC
                                                                                                                                                                                                                                                                                             (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
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PN JP 2002541795-A/4731
PD 10-DEC-2002
PP 11-APR-2000 2
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN 12-P21/02, 461K38/00, A61K48/00, A61P43/00, A61P43/10, PC C12P21/02,
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1 (bass 1 to 17)
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.

Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.

Brett, I., Zwick,M., Pavco,P. and Mcswiggen,J.

REGULATION Of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 4731 10-DEC-2002;

RIBOZYME PHARMACEUTICALS INC

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PN 2002541795-A/4731
PD 10-DEC-2002
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    .17
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(C12N5/00,C12R1:91)
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BD256938.1 GI:33066708
JP 2002541795-A/4731.
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PC (C12P2
PC A61K3:
PC (C12N8)
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Futreal, P.A., Wooster, R.F., Ashworth, A. and Stratton, M.R.
MATERIALS AND METHODS RELATING TO THE IDENTIFICATION AND SEQUENCING
OF THE BRCA2 CARES SUGGETIBLITY GENE AND USES THEREOF
PATENT: WO 9719110-A 208 29-MAY-1997,
CANCER RES CAMPAIGN TECH (GB)
Other publication AU 7635096 19970611
Cher publication GB 2307477 19970528.
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                                                   Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                  Telerman, A., Amson, R. and Tuijnder, M. Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as
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Unclassified.
1 (bases 1 to 17)
Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 1637 from patent US 5817796.
AR046844
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/db_xref="taxon:32644"
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A62967
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 AX759393.1 GI:32254009
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                                                                     PAT 08-MAY-2003
                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 03022177-A 2110 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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92.9%; Pred. No. 46;
tive 0; Mismatches 1;
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medicines
Patent: WO 03040369-A 1879 15-MAY-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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                                                                    AX736520 17 bp DNA
Sequence 2110 from Patent W003025177.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 92.9%; Pred. No. 46;
Matches 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="unassigned DNA"
/db_xref="taxon:9606"

    .17
/organism="Homo sapiens"

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                                                                                                                    AX736520.1 GI:30515808
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Homo sapiens
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Best Local Similarity 92.99
Matches 13; Conservative
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AX736520
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Regulation of repressor genes using nucleic acid molecules FH Location/Qualifiers
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Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
C-myb targeted ribozymes
Patent: 18 5646042-A 1637 08-JUL-1997;
Location/Qualifiers
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Location/Qualifiers
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82.4%; Pred. No. 51;
iive 0; Mismatches 3;
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US 6346398.
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Sequence 1637 from patent US 5646042.
153896 153896.1 GI:2475099
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llarity 82.4%; Pred. No. 51;
Conservative 0; Mismatches
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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(C12N5/00,C12R1:91)
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       unclassified.
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PN JP 2002441795-A/6077
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PF 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N15/09, A61X38/00, A61X48/00, A61P43/00, A61P43/00, C12N5/10, PC PC C12P21/02, C12P21/02, C12P21/02, C12P21/02, C12P21/02, C12P21/02, C12P21/02, C12P21/02, PC C12P21/02, C12P21/02, C12P21/02, C12P21/02, PC C12P21/02, C12P21/02/02, C12P21/02, C12P21/0
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BD258284.1 GI:33068054
unidentified unidentified
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1 (bases 1 to 17)

Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules Patent: JP 2002541795-A 6077 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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C-myb ribozymes having 2'-5'-linked adenylate residues
Patent: US 5817796-A 1637 06-OCT-1998;
Location/Qualifiers
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                                                                                       /organism="unknown"
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/organism="unidentified"
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/db_xref="taxon:32644"
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ORGANISM REFERENCE AUTHORS TITLE JOURNAL

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RESULT 63 BD258284

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PAT 20-APR-2002

SOURCE ORGANISM

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PAT 17-AUG-2003
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                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 17)
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 656127-A 2113 20-MAY-2003;
Location/Qualifiers
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 1312 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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9.4%; Score 12.2; DB 1;
Best Local Similarity 82.4%; Pred. No. 51;
Matches 14; Conservative 0; Mismatches 3;
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AR325311
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AX215870
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/organism="synthetic constr
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
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Pred. No. 51;
0; Mismatches
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1 Similarity 82.4%;
14; Conservative
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                                                    1433 GCAGACATATACATGGA
                                                                                      1 GCAGACATTGACATGCA
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AX217780/c
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AX215870/c
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AR325311/c
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TITLE
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(Dases 1 to 17)

Pavco, P., McSwiggn, J., Stinchcomb, D. and Escobedo, J.

Pavco, P., McSwiggn, for the treatment of diseases or conditions

Method and reagent for the treatment of diseases or conditions

related to levels of vascular endothelial growth factor receptor

Patent: US 6346398.A 5854 12-FEB-2002;
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Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Rathod and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 2447 20-MAY-2003;
Location/Qualifiers
                                                                 1 (bases 1 to 17)
Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A 5557 12-FEB-2002;
Location/Qualifiers
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9.4%; Score 12.2; DB 1;
Best Local Similarity 82.4%; Pred. No. 51;
Matches 14; Conservative 0; Mismatches 3;
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Sequence 5854 from patent US 6346398.
AR190366
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US 6566127.
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82.4%; Pred. No. 51;
tive 0; Mismatches
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/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 2447 from patent
AR325045
AR325045.1 GI:33710853
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Best Local Similarity 82.4
Matches 14; Conservative
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RESULT 68 AR325045

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AUTHORS TITLE

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PAT 18-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
              Jarvis,T., von Carlowitz,I., McBwiggen,J.A., Mclaughlin,F.G. and
Randi,A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. an Randi,A.M.
Method and reagent for the inhibition of erg
Patent: WO 0188124-A 1803 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
                                                    Method and reagent for the inhibition of erg
Patent: WO 0188124-A 1802 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butelo
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Patent: WO 03004526-A 73 16-JAN-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1803 from Patent WO0188124. AX423467
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Sequence 73 from Patent WO03004526.
AX671628
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                                                                                                                                                          /organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Best Local Similarity 82.4%;
Matches 14; Conservative (
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AX423467
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TITLE
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Homo sapiens
Eukarycia, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                        Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0153103-A 3222 16-AUG-2001;
RIBOXYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Mclaughlin, F.G. a Randi, A.M.
Method and reagent for the inhibition of erg
Patent: WO 0188124-A 1180 22-NOV-2001,
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
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/db xref="taxon:32630"
/nofe="Nucleic Acid"
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Pred. No. 51;
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/db_xref="taxon:9606"
Sequence 3222 from Patent WO0159103.
AX217780
AX217780.1 GI:15527841
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synthetic construct
artificial sequences.
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Mus musculus (house mouse)
Mus musculus
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 51;
0; Mismatches 3;
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Patent: WO 03025176-A 1326 27-MAR-2003;
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Patent: WO 03004526-A 744 16-JAN-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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/db_xref="taxon:10090"
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llarity 82.4%; Pred. No. 51;
Conservative 0; Mismatches
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/organism="Homo sapiens"
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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AX672299
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 51;
0; Mismatches 3; Indels
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 2221 from Patent WO03025175.
     AX727494 17 bp DNA Sequence 5181 from Patent WO03025176.
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Indels

Length 17;

PAT 08-MAY-2003

linear

suppression, tumour viruses and the use

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                Telerman,A., Amson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptoesis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 3032177-A 3552 27-WAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Patent: WO 03025177-A 4223 27-MAR-2003;
Molecular Engines Laboratories (FR)
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12.4%; Pred. No. 51;
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A human G protein coupled receptor
Patent: WO 03031621-A 226 17-APR-2003;
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/mol_type="unassigned DNA"
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 51;
0; Mismatches 3; Indels
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Sequence 3552 from Patent WO03025177.
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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                  AX732099 17 bp DNA Sequence 3733 from Patent W003025175.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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9.4%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 51;
Matches 14; Conservative 0; Mismatches 3; Indels
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Score 12.2; DB 1; Length 17; Pred. No. 51; 0; Mismatches 3; Indels
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Sequence 5321 from Patent W003040369.
AX762000
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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/db_xref="taxon:9606"

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/organism="Homo sapiens"
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/db_xref="taxon:9606"

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AX760612.1 GI:32255228
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       Query Match
Best Local Similarity 82.4<sup>†</sup>
Matches 14†, Conservative
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Patent: WO 03040369-A 1731 15-MAY-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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9.4%; Score 12.2; D
Best Local Similarity 82.4%; Pred. No. 51;
Matches 14; Conservative 0; Mismatches
     Amersham Biosciences (SV) Corp. (US)
Location/Qualifiers
                                                                                                                                   Score 12.2; D
Pred. No. 51;
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
                                                           /organism="Homo sapiens"
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Matches 14; Conservative
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Homo sapiens
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AX758410/c
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BD253926 17-JUL-2003
Regulation of repressor genes using nucleic acid molecules.
BD253926 161:33063696
JP 2002541795-A/1719.
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BD253927
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C12P21/02,C12P21/02//A61K31/711, (C12N5/10,C12R1:91), (C12P21/02, PC
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PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN CLINIS/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12P21/02,
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                                                                                                                                                                                                                                                                                                                                                 unclassified.

1 (bases 1 to 17)

Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002941795-A 1719 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 1720 10-DEC-2002;
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                                 ore 12; DB 1; Length 15; ed. No. 51; Mismatches 1; Indels
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100.0%; Pred. No. 57;
ive 0; Mismatches (
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/db_xref="taxon:32644"
                               9.2%; Score 12;
larity 85.7%; Pred. No.
Conservative 1; Mismatcl
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JP 2002541795-A/1719
10-DEC-2002
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BD253927/c
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A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
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JP 2002509721-A/5995
02-APR-2002
24-MAR-1999 JP 2000541291
27-MAR-1998 US 60/079678
PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
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                                                                  PAT 17-JUL-2003
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                                  Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.

BD202969
BD2025691 IG:33012739
Homo sapiens (human)
Homo sapiens
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1 (Dases 1 to 17)
Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A. Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response
Patent: JP 2002509721-A 5995 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
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Mammalia; Eutheria, Primates; Catarrhini, Hominidae; Homo.
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Location/Qualifiers
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9.4%; Score 12.2; D
Best Local Similarity 82.4%; Pred. No. 51;
Matches 14; Conservative 0; Mismatches
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                           RESULT 89
BD202969
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AUTHORS
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AX377083
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Regulation of repressor genes using nucleic acid molecules.
BD253929
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(CI2P21/02,CI2R1:91),(CI2P21/02,CI2R1:91),CI2N15/00,CI2N5/00,
A61K37/02,
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PR 12-APR-1999 US 60/129390
PI JAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
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Regulation of repressor genes using nucleic acid molecules.
BD255282
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1 (bases 1 to 17)
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Patent: JP 2002541795-A 1722 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 3075 10-DEC-2002;
STROZYME PHARMACEUTICALS INC
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     1;
Query Match 9.2%; Score 12; DB 1
Best Local Similarity 100.0%; Pred. No. 57;
Matches 12; Conservative 0; Mismatches
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JP 2002541795-A/1722
10-DEC-2002
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JP 2002541795-A/3075.
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JP 2002541795-A/1722.
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BD253929/c
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(C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH
Location/Qualifiers
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(C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH Location/Qualifiers
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                  OS EURATYONE

DN JP 2002541795-A/1720

PN JD 2002541795-A/1720

PD 10-DEC-2002

PF 11-APR-1999 US 60/129390

PR 12-APR-1999 US 60/129390

CL2N15/09, A61K38/00, A61K48/00, A61P43/00, CL2N5/10, PC CL2P21/02,
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PD 10-DEC-2002
PP 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12NS/09, A61K48/00, A61R43/00, A61R48/00, A61R43/00, C12NS/10, PC C12P21/02,
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Loses 1 to 17)

AUTHORS Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.

TILE Regulation of repressor genes using nucleic acid molecules batent: JP 2002541795-A 1721 10-DEC-2002;

NY OS Bukaryote Pharmaceuricals INC

NY DP 2002541795-A/1721

PD 10-DEC-2002

PF 11-ARP-2000 JP ?~~

PR 12-APR-1~~

PR 13-APR-1~~

PR 14-APR-1~~

PR 14-APR-1~~

PR 15-APR-1~~

PR 15
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9.2%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 12; Conservative 0; Mismatches 0; Indels

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    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

    .17
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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Regulation of repressor genes using nucleic acid molecules.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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PN JF 2002541795-A/3325
PD 10-DEC-202541795-A/3325
PP 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAMRENGE BLATT,MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN 1
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
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   Gaps
                                                                                                                                                                                                                                                                                  unclassified.

1 (bases 1 to 17)

Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation repressor genes using nucleic acid molecules Patent: JP 2002541795-A 3325 10-DEC-2002;
REGOZYME PHARMACEUTICALS INC
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Molecular Engines Laboratories (FR)
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(C12N5/00,C12N1:91)
Regulation of repressor genes us
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100.0%; Pred. No. 57;
rative 0; Mismatches
   Mismatches
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/organism="unidentified"
/mol_type="genomic DNA"
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Regulation of repressor genes using nucleic acid molecules.
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PN J2 2002541795-A/3324
PN J2 2002541795-A/3324
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/12339
PR 12-APR-1999 US 60/12338
CI2N15/09, A6IK38/00, A6IK48/00, A6IP43/00, A6IP43/00, CI2N5/10, PC
PN JP 2002541795-A/3075
PD 10-DEC-2002
PF 11-APR-1999 US 60/129390
PI LAWRENCE BLAIT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN 1
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/10, PC
PC PC PC 12P21/02,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unidentified
unclassified.
1 (base 1 to 17)
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Batt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Pacent: JP 2002541795-A 3324 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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100.0%; Pred. No. 57;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No.
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JP 2002541795-A/3324.
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Location/Qualifiers

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Woolf, \mathbf{T}. Method and reagent for inhibiting the expression of disease related
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  PAT 21-FEB-2003
                                                                                                                                                                          Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Direnzo, A., Karpeisky, A., Draper, K.G., Kisich, K., Matulic-Adamic, J., Mcswiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M., Seedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and
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A10125.
A10125.1 GI:412034
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  RNA
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RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
15 bp RN Sequence 2501 from Patent EP1260586.
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/db_xref="taxon:32644"

    .15
/organism="unidentified"
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1 (Dases 1 to 15)

2 (Bases 1 to 15)

2 (Bases 2 to 15)

3 (Bases 3 to 15)

5 (Bases 4 to 15)

6 (Bases 4 to 15)

7 (Bases 4 to 15)

7 (Bases 4 to 15)

7 (Bases 5 to 15)

8 (Bases 5 to 15)

8 (Bases 5 to 15)

1 (Bases 5 to 15)

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1 (Bases 5 to 15)
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Vogelstein, B., Kinzler, K.W., Zhang, L. and Zhou, W.
Gene expression profiles in normal and cancer cells
Patent: US 6333152-A 267 25-DEC-2001;
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9.1%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 56;
Matches 13; Conservative 0; Mismatches 2; Indels
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Sequence 105 from patent US 5616488.
139067
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Sequence 267 from patent US 6333152.
AR180199 1 GI:20222232
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/organism="unknown"
/wol_type="unassigned DNA"

    17 /organism="Mus musculus"
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/db_xref="taxon:10090"

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PEATURES

TITLE JOURNAL

I39067.1 GI:2083547

ACCESSION VERSION KEYWORDS

RESULT 99 139067 LOCUS DEFINITION

Unknown

SOURCE ORGANISM

REFERENCE AUTHORS

1406 ATTGTTAATGAT 1417

13 Arrgrrahrdar 2

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1433 GCAGACATATACATG 1447

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Unclassified. Unknown. Unknown

source

FEATURES

DEFINITION ACCESSION VERSION KEYWORDS

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RESULT 100 AR180199/c

15 GTAGACAGATACATG 1

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PAT 29-SEP-1997
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Artificial sequence; Genes.
Artificial sequence; Genes.
10-P1987181789-A/3
10-AUG-1987
07-NOV-1986 JP 1986265399
08-NOV-1986 ML 85 853074
YAM HENDORITGHKU BUAN EE
C12N15/00,C12N1/20,C12N9/28,C12P21/00,C12Q1/68//C07H21/04, PC
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JP 1987181789-A/3.
Synthetic construct
synthetic construct
artificial sequences.
I (bases I to 16)
Yan,H.B.E.E.
PLASMID FOR CLONING AND ANALYZING CONTROL REGION OF BATILLUS
Datent: JP 1987181789-A 3 10-AUG-1987;
GIST BROCADES IV
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                            ch 9.1%; Score 11.8; DB 1; Length 16; I Similarity 86.7%; Pred. No. 60; 13; Conservative 0; Mismatches 2; Indels
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unidentified
unclassified.
unclassified.
l (bases 1 to 16)
l (bases 1 to 16)
l Brysch, W and Schlingensiepen, K.
AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
PARENTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
IN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
IS BELGIONOSTIK GES (DE); BRYSCH WOLFGANG (DE)
LOCATION/Qualifiers
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strandedness: Double;

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A88762
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hypothetical: No;
anti-sense: No;
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A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR PREVENTION AND/OR TREATMENT OF NEURONAL INJURY, DEGENERATION AND CELL DEATH AND FOR THE TREATMENT OF NEOFLASMS
PATENT: WO 9502051-A 99 19-JAN-1995;
BIOGNOSTIK GES FUER BIOMOLEKUL (DE)
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Schlingensiepen, G., Schlingensiepen, R., Schlingensiepen, K. and
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1 (bases 1 to 16)
van BE,J.H.
Regulatory region cloning and analysis plasmid for bacillus
Patent: EP 0224294-A 7 03-JUN-1987;
GIST-EROCADES N.V
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A10140.
A10140.1 GI:412049
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Location/Qualifiers
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Best Local Similarity 86.7%; Pred. No. 60;
Matches 13; Conservative 0; Mismatches
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Best Local Similarity 86.7%; Pred. No. 60;
Matches 13; Conservative 0; Mismatches

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Sequence 89 from Patent W09502051.
A42573
A42573.1 GI:2298022
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1 (bases 1 to 15)
Ueda,I., Niwa,M., Saito,Y., Sato,S., Ono,H. and Kitaguchi,T.
Process for production of gamma-interferon
Process FP 0176916-A 32 09-APR-1986;
FUJISAWA PHARMACEUTICAL CO., LTD
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                               synthetic construct
artificial sequences.

1 (Dases 1 to 15)
Ueda,I., Niwa,M., Saitch,Y., Satch,S. and
Process for production of sometostatin
Patent: EP 0197558-A 50 15-OCT-1986;
FUJISAWA PHARMACEUTICAL CO., LTD
Location/Qualifiers
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/mol_type="unassigned DNA"
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92.3%; Pred. No. 69;
cive 0; Mismatches
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92.3%; Pred. No. 69;
tve 0; Mismatches
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/organism="unidentified"
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                                             /mol_type="genomic DNA'
/db_xref="taxon:32644"
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Oligonucleotide (E2).
A10647
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Matches 12; Conservative
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Best Local Similarity 92.3
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Method for detection of drug-induced mutations in the hiv reverse
transcriptase general
Patent: WO 02055741-A
INNOGENETICS N.V. (BE)
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Human immunodeficiency virus
Viruses; Retroid viruses; Retroviridae; Lentivirus, Primate
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Schlingensiepen, K.H. and Brysch, W.
An antisense oligonucleotide preparation method
Patent: JP 2001511000-A 910 07-AUG-2201;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-AUG-2001
30-JAN-1998 JP 1998532533
31-JAN-1997 BP 97101531.8
31-JAN-1997 BP 97101531.8
CL2N15/11,C07H21/04,A61K31/70
An antisense oligonuclectide preparation method FH
Location/Qualifiers
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/mol_type="unassigned DNA"
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        /organism="synthetic construct"
/mol_type="genomic DNA"
/mol_type="taxon:32630"

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                                                                                    Query Match 9.1%; Score 11.8; Dest Local Similarity 86.7%; Pred. No. 60; Matches 13; Conservative 0; Mismatches
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86.7%; Pred. No. 60;
tive 0; Mismatches
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JP 2001511000-A/910
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JP 2001511000-A/910.
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Matches 13; Conserva
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1 (Dases 1 to 15)
Vermoulen.N.M.J. and Schwartz,D.B.
Combinations and methods for reducing antimicrobial resistance
Patent: US 5872104-A 1 16-FEB-1999;
Location/Qualifiers
                             Stuyver, L., Louwagie, J. and Rossau, R. METHOD FOR DETECTION OF DRUG-INDUCED MUTATIONS IN THE REVERSE TRANSCRIPTASE GENE PAtent. WO 9727332-A 75 31-JUL-1997; INNOGENETICS NV (BE) Other publication AU 1444397 19970820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 15)
Grifantini,R., Galli,G., Carpani,G. and Grandi,G.
Process for the Preparation of D-.alpha.-amino acids
Patent: 18 5834258-A 1 10-NOV-1998;
Location/Qualifiers
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92.3%; Pred. No. 69;
tive 0; Mismatches
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    /db_xref="taxon:32644"

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Sequence 1 from patent US 5872104.
AR036330.1 GI:5952998
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Sequence 1 from patent US 5834258.
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AR053756.1 GI:5978618
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                                                                  PAT 16-NOV-1993
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synthetic construct
synthetic construct
artificial sequences.

1 (bases 1 to 15)
Ueda,I., Niwa,M., Satoh,S., Saitoh,Y. and Kusunoki,C.

Process for production of isulin-like growth factor I and plasmid
for production thereof
Patent: EP 0219814-A 65 29-APR-1987;
FUJISAWA PHARMACEUTICAL CO., LTD
Location/Qualifiers
                                                                                                                                                                  synthetic construct artificial sequences.

(base 1 to 15.)

Udda, I., Niwa, M., Saito, Y., Sato, S., Ono, H. and Kitaguchi, T.

9 Valine insulin-like growth factor I and process for production
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Pred. No. 69;
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FUJISAWA PHARMACEUTICAL CO., LTD
Location/Qualifiers
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ilarity 92.3%; Pred. No. 69;
Conservative 0; Mismatches
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PAT 20-APR-2002
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Unclassified.
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Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
Gene expression profiles in normal and cancer cells
Patent: US 6333152-A 210 25-DEC-2001;
Location/Qualifiers
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1 (bases 1 to 15)
Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
Vogelstein,B., Kinzler,K.W., Zhang,L. and zhou,W.
Patent: US 6333152-A 860 25-DEC-2001;
Location/Qualifiers
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1 (bases 1 to 15)
Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
Gene expression profiles in normal and cancer cells
Patent: US 6333152-A 197 25-DEC-2001;
Location/Qualifiers
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Sequence 860 from patent US 6333152.
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92.3%; Pred. No. 69;
ive 0; Mismatches
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/mol_type="unassigned DNA"
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/wol_type="unassigned DNA"
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Lieven, S., Joost, L. and Rudi, R.
Method for detection of drug-induced mutations in the reverse
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Patent: US 6087093-A 75 11-JUL-2000;
Location/Qualifiers
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Cellular factor ILF.
Patent: IOS 5534631.A 7 09-UUL-1996;
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 7 from patent US 5534631.
123532.
II33532.1 GI:1603402
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/organism="unknown"
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Best Local Similarity 92.39
Matches 12; Conservative
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Lieven, S., Joost, L. and Rudi, R.
Method for detection of drug-induced mutations in the reverse
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METHOD FOR DETECTION OF DRUG-INDUCED MUTATIONS IN THE REVERSE
TRANSCRIPTASE GENE
PATANT. WO 9727312-A 76 31-JUL-1997;
INNOGENETICS NV (BE)
Other publication AU 1444397 19970820.
Location/Qualifiers
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Pred. No. 69;
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Patent: US 6331389-A 75 18-DEC-2001;
Location/Qualifiers
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AR102587.
AR102587.1 GI:12814175

    .16
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

                              15 bp Sequence 75 from patent US 6331389.
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Sequence 76 from Patent W09727332.
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Matches 12; Conservative
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1 (bases I to 16)
Lieven, S., Joost, L. and Rudi.R.
Method for detection of drug-induced mutations in the reverse
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Lieven, S., Joost, L. and Rudi, R. Method for detection of drug-induced mutations in the reverse transcriptuses general patent: US 6087093-A 76 11-JUL-2000;
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Cellular regulators of infectious agents and methods of use
Patent: WO 0183754-A 34 08-NOV-2001;
Immusol Incorporated (US)
Location/Qualifiers
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8.8%; Score 11.4; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 12; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                  Length 16;
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/organism="synthetic construct"
/orl_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"
                                                                                                                                                                                    8.8%; Score 11.4; DB 1;
92.3%; Pred. No. 73;
tive 0; Mismatches 1;
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Patent: US 6331389-A 76 18-DEC-2001;
Location/Qualifiers
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Best Local Similarity 92.3%; Pred. No. 73;
Matches 12; Conservative 0; Mismatches
                                                                                                                         /organism="unknown"
/wol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 76 from patent US 6331389.
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Sequence 34 from Patent WO0183754.
AX328262
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/organism="unknown"
/mol_type="genomic DNA"
                                                                                  Location/Qualifiers
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synthetic construct
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/organism="Human immunodeficiency virus"
/mol_type="unassigned DNA"
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             GI:3021996
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Matches 13; Conserv
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AX572323
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AR435802
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                                                                                                 PAT 29-NOV-2002
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Method for detection of drug-induced mutations in the hiv reverse
transcriptase gene
Patent: WO 02055741-A 330 18-JUL-2002;
INNOGENETICS N.V. (BE)
Location/Qualifiers
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Method for detection of drug-induced mutations in the hiv reverse
transcriptase gene
Patent: WO 02055741.A 333 18-JUL-2002;
INNOGENETICS N.V. (BE)
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Human immunodeficiency virus
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
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Human immunodeficiency virus
Viruses, Retroid viruses, Retroviridae, Lentivirus, Primate
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// Organism="Human immunodeficiency virus"
//mol type="unassigned DNA"
//db_xref="taxon:12721"
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Pred. No. 73;
0; Mismatches 1;
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Pred. No. 73;
0; Mismatches
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                                                                                                AX572290 16 bp DI
Seguence 330 from Patent WO02055741.
AX572290
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/db_xref="taxon:12721"
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ilarity 92.3%;
Conservative
  TTGTTAATGATGAC 1420
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Best Local Similarity 92.3
Matches 12; Conservative
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Best Local Similarity
Matches 12; Conservat
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VERSION
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PAT 29-NOV-2002
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Human immunodeficiency virus
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
Unknown.

Unclassified.

(I (base 1 to 16)

Zhu,Q. and Lamb,C.J.

Plant defense genes and plant defense regulatory elements

Patent: US 5695939-A 26 09-DEC-1997;
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81.2%; Pred. No. 81;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                  Length 16;
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Eckstein, F., Ludwig, J. and Beigelman, L.
Nucleic acid catalysts with endonuclease activity
Patent: US 6656731-A 61 02-DEC-2003;
Location/Qualifiers
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Patent: WO 02055741.A 363 18-JUL-2002;
INNOGENETICS N.V. (BE)
Location/Qualifiers
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Seguence 363 from Patent WO02055741.
AX572323
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Best Local Similarity 81.2%; Pred. No. 81;
Matches 13; Conservative 0; Mismatches
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Sequence 61 from patent US 6656731.
AR435802.1 GI:40198886
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/mol_type="unassigned RNA"

    .16
    /organism="unknown"
    /mol_type="unassigned DNA"
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PAT 02-APR-2001

34

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Virulence genes of M. marinum and M. tuberculosis
Patent: WO 0119933-A 45 22-MAR-2001,
University of Maryland, Baltimore (US) ; The Department of Veterans
Affairs (US)
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8.5%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 11; Conservative 0; Mismatches 0; Indels
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   linear
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A01177
A01177.1 GI:410784
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Artificial sequence for oligonucleotide R247.
A00238
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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8.5%; Score 11; DB 1;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 11; Conservative 0; Mismatches
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Location/Qualifiers
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Location/Qualifiers
Sequence 45 from Patent W00119993.
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                                                    AX099210.1 GI:13538390
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artificial sequences.
1 (bases 1 to 14)
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artificial sequences.
1 (bases 1 to 14)
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synthetic construct
artificial sequences.
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A01177
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A00238
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Human immunodeficiency virus
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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Wang, C.-G. and Hepburn, A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US 5861244-A 296 19-JAN-1999;
Location/Qualifiers
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                                         DB 1; Length 16;
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    16
    7. organism="Human immunodeficiency virus"
/mol_type="unassigned DNA"
/db_xref="taxon:12721"

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Patent: WO 02055741-A 369 18-JUL-2002;
INNOGENETICS N.V. (BE)
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Sequence 369 from Patent WO02055741.
AX572329
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/organism="unknown"
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                                     Query Match
8.6%; Score 11.2; D
Best Local Similarity 81.2%; Pred. No. 81;
Matches 13; Conservative 0; Mismatches
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Best Local Similarity 100.0
...hes 11; Conservative
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AX099210/c
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AR030107/c
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AX357289.1 GI:18674441
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synthetic construct
artificial sequences.
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AX551046
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AX456096
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artificial sequences.
I (bases 1 to 14)
Bennett, A.D., Rhind, S.K., Lowe, P.A. and Hentschel, C.C.G.
Polypeptide and protein products, and processes for their
production and use
Patent: EP 0131363-A 10 16-JAN-1985;
CELLTECH LIMITED
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                                                      8.5%; Score 11; DB 1; Length 14; llarity 100.0%; Pred. No. 80; Conservative 0; Mismatches 0; Indels
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Gourse, R.L., Estrem, S.T., Ross, W.E. and Gaal, T. Promoter elements and methods of use Patent: US 6605431-A 6 12-AUG-2003;
Location/Qualifiers

    .14
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|mol type="unassigned DNA"
|db_xref="taxon:32630"

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Sequence 6 from patent US 6605431.
AR374275 GI:40076990
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A22508
A22508.1 GI:641532
                                                                                                                                                                                                                                                                                   synthetic construct
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PAT 13-FEB-2002
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                                                                                                                                                                                   Sebbel, P., Dunant, N., Bachmann, M., Tissot, A. and Lechener, F. Molecular antigen arrays and vaccines Patent: WO 0185208-A 13 15-NOV-2001; Cytos Biotechnology AG (CH); Sebbel, Peter (CH); Dunant, Nicolas (CH); Bachmann, Martin (CH); Tissot, Alain (CH); Lechener, Franziska (CH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli
Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Cytos Biotechnology AG (CH) ; Bachmann, Martin (CH) ; Renner,
Wolfgand Andreas (CH)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/bb_xref="taxon:32630"
/note="Modified ribosome binding site"
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/mol_type="unassigned DNA"
/db_xref="taxon:562"
AX357289 15 bp sequence 13 from Patent W00185208.
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Sequence 9 from Patent WO0209751.
AX456096
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PAT 20-JUN-2002
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Boyle, W.J., Lacey, D.L., Calzone, F.J. and Chang, M.-S.
Osteoprotegerin
Patent: US 6369027-A 86 09-APR-2002;
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Brysch, W.D. and Schlingensiepen, K.D.
An antisense oligonucleotide preparation method
Patent: EP 0856579-A 737 05-AUG-1998;
BIOGNOSTIK GES (DE)
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85.7%; Pred. No. 89;
ative 0; Mismatches
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Best Local Similarity 85.7%; Pred. No. 89;
Matches 12; Conservative 0; Mismatches
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Sequence 86 from patent US 6369027.
AR205552
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8.3%; Score 10.8; I
Best Local Similarity 85.7%; Pred. No. 89;
Matches 12; Conservative 0; Mismatches
                               /organism="unidentified"
/mol_type="unassigned DNA"
/db xref="taxon:32644"
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Sequence 737 from Patent BP0856579.
A90556
A90556.1 GI:6739070
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                                                Renner, W.A., Bachmann, M., Tissot, A., Maurer, P., Lechner, F., Sebbel, P. and Piossek, C.
Molecular antigen array
Molecular antigen array
Expects: Wo 02056907-A 13 25-JUL-2002;
Cytos Biotechnology AG (CH); Novartis Pharma AG. (CH); Renner,
Wolfgand Andreas (CH); Bachmann, Martin (CH); Tissot, Alain (CH); Maurer, Patrick (CH)
                                                                                                                                                                                                                                                                                                                     Gaps
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100.0%; Pred. No. 85;
ive 0; Mismatches 0; Indels
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1 (Lases 1 to 14)
Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLICONUCLEDOTIDE PREPARATION METHOD
PATEL: WO 9813904-A 737 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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/mol_type="unassigned DNA"
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/noTe="Modified ribosome binding site"
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/db_Xzef="texon:32630"
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synthetic construct
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                      artificial sequences.
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DD209438.1 GI:33019208
JP 2002512791-A/3028.
unidentified
unclassified.
1 (bases 1 to 14)
Blatt.L. Meswiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
Patent: JP 2002512791-A 3028 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
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PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1999 US 60/083217,18-SEP-1998 US 60/100842
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLAIT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism='Hepatitis virus (hepatitis C
Patent: JP 2001511000-A 737 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS UNCHOWN
DY 2001511000-A/737
DP 07-AUG-2001
PF 30-JAN-1999 JP 1998532533
PR 31-JAN-1997 FP 97101531.8
PR 73-LAN-1997 FP 97101531.8
PR 73-LAN-1997 EP 97101531.8
PR 73-LAN-1997 EP 97101531.8
PC C12N15/11, C07921/04, A61K31/70
CC An antisense oligonucleotide preparation method FH
                                            JP 2001511000-A/737
07-AUG-2010
30-JAN-1999 JP 1998532533
31-JAN-1997 EP 97101531.8
KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
C12N15/11,C07H21/04,A61K31/70
Location/Qualifiers
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JP 2002512791-A/3028
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Key Location/Qualifiers
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/organism='Unknown'
Location/Qualifiers
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8.3%; Score 10.8; D
Best Local Similarity 85.7%; Pred. No. 89;
Matches 12; Conservative 0; Mismatches
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                                   PAT 18-DEC-2003
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/note="part of oligonucleotide duplex used in vector
formation."
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Schlingensiepen, K.H. and Brysch, W.
An antisense oligonucleotide preparation method
                                                                                                                                                                  1 (bases 1 to 14)
Gourse, R.L., Estrem, S.T., Ross, W.E. and Gaal, T. Promoter elements and methods of use Patent: US 6605431-A 27 12-AUG-2003;
Location/Qualifiers
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                               AR374296 1 from patent US 6605431.
AR374296 1 GI:40077011
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Sequence 86 from Patent W00103719.
AX076570
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/note="unnamed protein product; Protein sequence is in conflict with the conceptual translation" /codon_start=1
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Pred, No. 94;
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Pred. No. 94;
0; Mismatches 2; Indels
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Cookson, W.O., Hopkin, J.M. and Shirakawa, T.
DIAGNOSTIC METHOD AND THERAPY
Patent: WO 9505481-A 4 23-FEB-1995;
             unclassified.

1 (bases 1 to 15)
Cookson, W.O., Hopkin, J.M. and Shirakawa, T.
DIAGNOSTIC METHOD AND THERAPY
Patent: WO 9505481-A 2 23-FEB-1995;
ISIS INNOVATION (GB)
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/db xref="GI:4529956"
/db_xref="REMTREMBL:CAA02703"
/translation="ELVVM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                                                                                  /protein id="CAA02702.1"
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/db xref="REMTREMBL:CAA02702"
/translation="ELVLM"
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Sequence 30 from patent US 5830650.
AR051085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                  /mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 bp
Sequence 4 from Patent WO9505481,

    .15
    /organism="unidentified"

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Best Local Similarity 85.7%;
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Best Local Similarity 85.7%;
Matches 12; Conservative
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AR051085
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                                                                              TITLE
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AUTHORS
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Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue gaston Cremieux, 91057 Bryz cedex, FRANCE
Gaston Cremieux, 91057 Bryz cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (versailles). The DNA fragment(s) resulting from the PCR were directly sequence from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutent line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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                                                                                                                                                                    ATH526531 14 bp DNA linear PLN 29-MAR-2003
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
                                                                                                                                                                                                                                                                                                                                                                                                                            Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

MRO Rep. 3 (12), 1152-1157 (2002)
                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="121G04"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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85.7%; Pred. No. 89;
tive 0; Mismatches 2; Indels
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/mol type="genomic DNA"
/cultivar="Wassillewskija"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l. .14<sup>-</sup>
/note="T-DNA flanking sequence
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AJ526531.1 GI:26794791
left border, T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Sequence 2 from Patent WO9505481.
A43116
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                           CGTCTTCTGATCAA 1395
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Best Local Similarity 85.7
Matches 12, Conservative
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PAT 06-MAR-1997

PAT 29-SEP-1999

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15 bp DNA linear PAT 29-SEP-1997 N-Terminal DNA sequence coding for human IL-2 analogue, 1-5. E00981
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Patent: US 6132967-A 699 17-OCT-2000;
                                                                                                                                                                                                                                                                                               Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
Patent: US 6132967-A 388 17-OCT-2000;
Location/Qualifiers
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Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
                                                                                                                                                                                                                                          Unclassified.
1 (Dases 1 to 15)
Grim.S., Stinchcomb.D.T., McSwiggen.J., Sullivan.S. and
Draper.K.G.
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Sequence 388 from patent US 6132967.
AR113942.1 GI:14094264
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85.7%; Pred. No. 94;
tive 0; Mismatches
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/organism="unknown"
/wol_type="unassigned DNA"
Best Local Similarity 85.7%; Pred. No. 94;
Matches 12; Conservative 0; Mismatches
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                                           1421 CAGTCGTTCTATGC 1434
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Best Local Similarity 85.75
Matches 12; Conservative
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Matches 12, Conservative
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E00981/c
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AR114253
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FEATURES
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AUTHORS
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1 (bases 1 to 15)
Grimbs.s. Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
Draper, K.G.
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Intercellular adhesion molecule-1 (ICAM-1) ribozymes
Patent: US 5837542-A 388 17-NOV-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 8.3%; Score 10.8; DB 1; Length 15; 1 Similarity 85.7%; Pred. No. 94; 12; Conservative 0; Mismatches 2; Indels
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Patent: US 5837542-A 699 17-NOV-1998;
Location/Qualifiers
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                                                                                                                                                                                                    DB 1; Length 15
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Seguence 699 from patent US 5837542.
AR056495
                                                                                Crea.R.
Walk-through mutagenesis
Patent: US 5830650-A 30 03-NOV-1998;
Location/Qualifiers
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Sequence 388 from patent US 5837542.
AROS6184
AROS6184.1 GI:5981761
                                                                                                                                                                                                 Query Match 8.3%; Score 10.8; Esst Local Similarity 85.7%; Pred. No. 94; Matches 12; Conservative 0; Mismatches
                                                                                                                                             1. .15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="unknown"
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  GI:5974449
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1 GACTTCTACATGGA 14
                                                        Unclassified.
1 (bases 1 to 15)
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Matches 12; Conserva
  AR051085.1
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AR056495
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Unclassified.
1 (bases 1 to 15)
Sullivan, S., Draper, K. G., McSwiggen, J. and Stinchcomb, D.T.
IL-5 targeted ribozymes
Patent: US 5616488-A 423 01-APR-1997;
                                                                                                                                    (Jasses 1 to 15)
Sullivan, S., Draper K.G., McSwiggen, J. and Stinchcomb, D.T.
IL-S targeted ribozymes
Patent: US 5616488-A 106 01-APR-1997;
Location/Qualifiers
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Unclassified.
Unclassified.
Unclassified.
Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
Gene expression profiles in normal and cancer cells
Patent: US 6331352-A 657 25-DEC-2001;
Location/Qualifiers
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                                 15 bp Di
Sequence 106 from patent US 5616488.
139068
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Seguence 423 from patent US 5616488.
139385
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85.7%; Pred. No. 94;
ative 0; Mismatches
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85.7%; Pred. No. 94;
ative 0; Mismatches
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/organism="unknown"
/mol_type="unassigned DNA"
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                                                                          I39068.1 GI:2083548
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Best Local Similarity 85.77
Matches 12; Conservative
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Best Local Similarity 85.7
Matches 12; Conservative
                                                                                                                           Unclassified.
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AR180589
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139068
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Sullivan, S., Draper, K.G., McSwiggen, J. and Stinchcomb, D.T.
IL-5 targeted ribozymes
Patent: US 5616488-A 104 01-APR-1997;
Location/Qualifiers
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/product='human IL-2 analogeu, 1-5'</pre>
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Larity 85.7%; Pred. No. 94;
Conservative 0; Mismatches 2; Indels
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Sequence 104 from patent US 5616488.
I39066.
I39066.1 GI:2083546
                                                                                                                                                                                                                                                                             *source: tissue type=Tonsil;
*source: clone=plasmid pHIG5-3;

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    .15
    /organism="unidentified"
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                                                                                                                                                                                                                          strandedness: Double;
topology: Linear;
hypothetical: No;
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Best Local Similarity
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Query Match Best Local S: Matches 12

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PAT 29-NOV-2002

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de Smet,K. and Stuyver,L.
Method for detection of drug-induced mutations in the hiv reverse
transcriptaes general
Patent: WO 02055741-A 406 18-JUL-2002;
INNOGENETICS N.V. (BE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roetger, A. Nucleotide carrier for diagnosing and treating oral diseases Patent: WO 02072883-A 48 19-SEP-2002; ROETGER, Antje (DE)
                                                                                                                Human immunodeficiency virus
Human immunodeficiency virus
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Capnocytophaga sputigena
Capnocytophaga sputigena
Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
Flavobacteriaceae; Capnocytophaga.
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                                 linear
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                                                                                                                                                                                                                                                                                                                       /organism="Human immunodeficiency virus"
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/db_xref="taxon:12721"

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/organism="Capnocytophaga sputigena"
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                          Sequence 406 from Patent WO02055741.
AX572366
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85.7%; Pred. No. 94;
tive 0; Mismatches
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Sequence 48 from Patent WO02072883.
AX587026.1 GI:27655901
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Sequence 382 from Patent EP1260586.
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llarity 85.7%; Pred. No. 94;
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Best Local Similarity 85.7%
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Matches 12; Conserv
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AX633243
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RESULT 165
AX572366
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 02059256-A 1762 01-AUG-2002;
MOLECULAR ENGINES LAB (FR)
Location/Qualifiers
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Best Local Similarity 85.7%; Pred. No. 94;
Matches 12; Conservative 0; Mismatches 2; Indels
                                                   8.3%; Score 10.8; DB 1; Length 15; larity 85.7%; Pred. No. 94; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                               DNA
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Patent: US 6649340-A 30 18-NOV-2003;
Location/Qualifiers
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/db_xref="taxon:9606"

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Seguence 30 from patent US 6649340.
AR430299
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/organism="unknown"
/mol_type="genomic DNA"
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                                                                                                                       1346 CAGGGAAGAAAA 1359
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Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                                                                                                                                                                                                 Unknown.
Unclassified.
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                                                                     Local Similarity
es 12; Conserv
                                                                                                                                                                                                                                                                                                                                 Unknown.
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JOURNAL FEATURES REFERENCE AUTHORS TITLE

LOCUS DEFINITION ACCESSION VERSION KEYWORDS

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ORGANISM

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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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REFERENCE AUTHORS TITLE

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PAT 21-FEB-2003

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Method and reagent for inhibiting the expression of disease related
                                                Woolf, \mathbf{T}. Method and reagent for inhibiting the expression of disease related
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Mcswiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and
                                                                                                                                                                                                                                                      Query Match

8.3%; Score 10.8; DB 1;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 12; Conservative 0; Mismatches 2;
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RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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                                                                                    genes
Patent: BP 1260586-A 2499 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Sequence 2793 from Patent EP1260586.
AX635654
AX635654.1 GI:28471268
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85.7%; Pred. No. 94;
Live 0; Mismatches
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/mol_type="unassigned RNA"
/db_xref="taxon:32644"
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/mol_type="unassigned RNA"
/db_xref="taxon:32644"
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Best Local Similarity
Matches 12; Conserv
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SOURCE
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AX635654/c
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ACCESSION
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AX635364
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Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
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Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
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Patent: EP 1260586-A 638 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Sequence 2499 from Patent EP1260586.
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Patent: BP 1260586-A 382 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:32644"
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/mol_type="unassigned RNA"
/db_xref="taxon:32644"
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AX633499.1 GI:28469113
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Best Local Similarity 85.7%;
Matches 12; Conservative
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Best Local Similarity
Matches 12; Conserv
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ACCESSION
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KEYWORDS
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AUTHORS
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AUTHORS
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PAT 21-FEB-2003

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LD DD RNA linear PAT 17-JUL-2003 Enzymatic nucleic acid treatment of diseases or conditions related BD208458
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1 (bases 1 to 15)

Blatt, L., Moswiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.

Blatt, L., Moswiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.

Brazymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection

Patent: JP 2002512791-A 2048 OB-MAY-2002;

RIBOZYME PHARMACEUTIOL INC

OS Hepatitis virus (hepatitis C virus)

PN JP 2002512791-A/2048

PP 26-APR-1999 JP 2000545991

PR 27-APR-1999 US 60/088217, 18-SEP-1999 US 60/100842 PR
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C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
A61K37/66,
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Method for production of recombinant protein
Patent: JP 2002272481-A 41 24-SEP-2002;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Artificial Sequence
ND JP 2002272481-A/41
PD 24-SEP-2002
PF 25-JUL-2001 JP 2001224117
PP TAKASHI ITO, YOKO TANAKA, MITSUYO KONDO
PC CI2N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02// NACH 184 00, PC A61K38/00, PC A61K38/00, PC A61K38/00, PC A61K37/02, PC A61K37/0
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PR 27-APR-1999 US 60/083217,18-SEP-1999 US 60/100842
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLAIT,JAMES A MCSWIGGEN, BLISABETH ROBERTS, PAMELA A
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/organism='Artificial Sequence'
Location/Qualifiers
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8.3%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 12; Conservative 0; Mismatches 2; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/mol_type="genomic RNA"
/db_xref="taxon:32644"
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BD208458.1 GI:33018228
JP 2002512791-A/2048.
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                                                Method and reagent for inhibiting the expression of disease related
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BD141513.1 GI:23236458

WO 0208417-A/41.

WO 0208417-A/41.

Synthetic construct
synthetic construct
artificial sequences.

1 (base 1 to 15)

1 (base 1 to 15)

In (base 1 to 15)

Method for production of recombinant protein
Patent: WO 0208417-A 41 31-JAN-2002;

MAKEDA CHEMICAL INDUSTRIES LTD, TAKASHI ITO, YOKO TANAKA, MITSUXO
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Method for production of recombinant protein.
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W0 0208417-A/41
31-JAN-2002
25-JUL-2001 W0 2001JP006392
25-JUL-2000 JP 00P 229064
TARASHI TIC, YOKO TRNAKA, MITSUYO KONDO
C12N15/10, C12N1/21, C12P21/02, C12Q1/02
Synthetic DNA
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/organism="synthetic construct"
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                                                                                                           Patent: EP 1260586-A 2793 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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85.7%; Pred. No. 94;
iive 0; Mismatches
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85.7%; Pred. No. 94;
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    forganism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

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Best Local Similarity 85.75
Matches 12; Conservative
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

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Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches
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Location/Qualifiers
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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8.2%; Score 10.6; DB 1; Length 15;
Best Local Similarity 90.9%; Pred. No. 1e+02;
Matches 10; Conservative 1; Mismatches 0; Indels
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85.7%; Pred. No. 1.2e+02;
tive 0; Mismatches 2; Indels
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Sequence 14 from Patent W002063044.
AX512687
AX512687.1 GI:23503905
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Sequence 5884 from Patent WO0179548.
AX294122
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/db_xref="taxon:9606"
       85.7%; Pred. No. 94; ative 0; Mismatches
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Homo sapiens
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GAARAAAATA 15
       Best Local Similarity 85.7
Matches 12; Conservative
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A04490.1 GI:410987
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels
                   Query Match
8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels
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Location/Qualifiers
1. .12
/organism="synthetic construct"
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels
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Matches 11; Conservative 0; Mismatches 1;
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Location/Qualifiers
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Location/Qualifiers
Patent: WO 8400380-A 4 02-FEB-1984;
Location/Qualifiers
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REFERENCE AUTHORS

PAT 22-DEC-1993

Matches

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synthetic construct
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artificial sequences.
1 (bases 1 to 12)
Craig,R.K. and MacIntyre,J.
Human calcitonin precursor polyprotein structural gene
Patent: RP 0070679-A 4 26-JAN-1983;
CELLIECH LIMITED
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Craig.R.K. and MacIntyre, J.

Human calcitonin precursor polyprotein structural gene
Patent: EP 001675-A 4 26-JAN-1983;

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1 (bases 1 to 12)
Craig, R.K. and MacIntyre, J.
Human calcitonin precursor polyprotein structural gene
Patent: EP 0070675-A 3 26-JAN-1983;
CELLTECH LIMITED
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/db_xref="taxon:32630"
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Craig, R.K. and MacIntyre, J.
Human calcitonin precursor polyprotein structural gene
Patent: EP 0070675-A 3 26-JAN-1983;
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Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1;
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A04491
A04491.1 GI:410988
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Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches
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Location/Qualifiers
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Direct Submission

Submitted (123-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue gaston Cremieux, 91057 Evry cedex, FRANCE

FR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program "Genoplante" (http://www.genoplante.com and http://genoplante-info.info.info.iogen.fr).
                                                                                                                                                                 Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechletold, N., Craud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                     Bukaryoja; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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Talmadge,K.D. and Hilliker,S.
RECOMBINANT DNA CONSTRUCTS CONTAINING AN 13 PROMOTER
Patent: WO 8902471-A 4 23-MAR-1989;
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11.7%; Pred. No. 1e+02;
ve 0; Mismatches 1;

    .13
    /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"

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/note="T-DNA flanking sequence
left border"
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                 AJ598136.1 GI:37947764
left border, T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/wol_type="unassigned DNA"
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109291
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EMBO Rep. 3 (12), 1152-1157 (2002)
22363535
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Balzergue, S.
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Arabidopsis thaliana T-DNA flanking sequence, left border, clone 462D11.
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Bell,G.I., Yamagata,K., Oda,N., Kaisaki,P.J., Furuta,H.,
Horikawa,Y. and Menzel, Bell,G.I., Mutations in the diabetes susceptibility genes hepatocyte nuclear factor (HNP) 1 alpha (alpha.), HNF1.beta. and HNF4.alpha Patent: US 618753-A 9 13-FBB-2001;
Location/Qualifiers
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Wang, C.-G. and Hepburn, A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US 5861244-A 190 19-JAN-1999;
Location/Qualifiers
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Pred. No. 1e+02;
0; Mismatches 2; Indels
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                   Score 10.4; DB 1; Length 12; Pred. No. 95;
                                                          1; Indels
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                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .12
/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
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               8.0%;
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Best Local Similarity 84.6%;
Matches 11; Conservative (
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PC C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC G01N37/00,
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1 (bases 1 to 10)
1 (bases 1 to 10)
1 Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 792 15-0CT-2002;
GENZYME CORP
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C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15,
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C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/56,
G01N37/00,
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/organism='Homo sapiens (human)'.
Location/Qualifiers
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100.0%; Pred. No. 1e+02;
iive 0; Mismatches 0; Indels
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Preparation and use of superior vaccines
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Location/Qualifiers
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Preparation and use of superior vaccines
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60/090031,19-UUN-1998 US
60/090031,19-UUN-1998 US
60/090001,19-UUN-1998 US
60/090001,19-UUN-1998 US
60/0900042,19-UUN-1998 US
60/0900042,19-UUN-1998 US
60/0900042,19-UUN-1998 US
60/0900041,19-UUN-1998 US
60/090080,19-UUN-1998 US
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60/090076,19-UUN-1998 US
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    /organism="Homo sapiens"
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/db_xref="taxon:9606"

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JP 2002534056-A/792
15-CCT-2002
18-JUN-1999 UP 2000554749
19-JUN-1998 US 60/090039
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Homo sapiens (human)
Homo sapiens
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Roberts, B.L. and Shankara, S.
Roberts, B.L. and Shankara, S.
Perparation and use of superior vaccines
Patent: JP 2002534056-A 535 15-OCT-2002;
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60/090079 PR
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60/090048 PR
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60/090047 PR
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60/090047 PR
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Wang, C.-G. and Hepburn, A.G.
Wang, C.-G. and Hepburn, A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US 5861244-A. 279 19-JAN-1999;
Location/Qualifiers
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Score 10.4; DB 1; Length 14; Pred. No. 1.1e+02; 0; Mismatches 1; Indels
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100.0%; Pred. No. 1e+02;
ive 0; Mismatches 0; Indels
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60/090080,19-JUN-1998 U
60/080994,19-JUN-1998 U
60/090078,19-JUN-1998 U
60/090076,19-JUN-1998 U
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
                                                                                                                                                                                                                             AR030090 10 bp D. Sequence 279 from patent US 5861244.
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19-JUN-1998 US 60/0900
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JP 2002534056-A/535
15-OCT-2002
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AR030090.1 GI:5943304
        8.0%;
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    Query Match
Best Local Similarity 91.7
Matches 11, Conservative
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Matches 10; Conservative
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13 AAATTTTTAAT 2
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PR 19-JUN-1998 U
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BD239117/c
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PAT 22-JUN-2001

RESULT 197
BD24027/c
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AUTHORS TITLE JOURNAL REFERENCE

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                              Unclassified.
1 (bases 1 to 10)
Shimamoto, A., Furuichi, Y., Shibata, Y., Funaki, H., Ohara, E. and
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Unknown.
Unclassified.
1 (bases 1 to 11)
1 Wang, C.-G. and Hepburn, A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US 5861244-A 25 19-JAN-1999;
Location/Qualifiers
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100.0%; Pred. No. 1e+02;
tive 0; Mismatches 0; Indels
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Patent: WO 0.1385.77-A 386 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
                                                                                                                                                             Watahiki,M.
Method for synthesizing cDNA from mRNA sample
Patent: US 6544736-A 113 08-APR-2003;
Location/Qualifiers
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AR303388 10 bp DNA Sequence 113 from patent US 6544736.
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Sequence 386 from Patent WO0138577.
AX152471
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                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
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AR029836.1 GI:5943050
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Homo sapiens
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Best Local Similarity 100.
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1 (bases 1 to 10)
1 (bases 1 to 10)
1 Preparation and Shankara, S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1445 15-OCT-2002;
GENZYME CORP
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60/080973 PR
60/080933 PR
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7.7%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 10; Conservative 0; Mismatches 0; Indels
                                   Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels
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C C12N15/00,C12N5/00,C12N15/00
C Preparation and use of superior vaccines
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60/08997, 19-JUN-1998 US
60/089992, 19-JUN-1998 US
60/089992, 19-JUN-1998 US
60/089992, 19-JUN-1998 US
60/09000, 19-JUN-1998 US
60/090042, 19-JUN-1998 US
60/090044, 19-JUN-1998 US
60/090080, 19-JUN-1998 US
60/090076, 19-JUN-1998 US
60/090078, 19-JUN-1998 US
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JP 2002534056-A/1445
15-0CT-2002
18-JUN-1999 JP 2000554749
19-JUN-1999 US 60/090039
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JP 2002534056-A/1445.
Homo sapiens (human)
Homo sapiens
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                               Hustert, E., Haberl, M. and Wojnowski, L.
Identification of the genetic determinants of the polymorphic cyplas expression
Patent: WO 02053775-A 67 11-JUL-2002;
EPIDAUROS BIOTECHNOLOGIE AG (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
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Sequence 396 from Patent WO02053774.
AX623355
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                AX472076.1 GI:22207117
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AX472076
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Wang, C. -G. and Hepburn, A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US 5861244-A 132 19-JAN-1999;
Location/Qualifiers
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Erlich, H.A.
HLA typing method and cDNA probes used therein
Patent: EP 0084796-A2 1 03-AUG-1983;
Location/Qualifiers
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Sequence 132 from patent US 5861244.
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Sequence 67 from Patent WO02053775.
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/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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Sequence 1 from Patent EP 0084796.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Sequence 7817 from Patent WO02053774.
AX630776
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/db_xref="taxon:9606"

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    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Matches 10; Conservative 0; Mismatches 0; Indels
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Method for determining homeostasis of the skin
Patent: WO 2023774-4, 6549 Il-UUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Petent: WO 2025374-A 2822 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Patent: WO 02053774-A 396 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Grinnel, B.W.
A method of using eukaryotic expression vectors comprising the bk virus enhancer
Patent: EP 0245949-A2 2 19-NOV-1987;
Location/Qualifiers
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JP 199946789-A/3
21-DEC-1999
17-MAY-1999 JP 1999135687
09-AFR-1986 US 849999
PRYAN WILLAM GHRINNERU
C12N15/09, C07K14/47, C12P21/02/ (C12P21/02, C12R1:91), C12N15/00
                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                 Petersohn, D., Conradt, M. and Hofmann, K.
Method for determining homeostasis of the skin
Patent: WO 0203774-A 7817 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers

    .12
    /organism='Unidentified'

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Human protein C produced by recombination.
E59615
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100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0;
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    .11
    /organism="Homo sapiens"
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2 Equance 2 from Patent EP 0245949.
105103.1 GI:591239
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/organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
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  AX630776.1 GI:28458816
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JP 1999346789-A/3.
unidentified
unidentified
                         Homo sapiens (human)
Homo sapiens
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Pryan, W.G.
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Best Local Similarity 100.
Matches 10; Conservative
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I05103/c
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E59615/c
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1 (bases 1 to 12)
Bang,N.U., Ehrlich,H.J., Grinnell,B.W. and Yan,S.-C.B.
Vectors and compounds for expression of zymogen forms of human protein C
Patent: EP 0323149-A2 7 05-JUL-1989;
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Hoskins,J.A. and Long,G.L.
Human protein S, A plasma protein regulator of hemostasis
Patent: EP 0247643-A2 5 02-DEC-1987;
Location/Qualifiers
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100.0%; Pred. No. 1.2e+02;
iive 0; Mismatches 0; Indels
                                                                    7.7%; Score 10; DB 1; Length 12;
100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0; Indels
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/organism="unknown"
/mol_type="unassigned DNA"
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/wol_type="unassigned DNA"
1. .12
/organism="unknown"
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Sequence 7 from Patent EP 0323149.
106650
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Sequence 5 from Patent BP 0247843.
105127
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PAT 27-AUG-2002
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10-OCT-2000 JP 2000309380
09-APR-1986 US 849999
PRYAN WILLIAM GRINNELL
CI2N15/09,CO7K14/47,CI2N5/10,CI2P21/02//A61K38/00,A61P7/02, P
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Grinnell, B.W.
Method of using eukaryotic expression vectors comprising the BK
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0
                                                                                                                                                                                                0;
             Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 12)
Berg, D.T. and Grinnell, B.W.
Improvements in or relating to eukaryotic expression
Patent: BP 0363127-A2 3 11-APR-1990;
Location/Qualifiers
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ative 0; Mismatches 0;
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1 (bases 1 to 12)
Grinnell, P. W.
Recombinant human protein C
Patent: JP 200145496-A 3 29-MAY-2001;
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/wol_type="unassigned DNA"
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Location/Qualifiers
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Sequence 3 from patent US 5681932.
171433
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Recombinant human protein C.

BD014692

BD014692.1 GI:2255475

DD 200114496-A/3.

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JP 2001145496-A/3
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Best Local Similarity 100.
Matches 10; Conservative
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I71433/c
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BD014692/c
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(I (bases 1 to 12)

Beavers, L. S., Eumol, T.F., Gadski, R.A. and Weigel, B.J.

Novel recombinant and chimeric antibodies directed against a human adenocarchinoma antigen

Patent: EP 0338767-A2 15 25-OCT-1989;

Location/Qualifiers
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Bumol,T.F., Gadski,R.A., Hamilton,A.E., Sportsman,J.R. and
Strnad,J.
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100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0; Indels
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Sequence 15 from Patent EP 0338767.
107402
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  0; Mismatches
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Sequence 10 from Patent EP 0326423.
106784
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2624ence 3 from Patent BP 0363127.
107634.1 GI:589743
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Best Local Similarity 100.
Matches 10, Conservative
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107634/c
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106784/c
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PHELIX: testis-specific protein expressed in cancer.
BD228587
                                                                                                                                                                                                         unidentified
unidentified
unclassified.
1 (basse 1 to 14)
2 I (basse 1 to 14)
3 Brysch, W. and Schlingensiepen, K.
ANTISENES OLIGONUCLEOTIDE PREPARATION METHOD
L. Patent: WO 9833904-A 724 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      7.7%; Score 10; DB 1; Length 14; 100.0%; Pred. No. 1.3e+02; trive 0; Mismatches 0; Indels
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Brysch, W.D. and Schlingensiepen, K.D.
An antisense oligonuclectide preparation method
Patent: EP 0856579-A 724 05-AUG-1998;
BIOGNOSTIK GES (DE)
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    .14
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/db_xref="taxon:32644"

 Mismatches
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Sequence 724 from Patent WO9833904.
A88576
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/organism="unidentified"
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Sequence 724 from Patent EP0856579.
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Best Local Similarity 100.
Matches 10; Conservative
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 10; Conservative
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                             1354 GAAAAATATT 1363
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                                                          GAAAATATT 2
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A88576/c
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A90543/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mang, C.-G. and Hepburn, A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US 5861244-A 33 19-JAN-1999;
Location/Qualifiers
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Covalently linked dimeric dna binding molecules
Patent: WO 011979-2-A 20 22-MAR-2001;
GENELABS TECHNOLOGIES, INC. (US)
Location/Qualifiers
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                                                           ce 1. .12
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Location/Qualifiers
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 7/02,
(C12NS/00,C12R1:91)
Recombinant human protein C
Location/Qualifiers
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    13
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|db_xref="taxon:9606"

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Sequence 20 from Patent W00119792.
AX098562
AX098562.1 GI:13537826

    .12
    /organism="unidentified"
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/db_xref="taxon:32644"

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Homo sapiens
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   A61K37/02,
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CC Recom
FH Key
FT source
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AR030144
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PAT 17-AUG-2003

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Gaps

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PAT 18-DEC-2003

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Unclassified.

1 (bases 1 to 14)
Raitano,A.B., Jakobovits,A., Faris,M., Afar,D.E.H., Hubert,R.S. and Mitchell,S.C.
36P6DS: secreted tumor antigen
Patent: US 6566078-A 3 20-MAY-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Uncassitude 14)
Afar, D.B.H., Hubert, R.S., Jakobovits, A. and Raitano, A.B.
Afar, D.B.H., Hubert, R.S., Jakobovits, A. and Raitano, A.B.
C-type lectin transmembrane antigen expressed in human prostate cancer and uses thereof
Patent: US 6602501-A 11 05-AUG-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.7%; Score 10; DB 1; Length 14; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 10; Conservative 0; Mismatches 0; Indels
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Gourse, R. L., Estrem, S.T., Ross, W.E. and Gaal, T. Promoter elements and methods of use Patent: US 6605431.A 10 12-AUG-2003;
Location/Qualifiers
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100.0%; Pred. No. 1.3e+02;
ative 0; Mismatches 0;
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Sequence 10 from patent US 6605431.
AR374279
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Sequence 11 from patent US 6602501.
AR372768 1 GI:40074490
AR322286 14 bp
Sequence 3 from patent US 6566078.
AR322286
                                                                                                                                                                                                                                                                                                                                       1. .14
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/organism="unknown"
                                                           AR322286.1 GI:33707875
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Best Local Similarity 100.
Matches 10; Conservative
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                                                             artificial sequences.

I (bases 1 to 14)

SA Far.D.E., Hubert.R.S. and Raitano, A.B.

PHELIX: testis-specific protein expressed in cancer

PATA.D.E., Hubert.R.S. and Paitano, A.B.

PHELIX: testis-specific protein expressed in cancer

UROGENESYS INC

OS Artificial Sequence

PN 30-JUL-2002;

PP 31-AUG-1999 JP 2000567696

PR 31-AUG-1999 US 60/106524 PI

PP 31-AUG-1999 US 60/10651031-OCT-1998 US 60/106524 PI

PP 31-AUG-1999 US 60/096610, 31-OCT-1998 US 60/106524 PI

PP 31-AUG-1999 US 60/1096610, 31-OCT-1998 US 60/106524 PI

PP 31-AUG-1999 US 60/1096610, 31-OCT-1998 US 60/106524 PI

PP 31-AUG-1999 US 60/1096610, 31-OCT-1998 US 60/106524 PI

PP 31-AUG-1999 US 60/096610, 31-OCT-1998 US 60/106524 PI

PP 31-AUG-1999 US 60/1096610, 31-OCT-1998 US 60/106524 PI

PP 31-AUG-1999 US 60/1096610, 31-OCT-1998 US 60/106524 PI

PP 31-AUG-1999 US 60/096610, 31-OCT-1998 US 60/106524 PI

PP 31-AUG-1999 US 60/096610, 31-OCT-1998 US 60/106524 PI

PP 31-AUG-1999 US 60/1096610, 31-OCT-1998 US 60/106524 PI

PP 31-AUG-1999 US 60/1096610, 31-OCT-1998 US 60/106524 PI

PP 31-AUG-1999 US 60/1096610, 31-OCT-1998 US 60/106524 PI

PP 31-AUG-1999 US 60/096610, 31-OCT-1998 US 60/106524 PI

PP 31-AUG-1999 US 60/096610, 31-OCT-1998 US 60/106524 PI

PP 31-AUG-1999 US 60/096610, 31-OCT-1998 US 60/106524 PI

PP 400-1990 US 60/096610, 31-OCT-1998 US 60/106524 PI

PP 500-1990 US 60/1096610, 31-OCT-1998 US 60/106524 PI

PP 600-1990 US 60/096610, 31-OCT-1998 US 60/106524 PI

PP 600-1990 US 60/096610, 31-OCT-1998 US 60/106524 PI

PP 600-1990 US 60/096610, 31-OCT-1998 US 60/106524 PI

PP 700-1990 US 60/09610, 31-OCT-1998 US 60/106524 PI

PP 700-1990 US 60/09610 US 60/10
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Unclassified.
1 (Dases I to 14)
S Afar, D.B., Hubert, R.S. and Mitchell, S.C.
Gene expressed in prostate cancer
Gene expressed in prostate cancer
Location/Qualifiers
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Sequence 5 from patent US 6509458.
AR277706 1 GI:29711494
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Raitano, A.B., Afar, D.B., Jakobovits, A., Faris, M., Hubert, R.S., Mitchell, S.C. and Saffran, D.C.
G protein-coupled receptor up-regulated in prostate cancer and uses
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Jakobovits,A.
Diagnosis and therapy of cancer using sgp28-related molecules
Patent: Wo 0131343-A 28 03-MAY-2001;
Urogenesys, Inc. (US)
Location/Qualifiers
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Sequence 28 from Patent WO0131343.
AX127613
AX127613.1 GI:14134282
AX107057

24 dequence 21 from Patent W00125434

AX107057

AX107057.1 GI:13922568
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AX083184.1 GI:13185070
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AR431453
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Raitano, A.B., Afar, D.B., Rastegar, G.S., Mitchell, S.C., Hubert, R.S., Challita-Bid, P.M., Faris, M. and Jakobovits, A.
103p2d6: tissue specific protein highly expressed in various
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Urogenesys, Inc. (US)
Location/Qualifiers
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AX233638.1 GI:15593340
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AX285303
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              Afar, D.E., Hubert, R.S., Raitano, A.B., Saffran, D.C., Mitchell, S.C., Faris, M. and Jakobovits, A. Serpentine transmembrane antigens expressed in human prostate cancers and uses thereof Patent: WO 0140276-A 23 07-JUN-2001; Urogenesys, Inc. (US)
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Mitchell,S.C. and Jakobovits,A.
34p3d7: a tissue specific protein highly expressed in prostate
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Urogenesys, Inc. (US)
Location/Qualifiers
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Urogenesys, Inc. (US)
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AX213287
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PAT 18-JUN-2002
                PAT 18-JUN-2002
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Nucleic acid and corresponding protein named 158plh4 useful in the treatment and detection of bladder and other cancers

Patent: WO 0216598-A 729 28-FEB-2002;

Agensys, Inc. (US)

Location/Qualifiers
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Nucleic acid and corresponding protein named 159ph4 useful in the treatment and detection of bladder and other cancers

Patent: WO 0216598-A 717 28-FEB-2002;

Agensys, Inc. (US)

Location/Qualifiers
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tive 0; Mismatches 0;
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Organism="synthetic construct"
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/db xref="taxon:32630"
/noTe="Primer"
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98p763: homeodomain protein highly expressed in various cancers Patent: WO 2001057-A 7 29-NOV-2001, Urogenesys, Inc. (US)
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55ph4: gene expressed in various cancers
Patent: WO 0196391-A 10 20-DEC-2001;
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/mol_trype="unassigned DNA"
/db xref="taxon:32630"
/note="primer"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"
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PAT 16-JUL-2002

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DNZ linear PAT 17-JUL-2003 BPC-1: secretory brain-specific protein expressed and secreted in prostatic and vesical cancer cells.
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artificial sequences.
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Afar,D.E., Hubert,R.S., Leong,K., Raitano,A.B., Saffran,D.C. and Jakobovits,A.
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Schlingensiepen, K.H. and Brysch, W.
An antisense Oligonucleotide preparation method
Patent: JP 2001511000-A 724 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
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31-JAN-1997 EP 97101531.8
KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
C12115/11, C077121/04, A61K31/70
An antisense oligonucleotide preparation method FH
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Plant genes involved in defense against pathogens Patent: WO 03000898-A 5831 03-4AN-2003; Syngente Participations AG (CH) Location/Qualifiers
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33.3%; Pred. No. 1.3e+02;
Ve 1; Mismatches 1;
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Location/Qualifiers

    .14
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    .14
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JP 2001511000-A/724.
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JP 2002522076-A/2.
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Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
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kukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                         Faris, M., Hubert, R.S., Raitano, A.B., Afar, D.E., Levin, E.,
Challita-Bid, P.M. and Jakobovits, A.
Nucleic acid and corresponding protein named 158pld7 useful in the
treatment and detection of bladder and other cancers
Patent: WO 0216593.A 661 28-FEB-2002;
Agensys, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                    /organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AX586901 14 bp DNA Sequence 2586 from Patent WO02060953.

    .14
/organism="Homo sapiens"
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/db_xref="taxon:9606"

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Location/Qualifiers
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AX655961.1 GI:29158775
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                        artificial sequences.
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         synthetic construct
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Best Local Similarity 100.
Matches 10; Conservative
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AX586901
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PAT 25-SEP-2002
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Adenovirus derived gene delivery vehicles comprising at least one element of adenovirus type 35.
BD273346
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Evans,R.M., Forman,B.M. and Weinberger,C.A.
Method for modulating process mediated by farnesoid activated
                                                                                                                                                                                                                                                                                                                                        /note='Partial sequence of an adenovirus ITR' FH
Location/Qualifiers
misc_feature (1)..(13).
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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AR305335
AR305535
BPFINITION Sequence 3 from patent US 6545162.
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Patent: US 6416957-A 5 09-JUL-2002;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Adenoviridae"
/mol_type="genomic DNA"
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                                                     DD273346.1 GI:33083114
JP 2002543846-A/42.
Adenoviridae
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Best Local Similarity 84.69
Matches 11; Conservative
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C12NS/00,
C12NS/00
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C12N1/19, C12N1/21, C12N5/10, C12N5/10, C12P21/02, C12Q1/68, G01N33/
              BPC-1: secretory brain-specific protein expressed and secreted in prostatic and vesical cancer cells Parent: JP 2002522076-A 2 23-JUL-2002; UROGENESYS INC
                                                                                                                                                                                                                                          A61K48/00, A61P13/08, A61P13/10, A61P35/00, C07K14/47, C07K16/18,
                                                              OSS ARTÍFICIAL Sequence

BN JP 2002522076-A/2

PD 23-JUL-2002

PF 10-AUG-1999 UP 2000565126

PR 10-NUG-1999 US 60/095982

PI DANIELE PAPAR,RENE S HUBERT,KAHAN LEONG,ARTHUR B RAITANO PI AYA JAKOBOVITS

PL AXA JAKOBOVITS
                                                                                                                                                                                                                                                                                                                                               Description of Artificial Sequence:cDNA synthesis primer FH Location/Qualifiers source 1..14
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1 (bases 1 to 13)
1 (bases 1 to 13)
Evans,R.M., Forman,B.M. and Weinberger,C.A.
Farnesoid activated receptor polypeptides, and nucleic acid
encoding the same
Patent: US 6005086-A 5 21-DEC-1999;
Location/Qualifiers
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        /organism="synthetic construct"
/mol type="genomic DNA"
        /db_xref="taxon:32630"

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/wol_type="unassigned DNA"
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AR096039
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BD273346/c
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Best Local Similarity 84.6%;
Matches 11; Conservative 0
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Balzergue, S.
Direct Submission
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AJ587409/c
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                                                    Unknown.
Unknown.
Unclassified.
1 (bases 1 to 13)
1 (bases 1 to 13)
Bervan, P.B. and Baird, E.E.
Method for the synthesis of pyrrole and imidazole carboxamides on a solid support
solid support
Patent: US 6545162-A 3 08-APR-2003;
Patent: US cation/Qualifiers
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Adenovirus derived gene delivery vehicles comprising at least one
element of adenovirus type 35
Patent: WO 0070071-A 42 23-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bahr, G., Cocude, C. and Capron, A. Rhilf polypeptides and its fragments and polymucleotides encoding said polypeptides and therapeutic uses said polyseptides and therapeutic uses Patent: WO 0185955-A 41 15-NOV-2001;
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/organism="Adenoviridae"
/mol_Lype="unassigned DNA"
/db_xref="taxon:10508"
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Sequence 41 from Patent W00185955.
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Seguence 42 from Patent WO0070071.
AX049941
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Location/Qualifiers
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                 GI:31694944
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Best Local Similarity 84.6
Matches 11; Conservative
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Submitted (23-0CT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue gaston Cremieux, 91057 Bvry cedex, FRANCE PCR was performed on DNA from transforments of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequence from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
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AJS87409
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AJS87409.

I GI:37937033

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Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Arabidopsis

Arabidopsis

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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/wol type="genomic DNA"
/cultivar="Wassillewskija"
/db xref="taxon:3702"
/clone="274E08"
/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
/nofe="Amorce"
                                                                                                                                                                              Score 9.8; DB 1;
Pred. No. 1.4e+02;
0; Mismatches 2

    .13 //note="T-DNA flanking sequence right border"
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Gaps

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PAT 22-JAN-2000

RESULT 254 A64290

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ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

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Query Match 7.5%; Score 9.8; DB 1; Length 14; Best Local Similarity 84.6%; Pred. No. 1.4e+02; Matches 11; Conservative 0; Mismatches 2; Indels
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                             1 (bases 1 to 14)
Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLICONUCLEOTIDE PREPARATION METHOD
PACENT: WO 9813904-A 787 06-AUG-1998;
BIOGNOSTIK GES (DE); RRYSCH WOLFGANG (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 14)
Brysch, W.D. and Schlingensiepen, K.D.
An antisense oligonucleotide preparation method
Patent: EP 08565/9-A 738 05-AUG-1998;
BIOGNOSTIK GBS (DE)
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Brysch, W.D. and Schlingensiepen, K.D.
An antisense oligonuclectide preparation method
Paten: BP 0856579-A 787 05-AUG-1998;
BIOGNOSTIK GES (DE)
Location/Qualifiers
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Sequence 787 from Patent EP0856579.
A90606.
A90606.1 GI:6739120
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Sequence 738 from Patent EP0856579.
A90557
A90557.1 GI:6739071
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

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A90557
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                                                                                  PAT 29-MAR-1999
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METHOD FOR DETECTION OF DRUG-INDUCED MUTATIONS IN THE REVERSE
TRANSCRIPTASE GENE
PATENT: WO 972732-A 78 31-JUL-1997;
INNOGENETICS NV (BE)
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7.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.4e+02;
Matches 11; Conservative 0; Mismatches 2; Indels
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Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
PATENT: WO 9833904-A 738 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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                                                                                                                                                                                                                                                                                                                   Other publication AU 1444397 19970820.
Location/Qualifiers
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Sequence 787 from Patent WO9833904.
A88639
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Sequence 738 from Patent WO9833904.
A88590
                                                                              14 bp
Sequence 78 from Patent W09727332.
A64290
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Best Local Similarity 84.69
Matches 11; Conservative
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PAT 22-JAN-2000

RESULT 256

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A88639/c

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PAT 08-AUG-2001

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BD271882 14 bp DNA linear PAT 17-JUL-2003 Expression of foreign genes from IRES transcription cassette in
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synthetic construct
artificial sequences.

1 (bases 1 to 14)
Pederson, F.S., Jesperson, T. and Duch, M.
Expression of foreign genes from IRES transcription cassette in
Patent: JP 2002542834-A 12 17-DEC-2002;
AARHUS UNIVERSITY
                                              1 (bases 1 to 14)
Wilson,J.M., Kozarsky,K. and Strauss,J. III.
Methods and compositions for gene therapy for the treatment of defects in lipoprotein metabolism
Patent: US 6174527-A 8 16-JAN-2001,
Location/Qualifiers
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JP 2002542834-A/12
17-DEC-2002
29-APR-2000 JP 2000615780
29-APR-1999 DK PA 199900584
FINN SKOU PEDERSON, THOMAS JESPERSON, MOGENS DUCH PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unclassified.
Unclassified.
1 (bases 1 to 14)
Wilson, J. M., Fisher, K. J., Chen, S. - J. and Weitzman, M. Wilson, U. M., Eisher, K. J., Chen, S. - J. and Weitzman, M. Walenovirus and method of use thereof Patent: US 6203975-A 8 20-MAR-2001;
Location/Qualifiers
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84.6%; Pred. No. 1.4e+02;
tive 0; Mismatches 2; Indels
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                                                                                                                                                 1. .14
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JP 2002542834-A/12.
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Best Local Similarity 84.6%
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Best Local Similarity 84.6%
Matches 11, Conservative
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AR142590/c
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1 (bases 1 to 14)
Lieven, S., Joost, L. and Rudi, R.
Method for detection of drug-induced mutations in the reverse transcriptase gene
transcriptase gene
Patent: US 6087093-A 78 11-JUL-2000;
Location/Qualifiers
                                   Gaps
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Wilson,J.M., Fisher,K.J., Chen,S.-J. and Weitzman,M.
Adenovirus and methods of use thereof
Patent: Use 6001557-A 8 14-DEC-1999;
Location/Qualifiers
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Score 9.8; DB 1; Length 14;
Pred. No. 1.4e+02;
0; Mismatches 2; Indels
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AR102589
AR102589.1 GI:12814177
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/mol_type="unassigned DNA"
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Sequence 8 from patent US 6174527.
AR141985.1 GI:15102285
                                                                                                                                                                             AR093390 14 bp
Sequence 8 from patent US 6001557.
AR093390
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 7.5%;
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                                                                  1351 GAAGAAAATATT 1363
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   Query Match
Best Local Similarity 84.64
Matches 11; Conservative
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PAT 03-SEP-2003
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1 (Dases 1 to 14)
Lieven, S., Joost, L. and Rudi, R.
Method for detection of drug-induced mutations in the reverse
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Wong, W.K.R. and Sutherland, M.L.
Word, W.K.R. and Sutherland, M.L.
Excretion of heterologous proteins from E. Coli
Patent: US 5223407-A 5. 29-JUN-1993;
Pred. No. 1.4e+02;
0; Mismatches 2;
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Patent: US 6331389-A 78 18-DEC-2001;
Location/Qualifiers
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Sequence 78 from patent US 6331389.
AR262892
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Sequence 5 from patent US 5223407.
AR363706
AR363706.1 GI:34425645
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AR363707
AR363707.1 GI:34425646
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/wol_type="genomic DNA"
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Best Local Similarity 84.6%;
Matches 11; Conservative
 Best Local Similarity 84.6%;
Matches 11; Conservative
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                                          1430 TATGCAGACATAT 1442
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Best Local Similarity 84.6
Matches 11; Conservative
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AR262892
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                                                                        of AENGFMK2
                              CI2N7/00,C12N7/02,G01N33/569//(C12N7/00,C12R1:93),C12N15/00,
C12N5/00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        December 1 to 14)
Wilson,J.M., Kozarsky,K. and Strauss,J. III.
Wilson,J.M., Kozarsky,K. and Strauss,J. III.
Wethods and compositions for gene therapy for the treatment of defects in lipoprotein metabolism
Patent: US 5652224-A 8 29-JUL-1997;
Location/Qualifiers
C12N15/09, A61K35/12, A61K35/76, A61K48/00, A61P43/00, C12N5/06, PC
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Unclassified.
Unclassified.
1 (bases 1 to 14)
Garner,H.R. Wren,J.D., Minna,J.D. and Fondon,J.W. III.
Polymorphic repeats in human genes
Polymorphic repeats 29-0CT-2002;
Location/Qualifiers
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                                                                      Description of Artificial Sequence:5 prime of PL
Key
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/organism='Artificial Sequence'
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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AR241718
AR241718.1 GI:27287530
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                                                                                                                                                                                                                                                                                                                                                                               1. .14
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/wol_type="genomic DNA"
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/organism="unknown"
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Matches 11; Conserv
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PC C12N7
PC C12N6
PC C12N6
PC C12N6
FC C12N6
FT Key
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Matches 11; Conservative
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                            1346 CAGGGGAAGAAA 1358
                                                                                                                                                                                                Homo sapiens (human)
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Best Local Similarity 84.69
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AX572338
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AX571850
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Fauchet, C.R.J.
Fixing unit with an end imprint in a threaded terminal portion Patent: US 6632057-A 123 14-OCT-2003;
Location/Qualifiers
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Expression of heterologous genes from an ires translational cassette in retroviral vectors
Patent: WO 0066755-A 12 09-NOV-2000;
Aarhus University (DK)
Location/Qualifiers
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84.6%; Pred. No. 1.4e+02;
tive 0; Mismatches 2; Indel8
                                                                                                                                                         Length 14;
                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                     2; Indels
             Unclassified.

1 (bases 1 to 14)

1 (bases 1 to 14)

Wong, W.K.R. and Sutherland, M.L.

Excretion of heterologous proteins from E. Coli

Patent: US 5223407-A 6 29-JUN-1993;

Location/Qualifiers
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// Organism="synthetic construct"
// Mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="5 prime of PL of AENGFMK2"
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84.6%; Pred. No. 1.4e+02;
                                                                                                                                                         7.5%; Score 9.8; DB 1;
84.6%; Pred. No. 1.4e+02;
tive 0; Mismatches 2.
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Sequence 123 from patent US 6632057.
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/mol_type="unassigned RNA"
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Sequence 12 from Patent WO0066758.
                                                                                                      1. .14
/organism="unknown"
/wol_type="genomic DNA"
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synthetic construct
artificial sequences.
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Matches 11; Conservative
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AR408030/c
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Method for detection of drug-induced mutations in the hiv reverse
transcriptages general parts.
Patent: WO 02055741-A 361 18-JUL-2002;
INNOGENETICS N.V. (BE)
Location/Qualifiers
                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                    Blanche, F. and Cameron, B. Methods for purifying and detecting double stranded dna target sequences by triple helix interaction Patent: WO 02077274-A 9 03-OCT-2002; Aventis Pharma S.A. (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Human immunodeficiency virus
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
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84.6%; Pred. No. 1.4e+02;
tive 0; Mismatches 2; Indels
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/db_xref="taxon:12721"
      linear
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34.6%; Pred. No. 1.4e+02;
tve 0; Mismatches 2; Indels
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        DNA
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AX572321.1 GI:26004411

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/db_xref="taxon:9606"

Sequence 9 from Patent WO02077274,
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Wed Apr

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AX017787
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AX017787
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  PAT 29-NOV-2002
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Method for detection of drug-induced mutations in the hiv reverse
transcriptase gene
Patent: WO 020555741.378 18-JUL-2002;
INNOGENETICS N.V. (BE)
Location/Qualifiers
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                                                               Human immunodeficiency virus
Human immunodeficiency virus
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
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Schlingensiepen, K.H. and Brysch, W.
An antisense Oligomucleoride preparation method
Patent: JP 2011511000-A 738 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
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31-07M-1999 bp 1998512533
31-07M-1997 EP 97101531.8
KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
C12M15/11.(007H21/04, AGIK31/70
An antisense oligonucleotide preparation method FH
Location/Qualifiers
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  linear
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Location/Qualifiers
  DNA
 AX572338 14 bp DN
Seguence 378 from Patent WO02055741.
AX572338

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/db_xref="taxon:32644"

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                                       AX572338.1 GI:26004428
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BD066103
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RESULT 275 BD066152/c

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        PAT 27-AUG-2002
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Pooideae, Triticeae, Hordeum.
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Schlingensiepen, K.H. and Brysch, W.
An antisense Oligonucleotide preation method
Patent: JP 2011511000-A 747 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MEH
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JP 2001511000-A/787
JP 2001511000-A/787
30-AUG-2001
30-JAN-1998 JP 1998532533
31-JAN-1997 EP 97101531.8
KARL HERMANN SCHLINGENSIEPER, WOLFGANG BRYSCH
CI2N15/11, CO7721/04, A61K31/70
An antisense oligonucleotide preparation method FH
Location/Qualifiers
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Pred. No. 2.3e+02;
0; Mismatches 8; Indel8
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14 bp DNA line:
An antisense oligonucleotide preparation method.
BD066152
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84.6%; Pred. No. 1.4e+02;
ative 0; Mismatches 2;
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Sequence 16 from Patent WO9946404.
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                                                          BD066152.1 GI:22611755
JP 2001511000-A/787.
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Nuclectide sequence 13 from patent number WO8300346.
A04336
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                                                                                                                  SM Unknown.
Unclassified.

I (bases I. barea.)

SGOUTES, R.L., Estrem, S.T., Ross, W.E. and Gaal, T. Promoter elements and methods of use Promoter elements and methods of use IAL Patent: US 6605431-A 10 12-AUG-2003;

SS I. 14 / Organism="unknown" / mol_type="genomic DNA" / mol_type="genomic DNA"
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Location/Qualifiers
                        AR374279 14 bp I Sequence 10 from patent US 6605431. AR374279
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The invention relates to a new compound having a sequence comprising 8-50 bp targeted to a nucleic acid encoding human collapsin response mediator protein 2 which specifically hybridizes with the nucleic acid encoding human collapsin response mediator protein 2 and inhibits its expression. The compound is useful for preparing a composition for treating neurodegenerative disease, e.g., Alzheimer's disease, Down syndrome or schizophrenia. This sequence represents the human collapsin response mediator protein 2 gene intron 1 sequence against which the antisense oligonucleotides may be targeted.
                                                                                                                                                                                                                                                                                                                        New compound, having a sequence targeted to a nucleic acid encoding human collapsin response mediator protein 2, useful for preparing a composition for treating neurodegenerative disease, e.g., Alzheimer's disease.
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/note= "contains phosphorothicate internuclectide
/notes all cytidine nuclectides are 5-methylcytidine
residues"
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human collapsin response mediator protein 2; neurodegenerative disease;
Alzheimer's disease; Down syndrome; schizophrenia; H-ras; 88; antisense.
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/*tag= a
/note= "2'-0-methoxyethyl modified nucleotitides"
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Homo sapiens.
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human collapsin response mediator protein 2; neurodegenerative disease;
Alzheimer's disease; Down syndrome; schizophrenia; H-ras; ss; antisense.
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/note= "contains phosphorothioate internucleotide
linkages, all cytidine nucleotides are 5-methylcytidine
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ABF65197
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ABF91286
ABH50638
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ABF73476
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The invention relates to a new compound having a sequence comprising 8-50 bp targeted to a nucleic acid encoding human collapsin response mediator protein 2 which specifically hybridizes with the nucleic acid encoding human collapsin response mediator protein 2 and inhibits its expression. The compound is useful for preparing a composition for treating neurodegenerative disease, e.g., Alzheimer's disease, Down syndrome or schizophrenia. This sequence represents the human collapsin response mediator protein 2 gene intron 1 sequence against which the antisense oligonucleotides may be targeted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New compound, having a sequence targeted to a nucleic acid encoding human collapsin response mediator protein 2, useful for preparing a composition for treating neurodegenerative disease, e.g., Alzheimer's disease.
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human collapsin response mediator protein 2; neurodegenerative disease;
Alzheimer's disease; Down syndrome; schizophrenia; H-ras; 88; antisense.
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|Inkages, all cytidine nucleotides are 5-methylcytidine
residues"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New compound, having a sequence targeted to a nucleic acid encoding human collapsin response mediator protein 2, useful for preparing a composition for treating neurodegenerative disease, e.g., Alzheimer's disease.
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human collapsin response mediator protein 2; neurodegenerative disease;
Alzheimer's disease; Down syndrome; schizophrenia; H-ras; ss; antisense.
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linkages, all cytidine nucleotides are 5-methylcytidine
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/note= "2'-O-methoxyethyl modified nucleotitides"
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Pred. No.
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human collapsin response mediator protein 2; neurodegenerative disease;
Alzheimer's disease; Down syndrome; schizophrenia; H-ras; ss; antisense.
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100.0%; Pred. No. >...
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human collapsin response mediator protein 2; neurodegenerative disease;
Alzheimer's disease; Down syndrome; schizophrenia; H-ras; ss; antisense.
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linkages, all cytidine nucleotides are 5-methylcytidine
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                                                                                                                                            (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                     WPI; 2003-449447/42.
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New compound, having a sequence targeted to a nucleic acid encoding human collapsin response mediator protein 2, useful for preparing a composition for treating neurodegenerative disease, e.g., Alzheimer's disease.
                                                                                                                                                                                                                                                                                                   The invention relates to a new compound having a sequence comprising 8-50 bp targeted to a nucleic acid encoding human collapsin response mediator protein 2 which specifically hybridizes with the nucleic acid encoding human collapsin response mediator protein 2 and inhibits its expression. The compound is useful for preparing a composition for treating neurodegenerative disease, e.g., Alzheimer's disease, Down syndrome or schizophrenia. This sequence represents the human collapsin response mediator protein 2 gene intron 1 sequence against which the antisense oligonucleotides may be targeted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer; microsatellite marker; barley; chromosome 7 marker; cereal; fermentability; group 5 chromosome; ethyl carbamate production; Bmac2l3; wort fermentation; Triticeae; Bmac96; epi-heterodendrin production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening cereals for fermentability, especially useful in barley.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.4%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 9.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                 claim 3; SEQ ID NO 40; 102pp; English
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04-NOV-2002; 2002WO-US035323
                                    08-NOV-2001; 2001US-00006911
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ID AAZ20454 standard; DNA; 22
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                                                                          (ISIS-) ISIS PHARM INC
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                                                                                                                Watt AT;
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Best Local Similarity
Matches 20; Conserv
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Hordeum vulgare.
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                                                                                                                                                                                                                               New compound, having a sequence targeted to a nucleic acid encoding human collapsin response mediator protein 2, useful for preparing a composition for treating neurodegenerative disease, e.g., Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human collapsin response mediator protein 2 gene antisense oligo #138030
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human collapsin response mediator protein 2, neurodegenerative disease,
Alzheimer's disease, Down syndrome, schizophrenia, H-ras, ss, antisense.
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"2'-0-methoxyethyl modified nucleotitides'
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/note= "2'-O-methoxyethyl modified nucleotitides"
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                                                                                                                                                                                                                                                                                                           Claim 3; SEQ ID NO 39; 102pp; English
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linkages, all cyt
residues"
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                                                                              08-NOV-2001; 2001US-00006911.
                                        04-NOV-2002; 2002WO-US035323
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/note= '
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                                                                                                                  (ISIS-) ISIS PHARM INC
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nes 20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_difference
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misc_difference
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-2003
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    15-MAY-2003
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Query Match

Matches

ADC66362

RESULT 7 ADC66362/c

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Gaps

This sequence represents a PCR primer for a barley chromosome 7

microsatellite marker, and can be used in the method of the invention.

The method is for screal for fermentability, comprising

analysing cereal genomic DNA to determine which allele(s) of a gene/gene

complex affecting fermentability at a locus close to the centromere on

bomologous Triticeae group 5 chromosome (barley chromosome 7) is/are

present. The invention also relates to a method for screening cereal for

chyl carbamate production on wort fermentation and distillation,

comprising analysing barley genomic DNA to determine which allele(s) of

the locus, designated eph on the short arm of homologous Triticeae group

che locus, designated eph on the short arm of homologous Triticeae group

che locus, designated eph on the short arm of homologous friticeae group

che locus, designated eph on the short arm of homologous friticeae group

che locus, designated eph on the strangement in methods and

primers are useful for determining fermentability and/or epi-heterodendrin

comprision in cereals, especially barley. Current methods for determining

fermentability are difficult to apply within barley breeding programs.

Prior art methods using molecular markers have difficulty in detecting

Sequence 22 BP; 6 A; 3 C; 6 G; 7 T; 0 U; 0 Other;

Gaps ô 12.0%; Score 15.6; DB 1; Length 22; 81.8%; Pred. No. 79; 4; Indels iive 0; Mismatches 4; Indels 18; Conservative Local Similarity Query Match Matches 8

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AAF83488 standard; DNA; 20 AAF83488/c

BP

(first entry) 23-JUL-2001

Human ADAM10 mRNA specific antisense oligo ISIS #100751.

human; ss; cytostatic. disintegrin and metalloproteinase 10; ADAM10; antisense; onnective tissue disorder; antiinflammatory; hematologic; connective tissue

Homo sapiens

US6228648-B1

17-MAR-2000; 2000US-00527154

17-MAR-2000; 2000US-00527154

(ISIS-) ISIS PHARM INC

Condon TP, Flournoy SC;

WPI; 2001-342677/36.

antisense oligonucleotides targeted to nucleic acids encoding A disintegrin and metalloproteinase 10 (ADAM10), useful for treating diseases associated with ADAM10 expression, e.g. inflammation or hematologic malignancies, Claim 1; Col 41-42; 29pp; English.

The invention provides antisense compounds targeted to the nucleic acid molecule encoding A disintegrin and metalloproteinase 10 (ADMA10). The antisense compounds specifically hybridize with and inhibit the expression of ADMA10. The antisense oligonucleotides are useful for treating or diagnosing an animal, particularly a human, suspected of having or being prone to a disease or condition associated with expression of ADMA10, e.g. connective tissue disorders, inflammation or hematologic malignancies. The antisense oligonucleotides are also useful

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The invention relates to a compound of 8-50 nucleobases in length targeted to a nucleic acid encoding protein phosphatase 1B (PTP1B), where targeted to a nucleic acid encoding protein phosphatase 1B (PTP1B), where the compound specifically hybridises with and inhibits the expression of PTP1B (e.g. an antisense oligonucleotide). Also included are (1) a compound of 8-50 nucleobases in length which specifically hybridises with an 8 nucleobase portion of an active site on a nucleic acid encoding PTP1B; (2) inhibiting the expression of PTP1B in cells or tissues or complition associated comprising contacting the cells or tissues with the compound; treating an animal having or suspected of having a disease or condition associated sugar levels in an animal comprising administering the compound; (5) preventing or delaying the onset of a disease or condition associated preventing or delaying the onset of a disease or condition associated correcting or delaying the onset of an increase in blood glucose levels in an animal comprising administering the compound; and (6) preventing or delaying the onset of an increase in blood glucose levels in an animal comprising the compound. The compound is used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein phosphatase 1B (PTP1B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and for treating diabetes, cancer, or obesity, comprises an antisense oligonucleotide targeted to nucleic acid encoding PTPIB.
in research applications for the modulation of ADAM10 expression. The present sequence represents an antisense oligo specific for the human ADAM10 mRNA
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; protein phosphatase 1B; PTP1B; ss; probe; human;
type 2 diabetes; obesity; ovarian cancer; chronic myeloid leukaemia;
hyperproliferative disease; antidiabetic; anorectic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mckay R;
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                                                                                                                    DB 1; Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PTP1B antisense oligonucleotide ISIS 142076.
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                                                                                Sequence 20 BP; 8 A; 4 C; 2 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                          0; Mismatches
                                                                                                                    Score 15.2; Pred. No. 82;
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                                                                                                                                                                                               1424 TCGTTCTATGCAGACATATA 1443
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31-JUL-2000; 2000US-00629644.
                                                                                                                      11.7%;
85.0%;
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                                                                                                                                                                                                                                                                                                                             ABK85325 standard; DNA; 20
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                                                                                                                  Query Match
Best Local Similarity 85.0
Matches 17; Conservative
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FREIER S M.
MONIA B P.
BUTLER M M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-462914/49.
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(MONI/)
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to inhibit the expression of PTPIB in cells or tissues, to treat or prevent or delay the onset of a disease or condition associated with PTPIB, such as type 2 diabetes, obesity, cancer (especially ovarian cancer. Chronic myeloid leukaemia and hyperproliferative diseases in an animal having or suspected of having the disease or condition, and for decreasing blood sugar levels or preventing or delaying the onset of an increase in blood glucose levels in an animal. The compound is also used in diagnostics, therapeutics, prophylaxis, and in research reagents and ktts. The present sequence is an antisense compound of the invention targetting human PTPIB
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Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

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Gaps
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  DB 1; Length 20;
                         3; Indels
Score 15.2; DB; Pred. No. 82; 0; Mismatches
                                                 1435 AGACATATACATGGAAGATG 1454
11.7%;
85.0%;
 Query Match
Best Local Similarity 85.0
Matches 17; Conservative
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1 AGCCATGTACTTGGAAGATG 20

Capture oligonucleptide Zip ID#1251 oligo #9. ВÞ ABI94164 standard; DNA; 20 (first entry) 16-FEB-2002 ABI94164; RESULT 11 ABI94164

Human, K-ras, PCR primer, probe, capture probe, mutation detection, ligase detection reaction; LDR, p53; BRCAL; BRCA2; infectious disease; infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer, oncogene; tumour suppressor; human papillomavirus; forensic; environmental monitoring; food industry; feed industry; ss.

Synthetic

WO200179548-A2. 25-OCT-2001 04-APR-2001; 2001WO-US010958.

14-APR-2000; 2000US-0197271P.

(CORR) CORNELL RES FOUND INC

Kliman R; Favis R, Gerry NP, Zirvi M, WPI; 2002-034366/04 Barany F,

Example 5; Fig 29; 300pp; English.

Designing capture oligonucleotide probes for use on a support to which complementary oligonucleotides hybridize with little mismatch.

The present invention describes a method (M1) for designing capture oligomucleotide probes (I) for use on a support to which complementary oligomucleotide probes (I) will hybridise with little mismatch, where (I) have melting temperatures within a narrow range. The method is useful for detecting infectious diseases caused by bacterial infectious agents or Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal infectious agents e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal infectious agents e.g. Troptococcus neoformans, Candida albicans and Aspergillus funigautus, viruses e.g. T-cell lymphocytotrophis cirus, Espstein-Barr virus and polio virus, and parasitic infectious agents medinesis. The method is also useful for detecting genetic diseases such as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.

Detecting cancer involving oncogenes, tumour suppressor genes, or genes involved in DNA amplification, replication, recombination or repair, the

Novel compound hybridizing with nucleic acid molecule encoding CD81 and inhibiting the expression of CD81, useful for treating infections and disease associated with expression of CD81 such as inflammation disorder.

Dobie K;

Graham MJ,

WPI; 2003-810907/76.

Example 15; SEQ ID NO 25; 55pp; English

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cancer is specifically associated with a gene selected from BRCAl gene, p53 gene, human papillomavirus types 16 and 18 and liver cancers. The method is also used for environmental monitoring, forensics and the food and feed industry, detecting comprises scanning (using e.g. a scanning electron microscope and infrared microscope) the support at the particular sites and identifying if ligation of the oligonuclectide probe sets occurred and correlating (using a computer) identified ligation to a presence or absence of the target nucleotide sequences. ABI82074 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Phosphorothioate backbone and all cytidines are 5 -methyl cytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense; es; human; CD81; TAPA-1; tetraspanin; viral infection; occaine addiction; autoimmune disorder; antinflammatory; antibacterial; virucide; antiparasitic; inflammatory disorder; parasitic infection; bacterial infection.
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                                                                                                                                                                              DB 1; Length 20;
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16. .20
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/note= "2'-methoxyethyl nucleotide"
                                                                                                                                                  Sequence 20 BP; 6 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                           Human CD81/TAPA-1 antisense oligonucleotide #13.
                                                                                                                                                                           Score 15.2; DB; Pred. No. 82; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                  1364 CCACGCATCACGAGCGATCG 1383
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                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                             11.7%;
85.0%;
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                                                                                                                                                                             Query Match
Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                         of the present invention
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Sequence 20 BP; 9 A; 1 C; 6 G; 4 T; 0 U; 0 Other;

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                 The invention relates to a compound (antisense oligonucleotide) hybridising with the eighth nucleobase portion of an active site on a mucleic acid melecule encoding CDB1 (also known as TAPA-1, a tetraspania) and inhibiting the expression of CDB1. Also included is a composition comprising the antisense oligonucleotide and a carrier or a diluent. The antisense oligonucleotide is useful for inhibiting the expression of CDB1 in cells or tissues. The antisense oligonucleotide is useful for treating infections preferably viral, bacterial and parasitic and diseases such as inflammatory disorders and autoimmune disorders. The disease or condition is characterised by chemical dependency (e.g. cocaine addiction). The present sequence is a CDB1 antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Compsn. contg. sequence specific glyco-conjugate DNA ligand - for modulating gene transcription, e.g. to induce immunosuppression, does not cause DNA cleavage, also new ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New glycoconjugates are able to modulate transcriptional activity of specific genes in eukaryotic cells by selectively inhibiting binding interactions between DNA-binding proteins and their recognition sites. Glycoconjugate DNA ligands which preferentially bind to an NFAT recognition sequence as compared to an API or Spl sequence are preferred. Such ligands inhibit NPAT-DNA complex formation or displace pre-formed complexes and are useful for inducing immune suppression. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear factor of activated T-lymphocytes; NFAI; interleukin 2; transcriptional regulator; early activation gene; glycoconjugate; calicheamicin-MG; purine-rich core sequence; immune suppression; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative NFAT binding site from human IL-2 gene (-289 to -270).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 8 A; 3 C; 4 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 24; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1427 TTCTATGCAGACATATACAT 1446
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(first entry)
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ses 17; Conservative
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12-OCT-1995
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AA084976
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                                                                                                                                                                                                                                                          Human; immunosuppressive; cytoplasmic nuclear factor of activated T cell; NF-ATc; nuclear translocation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for identifying an immunosuppressive agent. The method comprising: contacting a cell containing cytoplasmic nuclear factor of activated T cell (NF-ATC) polypeptide with a compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying immunosuppressive agent comprises contacting cell having cytoplasmic NF-AT polypeptide with inducer of polypeptide cytoplasmic translocation, in presence and absence of test agent, and assaying the
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                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        that induces nuclear translocation of the polypeptide, and nuclear translocation of the NF-ATC is assayed. The method is useful for identifying an immunosuppressive agent and an immune regulating age The present sequence is human NF-AT binding site DNA
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  DB 1; Length 20;
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                Pred. No. 97;
0; Mismatches
  11.4%; Score 14.8;
88.9%; Pred. No. 97
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                                                         1394 AAAGGAGGTAAAATTGTT 1411
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                                                                                                                                                                                                                                 Human NF-AT binding site DNA #3.
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93US-00124981.
94US-00228944.
94US-00260174.
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                                                                                                                                                   AAD34038 standard; DNA; 20
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                              Conservative
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Query Match
Best Local Similarity
Matches 16; Conser
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18-APR-1994;
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ADA66410
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AAD34038
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cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
primer; probe; tumour suppression; tumour reversion; apoptosis;
virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related
                                                                                                                Tumour suppression/reversion associated nucleotide #5021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 619; 771pp; French.
ADB44698 standard; DNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR ENGINES LAB.
                                                                                                                                                                                                                                                                                                                                                                          17-SEP-2002; 2002WO-IB004219.
                                                                                                                                                                                                                                                                                                                                                                                                                  17-SEP-2001; 2001FR-00011981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful e.g. for treatment of polypeptide and antibodies.
                                                                           (first entry)
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                                                                           18-DEC-2003
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                                                                                                                                                                                                                  diagnosis.
                                     ADB44698;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of identifying an immunosuppressive agent which comprises contacting a cell containing or capable of expressing NF-ATC and NF-ATD with one or more compounds that induces nuclear translocation of NF-ATC and NF-ATD. The method is useful in determining or controlling the expression of early T lymphocyte cartivation genes and the expression of selected constitutive genes that can be advantageously expressed in T lymphocytes. Agents that modulate the nuclear import of the cytoplasmic subunit of NF-AT or the induction of the cytoplasmic subunit of NF-AT or the induction.

The NF-AT polymucleotides may be used for diagnosing pathological conditions or genetic diseases involving T cell neoplasms or T cell hyperfunction or hypofunction, and conditions or diseases that involve alterations in the structure or abundance of NF-ATC polymptide.

Conditions or Apportmention, and sonditions or diseases that involve alterations in the structure or abundance of NF-ATC mcNA to diagnose a disease and for forensic identification of individuals, e.g. for the cidentification of descendents, paternity or criminal identification. The present sequence represents an NF-AT DNA binding site.
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O
                                                                                                                               ds; human; immunosuppression; NF-ATC; NF-ATn;
T lymphocyte activation gene expression; T lymphocyte; T cell neoplasm;
T cell hyperfunction; T cell hypofunction; forensic identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying an immunosuppressive agent comprises contacting a cell containing or capable of expressing NF-ATc and NF-ATn with one or more compounds that induces nuclear translocation of NF-ATc and NF-ATn.
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Pred. No. 97;
0; Mismatches 2; Indels
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93US-00124981.
94US-00228944.
94US-00260174.
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88.9%;
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                                                      (first entry)
                                                                                         NF-AT DNA binding site #2.
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Best Local Similarity 88.9
Matches 16; Conservative
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NORTHROP J P.
HO S N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HOSN/) HO S N.
(FLAN/) FLANAGAN W M.
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20-SEP-1993;
18-APR-1994;
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                                                      20-NOV-2003
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15-JAN-1999;
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                ADA66410;
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fragments of at least 15 consecutive nucleotides of these nucleotides, a fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 89 identity, after optimal alignment, with the nucleotides, or the complement, or corresponding RNA, of the nucleotides. The nucleotides are used as probes or primers for detecting, identifying, quantifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour suppression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies (Ab) against the polypeptide are useful for prevention and/or treatment of viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

Analysis of the expression of the nucleotides can be used for diagnosis and polypeptides can be used to screen for their specific interactive modecules.

Cond/or prognosis of these diseases. The nucleotides and polypeptides can also be useful for treating diseases associated with abnormal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.1%; Score 14.4; D 93.8%; Pred. No. 92; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression of the nucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ02237 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1402 TAAAATTGTTAATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 TAAACTTGTTAATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 17
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2 AAAGGAGGAAAAACTGTT 19

d ò

RESULT 16 ADB44698/c

27-NOV-1998;

28-NOV-1997; 17-DEC-1997; 04-NOV-1998;

Griffais R;

W09928475-A2

Synthetic

10-JUN-1999

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AAX91991-X97517 represent PCR primers used to amplify open reading frames and other nucleic acid sequences from the genome of Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent critis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAX34884- AAX35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae especially where the vector directs the expression of a neutralising epitope of C. pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New radiation hybrid map of the dog, Canine familiaris, genome, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dog; genome; genomic marker; radiation hybrid map; identification; chromosome location; gene marker; polymorphic microsatellite marker; phenotype; behaviour; pedigree; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14.2; DB 1; Length 20;
Pred. No. 1.3e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic marker oligonucleotide sequence SEQ ID NO:58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 20 BP; 3 A; 4 C; 4 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                  Genome sequence of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                         Page 1670; Disclosure; 1912pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1354 GAAAAATATTCCACGCATC 1372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAAAAATGCGACGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0108193P
                                                                                                                  97FR-00014673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.9%;
84.2%;
                                                                              98WO-IB001890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA66196 standard; DNA; 20
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                                                                                                                                                                                                                                                            WPI; 1999-357842/30
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Best Local Similarity
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                                                                                                                                                                              GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-NOV-1999;
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WO9927105-A2
                                                                              20-NOV-1998;
                                                                                                                                        04-NOV-1998;
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                                                                                                                    21-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salibert F,
                                       03-JUN-1999
                                                                                                                                                                                                                     Griffais R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primers AAZ01426-Z06209 were used to amplify open reading frames cocke by the genome of Chlamydia trachomatis (see AAZ01425). These ORFs encode polypeptides (see AAX36754-Y37949) which can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases unch as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis, genital diseases such as nongonococcal uretritis, pendydmitis, cervicitis, salpingtitis, perihapatitis, bartholinitis, peneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
                                                                          Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer; bartholinitis; preumopathy; venereal lymphogranulomatosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 1.3e+02;
0; Mismatches 3; Indels
                                       PCR primer used to amplify an ORF of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primer used to amplify an ORF of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 1508; 1755pp; English.
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97FR-00016034.
98US-0107077P.
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84.2%;
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07-OCT-1999 (first entry)
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Chlamydophila pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                  Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-371125/31
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                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEST ) GENSET
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13-SEP-1999

16;

Matches

Query Match

diseases

1385

g ð

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Gaps

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for e.g. identifying genes implicated in phenotypic and behavioral traits or in genetic diseases and for studying dog pedigrees.
                      Claim 1; Page 55; 87pp; English.
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The present invention describes a radiation hybrid map of the dog (Canine familiaris) genome comprising the genome location of a marker selected from AAA66139 to AAA66942. The radiation hybrid map is useful for identifying and localising dog genes, since it covers approximately 80 % of the dog genome and provides a dense map integrating different types of the dog genome and provides a dense map integrating different types (or complementary sequences) are especially useful to identify genes responsible for phenotypic and behavioural traits in dogs, to identify marked genes, to analyse diseases and identify implicated genes in such diseases and to analyse and to study dog pedigrees. They may also be useful for isolating corresponding human gene sequences e.g. genes Sequence 20 BP; 9 A; 2 C; 6 G; 3 T; 0 U; 0 Other; involved in genetic diseases

Score 14.2; DB 1; Length 20; Pred. No. 1.3e+02; 3; Indels 0; Mismatches 1435 AGACATATACATGGAAGAT 1453 2 AGACATGGACAAGGAAGAT 20 10.9%; 84.2%; Query Match Best Local Similarity 84.2 Matches 16, Conservative q ð

ABZ93979 standard; DNA; 20 (first entry) 17-OCT-2003 ABZ93979; RESULT 20 **ABZ**93979/

Human; antisense; lung dysfunction; nasal airway dysfunction; antinflammatory steroid; ubiquinone; antinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchodonstriction; lung allergy; lung inflammation; respiratory disease; ds. Human oligonucleotide sequence.

Homo sapiens.

31-OCT-2002

WO200285308-A2.

23-APR-2002; 2002WO-US013135

(EPIG-) EPIGENESIS PHARM INC

24-APR-2001; 2001US-0286137P

Aguilar Pabalan J, Katz E, Sandraвagra A, Ka b, Shahabuddin S; Li Y, San . Tang L, Willer S, Nyce JW,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired ö respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid ubiquinone

Disclosure; SEQ ID NO 9221; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions,

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James 2 introversion junctions, or regions within a club collections of punctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention of the invention and antiinflammatory, antiallargic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a consenting a respiratory lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antistant servicid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing bronchoconstriction, lung aurfactant in a subject's tissue, or treating bronchoconstriction, note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
or regions within 2-10 nucleotides of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14.2; DB 1; Length 20;
Pred. No. 1.3e+02;
0; Mismatches 3; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 11 A; 2 C; 0 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.9%;
84.2%;
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Best Local Similarity 84.2'
Marches 16; Conservative
     $$$$$$$$$$$$$$$$$$$$$$$$$$$$$
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Gaps

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ABX04789 standard; DNA; 18 ABX04789 RESULT

15-JAN-2003 (first entry) ABX04789;

Guanylate kinase gene associated oligonucleotide #7.

Herpesviridae; thymidlne kinase; TK; DRH nucleoside binding region; viral inhibitor; bacterial inhibitor; parasite inihibitor; tumour; autoreactive immune cell; cancer; hyperkeratosis; psoriasis; prostate hypertrophy; hyperthyroidism; endocrinopathy; allergy; autoimmune disease; restenosis; viral disease; AIDS; hepatitis; HCV; HBV; acquired immunodeficiency syndrome; intracellular parasitic disease; gene therapy; adenosine deaminase deficiency; Alzheimer's disease; ss; guanylate kinase.

Homo sapiens US6451571-B1

17-SEP-2002.

94US-00237592. 95US-00432871. 95US-00552304. 99US-00270956. 17-MAR-1999; 02-MAY-1994; 02-MAY-1995; 02-NOV-1995;

(UNIW) UNIV WASHINGTON

Loeb LA, Black ME;

WPI; 2003-045581/04.

Novel Herpesviridae thymidine kinase mutant useful for inhibiting pathogens e.g. viruses, bacteria, tumor in animals, has one or more mutations encoding amino acid substitutions upstream from the DRH nucleoside binding

Example 9; Col 47; 78pp; English

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The invention describes an isolated Herpesviridae thymidine kinase (TK) comprising a 12 amino acid (aa) nucleoside binding region having a site 3 made up of a DRH nucleoside binding site and a site 4 and mutation(s), at least one of the mutations being an a substitution 2 or 3 aa upstream or 5 or more as downstream from the DRH motif that increases a biological activity, preferably ability of TK to phosphorylate a nucleoside analogue, as compared to unmutated TK TK mutants are useful for inhibiting a pathogenic agent such as viruses, bacteria, parasites, tumour cells or autoreactive immune cells in a warm-blooded animal. TK mutant is useful for inhibiting a tumour or cancer in a warm-blooded animal. (or treating a variety of disease e.g., hyperkeratosis (psoriasis), prostate hypertrophy, hyperthyroidism, endocrinopathies, autoimmune diseases, lalexipes, restenosis, viral diseases such as acquired immunodeficiency syndrome (AIDS) hepatitis (HCV or HBV), intracellular parasitic diseases, and to correct aberrant expression of a gene within a cell, or to replace a specific gene which is defective in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                 proper expression using gene therapy, e.g. including adenosine deaminase deficiency, and Alzheimer's diseases. The mutants are utilised as a conditionally lethal marker for homologous recombination. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gene therapy, tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                        represents an oligonucleotide used in the isolation, purification and characterisation of guanylate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 BP; 6 A; 4 C; 3 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human HTPL scanning oligonucleotide SEQ ID 1131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14; DB 1;
Pred. No. 1.2e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. No. 1.2 ive 0, Mismatches
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30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000668.
30-JAN-2001; 2001WO-US000669.
23-MAY-2001; 2001US-00864761.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and

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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL mas two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL startes an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome lDpl2.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorders associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, and cotal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful disorder: The present oligonucleotide was used in an example from the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotide which down regulates expression of Ets-related gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; hammerhead ribozyme, cytostatic, antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour andiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tubercous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ERG hammerhead ribozyme target sequence, Seq ID No 555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 13.8; DB 1; Length 17;
Pred. No. 1.2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Von Carlowitz I, Mcswiggen JA, Mclaughlin F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 4 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
for treating subjects having defects in HTPL.
                                           Example 2; Page 212; 718pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1457 TTGATCAAGCAAATAGG 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK17908 standard; RNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAY-2001; 2001WO-US015866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAY-2000; 2000US-00572021.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.6%;
88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-082995/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200188124-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amberzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jarvis T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK17908;
  à
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Magnoliophyta Quercus; ss. 29-JAN-2004 Matches à g

conditions selected from cancer, lynphoma, Ewing's sarcoma, melanoma, theory and in the cancer, lynphoma, Ewing's sarcoma, melanoma, theory and conditions selected from cancer, lynphoma, Ewing's sarcoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, variation, architis, psoriasis, verruca vulgaris, angiofibroma of tuberous solerosis, port-wine stains, Sturge Weber syndrome, Rippel-Trenaunay-Weber syndrome, Osler-Weber-rendu syndrome, leukemia, osteoporosis and wound healing. [1] is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with [1] under conditions suitable for the treatment. Leukemia or tumour the reatment. The method comprises the use of one or more therapies under conditions suitable for the treatment. Leukemia or tumour conditions suitable for the treatment. Leukemia or tumour conditions with one or more of other therapies such as radiation or chemotherapy treatment. [1] is useful for reducing ERG activity in a coll. by contacting (1) with RNA, in the pateence of a divalent cation such as Mg2+. [1] is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations with RNG and as diagnostic tool to the presence of ERG RNA in a cell. [1] is useful for specifically cancering genes that share homology with ERG gene or ERG fusion genes. ABKI7319 represent nucleic acid molecules which regulate expression of ERG, and enarmatic nucleic acid molecules acid significance of ERG, and enarmatic nucleic acid molecules acid significance of ERG, and enarmatic nucleic acid molecules acid significance of ERG, and enarmatic nucleic acid molecules acid significance of ERG, and enarmatic nucleic acid molecules acid cide enarmatic nucleic acid molecules acided enarmatic mucleic acid molecules acided enarmatic nucleic acid molecu The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome. Claim 4; Page 69; 149pp; English.

.. 0 10.6%; Score 13.8; DB 1; Length 17; 58.8%; Pred. No. 1.2e+02; cive 5; Mismatches 2; Indels Sequence 17 BP; 3 A; 3 C; 6 G; 0 T; 5 U; 0 Other; 1414 TGATGACCAGTCGTTCT 1430 1 UGAGGACCAGUCGUUGU 17 10; Conservative Query Match Best Local Similarity

plant growth; plant growth trait modulation; Brassicaceae; Arabidopsis; Brassica; Zea; Oryza; Triticum; Hordeum; Lolium; Sorghum; Glycine; Medicago; Helianthus; Lactuca; Beta; Vitis; Solanum; Lycopersicon; Capsicum; Gossypium; Hevea; Linum; Prunus; Citrus; Populus; Pinus; Plant growth associated polynucleotide seq id 205. 230/c ADE25230 standard; DNA; 17 BP. (first entry)

US2003188343-A1.

02-OCT-2003.

09-JAN-2002; 2002US-0347288P.

07-JAN-2003; 2003US-00338777.

(LYNX-) LYNX THERAPEUTICS INC

Haudenschild CD, Buckler ES; WPI; 2003-803305/75. Bowen BA,

ö New isolated or recombinant polypeptide for use in modulating a plant growth trait in a flowering plant e.g. in Arabidopsis, Brassica, Zea, Oryza.

English NO 205; 81pp; 2; SEQ ID Example

The invention describes an isolated or recombinant polypeptide (I) the invention describes an isolated or recombinant polypeptide (I) the specification, or a conservative variant; (b) encoded by 1 of 30 sequences (S2), as given in the specification, or a conservative variant; (c) encoded by a sequence that hybridises under stringent conditions to S2; and (d) encoded by a sequence to \$\frac{1}{2}\$ independent of \$\frac{ primer, probe or genetic marker.

Sequence 17 BP; 6 A; 5 C; 1 G; 5 T; 0 U; 0 Other;

ö Gaps ö 10.6%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 1.2e+02; Live 0; Mismatches 2; Indels Conservative Query Match Best Local Similarity Matches 15; Conserv

1446 TGGAAGATGGGTTGATC 1462 TGGAAGATGATTTGATC 1 17 셤 ò

BP ACA96828 standard; DNA; 18 (first entry) 24-JUL-2003 ACA96828; ACA96828

RESULT 25

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Gaps

Human; glial cell derived neurotrophic factor; GDNF; PCR; primer; ss; Human glial cell derived neurotrophic factor (GDNF) PCR primer #22

nervous system disease.

Homo sapiens JN1364812-A.

21-AUG-2002.

11-JAN-2001; 2001CN-00107450.

11-JAN-2001; 2001CN-00107450.

(YISH-) YISHENG BIOLOGICAL PHARM CO LTD SHUHAI.

Feng H; Zheng Z, Zhou S,

WPI; 2003-000523/01.

Human glial cell derived neurotrophic factor and its derivatives and use. Claim 6; Page 3 (Claims); 28pp; Chinese. The invention relates to the human glial cell derived neurotrophic factor (GDNF) and its derivatives and use. The invention also relates to a method of obtaining DNA encoding human glial cell derived neurotrophic factor or its active segments and a method of purifying and fining coarse GDNF. A composition comprising human glial cell derived neurotrophic factor and a medicinal acceptable carrier can be used in the treatment of

(first entry)

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Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
                                                                                                                                                                                                                                                                           Cyclin Al ribozyme binding site #63.
  2 CACAGGAGGTAAAACTG 18
                                                                                                                          AAA85441 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                          WO200032765-A2.
                                                                                                                                                                                                                          04-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ71553;
                                                                                                                                                                           AAA85441;
                                                                                                                                                                                                                                                                                                                                                                         Mammalia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tritz R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ71553,
                                                                           RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the novel human nucleic acid encoding an epithelial stromal interaction 1 (EPSTI1) polypeptide. The protein of the invention has cytostatic activity. The polynucleotide may have a use in gene therapy. The methods and compositions of the present invention utilising the EPSTI1 gene are useful for the diagnosis and prognosis of cancer, in particular metastatic cancer of the breast, placenta, lymphoid tissue, ovary, testis, thymus, lung, stomach, small intestine, colon, pancreas, spleen, skin or extracellular body fluids. The oligonucleotides are used in the treatment of the above. The sequences shown in ABZ75438-ABZ75457 represent splice donor/acceptor sites at the exon boundaries of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated EPSTII nucleic acid molecule upregulated upon direct interaction between tumor and stromal cells, useful for the diagnosis and prognosis of breast, ovarian, lung, stomach, colon, pancreatic, spleen and skin cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; epithelial stromal interaction 1; BPSTI1; cytostatic; cancer; gene therapy; metastatic cancer; breast; placents; lymphoid tissue; ovary; testis; thymus; lung; stomach; small intestine; colon; pancreas; spleen; skin; exon; splice acceptor; splice donor; ds.
                                                                                                                                                                              Gaps
nervous system diseases. Sequences ACA96807-ACA96859 represent PCR primers used to amplify human GDNF CDNA
                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.6%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 1.3e+02; ive 0; Mismatches 2; Indels
                                                                                                                       Length 18;
                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 BP; 8 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
                                                                        Sequence 18 BP; 3 A; 3 C; 5 G; 7 T; 0 U; 0 Other;
                                                                                                                       Score 13.8; DB 1;
Pred. No. 1.3e+02;
                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Petersen LR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 40; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human EPSTI1 exon 9 splice donor.
                                                                                                                                                                                                                          1410 TTAATGATGACCAGTCG 1426
                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-JUL-2001; 2001DK-00001074.
22-APR-2002; 2002DK-00006601.
                                                                                                                    10.6%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUL-2002; 2002WO-DK000478
                                                                                                                                                                                                                                                                                                                                                                                                     ABZ75456 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Petersen OW, Nielsen HL,
                                                                                                                                                                           15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the human EPSTI1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-221745/21.
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Best Local Similarity
                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABZ75456;
                                                                                                                       Query Match
                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                 RESULT 26
ABZ75456
ABZ7546
AB
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                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.

Representative examples of ribozyme recognition sites are given in AAA88215 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in
                                                                                                                                                                                                                                          cleaves
                                                                                                                                                                                                                                     New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PCNA and Cyclin B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human biallelic marker upstream amplification primer SEQ ID NO:5909.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome, biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; dentification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.6%; Score 13.8; DB 1; Length 19; 88.2%; Pred. No. 1.4e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19 BP; 6 A; 3 C; 4 G; 6 T; 0 U; 0 Other;
                                                                                                                                           Robbins JM;
                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 92; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1452
                                                                                                                                           Barber JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13
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99WO-US028772.
                                            98US-0110954P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1436 GACATATACATGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GACATCTACATGGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ71553 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.6
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restenosis treatment
                                                                                                                                           Welch PJ,
                                                                                            (IMMU-) IMMUSOL INC.
                                                                                                                                                                                        WPI; 2000-412314/35
                                               04-DEC-1998;
06-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-SEP-2001
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Gaps

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1393 CAAAGGAGGTAAATTG 1409

Conservative

15;

Matches

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schultz911-3.rng

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AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ740 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and dispostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment.

N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 327, 3297 and
                                                                                                                                                                                                                                                                                                     Novel biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19 BP; 2 A; 3 C; 4 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                     Chumakov I;
                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Page 1490; 2745pp; English
                                                                                                        99WO-IB000822
                                                                                                                                           98US-0082614P
                                                                                                                                                            98US-0109732P
                                                                                                                                                                                                                                     Cohen D, Blumenfeld M,
                                                                                                                                                                                                                                                                                                                            map of the human genome
                                                                                                                                                                                                                                                                       WPI; 2000-013267/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention
                                                                                                                                                                                                (GEST ) GENSET
 Homo sapiens
                                WO9954500-A2
                                                                                                        21-APR-1999;
                                                                                                                                           21-APR-1998;
                                                                                                                                                                23-NOV-1998;
                                                                    28-OCT-1999.
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0, Gaps
Query Match 10.6%; Score 13.8; DB 1; Length 19; Best Local Similarity 88.2%; Pred. No. 1.4e+02; Matches 15; Conservative 0; Mismatches 2; Indels
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1354 GAAAATATTCCACGCA 1370 19 GAAAATAGTACACGCA 3 ò ద

AAH60603 standard; DNA; 19 BP 10-SEP-2001 (first entry) AAH60603;

Cyclin Al ribozyme binding site SEQ ID NO:3027.

Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnerary; prolliferative disease; skin disease; psoriasis; diabetic retinopathy; cytokine; inflammation; cell-cycle dependent kinase; cyclin; MWP; matrix metalloproteinase; growth factor; reductase; scarring; cytostatic; antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide; antisickling; ophthalmological; keraclolytic; gene therapy; viral wart; atopic dermatitis; actinic keratosis; squamous cell carcinoma; basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar; sickle cell retinopathy; ss.

Homo sapiene Synthetic.

The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme (1) which cleaves RNA encoding a cytckine involved in inflammation, matrix metalloproteinase (MME), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid segment encoding (1). (1) can have antipsoriatic, erratological, cytostatic, antiseborrheic, antidiabetic, antisickling, dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling, coptibalmological, vulnerary, keratolytic and vincide activities, and cleaves RNA encoding cytokine involved in inflammation. (1) can be used in gene therapy. (1) and (II) are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing scarring such as keloid, adhesion and hypertrophic or hypertrophic burn and some and in the Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases. Sequence 19 BP; 6 A; 3 C; 4 G; 6 T; 0 U; 0 Other; exemplification of the present invention Example 1; Page 292; 408pp; English. 26-OCT-2000; 2000WO-US029500. 99US-0161532P. Tritz R; WPI; 2001-300427/31. (IMMU-) IMMUSOL INC. WO200130362-A2. 26-OCT-1999; 03-MAY-2001 Robbins JM,

10.6%; Score 13.8; DB 1; Length 19; 88.2%; Pred. No. 1.46+02; tive 0; Mismatches 2; Indels Local Similarity

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Gaps ö

> 1436 GACATATACATGGAAGA 1452 GACATCTACATGGATGA 19 ð 셤

15; Conservative

Matches

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AAV93431 standard; RNA; 17 BP. AAV93431; RESULT 30 AAV93431

Human B-raf substrate nucleotide position 906. 18-FEB-1999 (first entry)

Human, c-raf, A-raf, B-raf, hammerhead ribozyme; hairpin ribozyme; target, substrate, catalyst, modulation; expression; Raf gene, delivery; screening; identification; synthesis, deprotection; purification; cancer; inflammation, psoriasis; non-heatic ascites; infection; genetic drift; restenosis; rheumatoid arthritis; ss.

Homo sapiens

WO9850530-A2.

12-NOV-1998.

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Parry T, Beigelman L, Mcswiggen JA, Karpeisky A,
Thompson J, Workman CT, Beaudry A, Sweedler D;
                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 6 A; 3 C; 2 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human B-raf substrate nucleotide position 905.
                                                                                                Jarvis T, Matulic-Adamic J, Reynolds M,
                                                                                                                                                                                Claim 177; Page 167; 259pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                1408 TGTTAATGATGACCA 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV93430 standard; RNA; 17 BP
                     97US-0051718P.
97US-0051718P.
97US-0056808P.
                                           97US-0061321P.
97US-0061324P.
97US-0064866P.
98WO-US009249
               97US-0046059P
                                                                  97US-0068212P
                                                                                                                                                                                                                                                                                                                                                                                                         1 UGUUAAUUAUGACCA 15
                                                                                 (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                            WPI; 1999-009494/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-1999
                                           02-OCT-1997;
02-OCT-1997;
05-NOV-1997;
05-MAY-1998;
                                                                  19-DEC-1997;
                            03-JUL-1997
              09-MAY-1997
                       09-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV93430;
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 31
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capable of modulating a process in a biological system. The method comprises: (a) introducing into the system a random library of nucleic acid catalysts (NAC) having a substrate binding domain (SBD), comprising a random sequence, and a catalytic domain (CD); and (b) identifying NAC in systems where modulation has occurred and/or determining the sequence of at least part of the SBDs in such systems. Nucleic acid molecules with conditionable activity from the present invention, are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepptic actives and infection. They may also be used to detect genetic drift and mutations in diseased cells and to determine c-raf RNA. Specifically NAC with RNA-cleaving activity that modulate expression of the Raf gene, are consect to treat cancer, restences, psoriasis or rheumatoid arthritis, or used to treat cancer, restences, with the level of c-raf. Introduction of sugar/phosphate modifications increases stability against nuclease and context and processed with the level of c-raf. Introduction associated with the level of c-raf. Introduction context of an expression of the cataly any condition associated with the level of c-raf. Introduction approximately and processes are activity. ANYOSO22 to AANYOSATY represent NACS that can be used in the context of an expression of the catalogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying new catalytic nucleic acid that modulates selected processes -especially ribozymes that cleave Raf RNA for treating cancer, restenosis, and also new ribozymes and modified nucleoside triphosphates used as antiviral agents and synthons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity. AAV90922 to AAV93877 represent NACs that can be used in the method, specifically for modulating the expression of a Raf gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A method has been developed for the identification of a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ERG hammerhead ribozyme target sequence, Seq ID No 554.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kisich K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K,
Parry T, Beigelman L, Mcswiggen JA, Karpeisky A,
Thompson J, Workman CT, Beaudry A, Sweedler D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 177; Page 167; 259pp; English.
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97US-005171BP.
97US-005680BP.
97US-0061321P.
97US-0064866P.
97US-0068212P.
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UGUUAAUUAUGACCA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RIBO-) RIBOZYME PHARM INC.
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I, Workman CT,
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Best Local Similarity
Homo sapiens.
                                                        WO9850530-A2.
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                                                                                                                12-NOV-1998
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XEXEXEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amethod has been developed for the identification of a nucleic acid
capable of modulating a process in a biological system. The method
comprises: (a) introducing into the system a random library of nucleic
acid catalysts (NAC) having a substrate binding domain (SBD), comprising
acid catalysts (NAC) having a substrate binding domain (SBD), comprising
acid catalysts (NAC) having a substrate binding domain (SBD), comprising
acid catalysts (NAC) having a substrate binding domain (SBD), comprising
at least part of the SBDs in such systems. Nucleic acid molecules with
conditions activity, and catalytic activity, from the present invention,
are used to modulate gene expression in plant and mammalian cells and to
cleave target nucleic acid, particularly for treating systemic diseases
caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepstic
ascites and infection. They may also be used to detect genetic drift and
untations in diseased cells and to determine craf RNA. Specifically NACs
with RNA-clearing activity that modulate expression of the Raf gene, are
used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
cused to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
cused to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
cused to treat modifications increases stability against nuclease and
activity. AAV90922 to AAV38377 represent NACs that can be used in the
customy appearance of supering the expression of a Raf gene
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target; substrate; catalyst; modulation; expression; Raf gene; delivery;
screening; identification; synthesis; deprotection; purification; cancer;
inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
restenosis; rheumatoid arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying new catalytic nucleic acid that modulates selected processes - especially ribozymes that cleave Raf RNA for treating cancer, restenosis, and also new ribozymes and modified nucleoside triphosphates used as antiviral agents and synthons.
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Bellon L; Burgin A;

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Gaps

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Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme; detection; mutation; anti-HIV drug resistance; polymorphism; resistance;

Human immunodeficiency virus 1.

probe; ss.

WO200255741-A2.

Synthetic

18-JUL-2002

11-JAN-2001; 2001EP-00870005. 20-APR-2001; 2001EP-00870085. 24-APR-2001; 2001US-0286102P.

(INNO-) INNOGENETICS NV

Stuyver L;

De Smet K,

WPI; 2002-590680/63.

09-JAN-2002; 2002WO-EP000153

HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:357.

(first entry)

31-JAN-2003

ABZ34115;

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The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, conditions selected from cancer, lymphoma, arthritis, psoriasis, verruca tumour angiogenesis, diabetic retinopathy, macular degeneration, neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca continue, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (I) to the patient in conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or callon such as Mg2+. (I) is useful for reducing ERG activity in a cell, by contacting the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RMA in a cell. (I) is useful for claving such as the stare homology with ERG gene or ERG fusion genes. ABK17354-ABK22719 represent nucleic acids, including antisense and cargatical propertion of the expression of ERG, and expression of ERG, and enzymatic nucleic acide which regulate expression of ERG, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polynucleotide which down regulates expression of Ets-related gene, useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofizoma of tuberous sclerosis; port.wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mcswiggen JA, Mclaughlin F, Randi AM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAY-2001; 2001WO-US015866.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Von Carlowitz I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RIBO-) RIBOZYME PHARM I.
(GLAX ) GLAXO GROUP LTD.
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                                                                                                                                                                                                                                                                               Homo sapiens.
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        %XCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCX
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detecting at least one of the mutations in the HIV reverse transcriptase gene by using probes optimized to function together in a reverse-hybridization assay.

Claim 2; Page 25; 117pp; English.

Detecting mutations associated with anti-HIV drug resistance comprises

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The present invention describes a method for detecting mutations associated with anti-HIV drug resistance in a patient by detecting at associated with anti-HIV drug resistance in a patient by detecting at least one of the mutations K103N/R, V106A/I/L, V18IC/I, M184V/I, V18BL, G190A/S/R, T215Y/F/D/S/A and/or C151M/L in the reverse transcriptase (RT) of HIV strains in a biological sample using a specific set of probes optimised to function together in a reverse-hybridisation assay. The method and the nucleic acid sequences used in the method are useful for determining viral mutations and/or polymorphisms in the HIV RT gene associated with resistance. The probes are useful for the genetic detection, preferably in vitro detection of the mutations K103N/R, V106A/I/L, X181C/I, O151M/L, M184VI, Y188L, G190A/S/R and/or T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the mutation is associated with anti-HIV drug resistance. The method provides a rapid, reliable and precise assay or determination and monitoring of a rapid, reliable and precise assay or determination and monitoring of a rapid, and probes which are used in the exemplification of the present in the present in the area of the present in the area of the present in the semplification of the present in the semplification of the present in the area of the present in the semplification of the present in the semination in the exemplification of the present in the seminary in the seminary in the exemplification of the present in the seminary 
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10.3%; Score 13.4; DB 1; Length 17; 66.7%; Pred. No. 1.46+02; ive 4; Mismatches 1; Indels
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Best Local Similarity
Matches 10; Conserv
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10.3%; Score 13.4; DB 1; Length 17;
llarity 93.3%; Pred. No. 1.4e+02;
Conservative 0; Mismatches 1; Indels
                                                                                                                      ABZ34117 standard; DNA; 17 BP.
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                                            1441 ATACATGGAAGATGG
                                                                3 ATACATGGACGATGG
           Similarity
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Local S...
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                       Matches
                                                                                                RESULT 34
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1414 TGATGACCAGTCGTT 1428

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10; Conservative

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ABZ34115 standard; DNA; 17

RESULT 33 ABZ34115 ID ABZ

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Gaps

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AAD56453 standard; DNA; 17
                                                                     (INNO-) INNOGENETICS NV
                                                                                  WPI; 2002-590680/63.
                                                                                                   hybridization assay.
                                                                                                                                                                                     Query Match
Best Local Similarity
                                    WO200255741-A2.
                                                                                                                                                                                                                                       07-AUG-2003
                                           18-JUL-2002.
                                                                            De Smet K,
                    probe; ss.
                                                                                                                                                                         invention
                             Synthetic
                                                                                                                                                                                                                                 AAD56453;
                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                       AAD56453,
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/note = "Bases 9 and 10 are linked by butanediol linker which is represented as B in page 49 and X in page 54 and 64 of the specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel acyclic linker-containing oligonucleotide useful for preventing decreasing translation, reverse transcription and/or replication of a target RNA in a system, comprises a modified deoxyribonucleotide.
                  gene expression; gene therapy; ribonuclease; RNase H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mod_base= OTHER
/note= "2'-deoxy-2'-fluoroarabinothymidine"
                                                                                                                                                                             /mod_base= OTHER
/note= "2'-deoxy-2'-fluoroarabinothymidine"
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/note= "2'-deoxy-2'-fluoroarabinoadenosine"
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/note= "2'-deoxy-2'-fluoroarabinothymidine"
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/note= "2'-deoxy-2'-fluoroarabinoadenosine"
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/note= "2'-deoxy-2'-fluoroarabinothymidine"
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/note= "2'-deoxy-2'-fluoroarabinothymidine"
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/note= "2'-deoxy-2'-fluoroarabinocytidine"
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                                                                                                                   Location/Qualifiers
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                Acyclic linker;
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                                       antisense; ss.
                                                                                                                   Key
modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Damha MJ,
The present invention describes a method for detecting mutations associated with anti-HIV drug resistance in a patient by detecting at least one of the mutations K1030/R, V1064/I/L, V181C/L, M184V/I, V181BL, C190A/S/R, T215Y/F/D/S/A and/or C151M/L in the reverse transcriptase (RT) of HIV strains in a biological sample using a specific set of probes optimised to function together in a reverse hybridisation assay. The method and the nucleic acid sequences used in the method are useful for determining viral mutations and/or polymorphisms in the HIV RT gene associated with resistance. The probes are useful for the genetic detection, preferably in vitro detection of the mutations K103N/R, C106A/I/L, V131C/I, O151M/L, M184V/I, Y188L, G190A/S/R and/or T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the mutation is associated with anti-HIV drug resistance. The method provides a rapid, reliable and precise assay or determination and monitoring of a rapid, rallable and precise assay or determination and monitoring of a rapid, rallable successive mutations associated with drug resistance of antivitation and monitoring of viruses containing RT genes. ABZ34542 represent HIV RT sequences and probes which are used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting mutations associated with anti-HIV drug resistance comprises detecting at least one of the mutations in the HIV reverse transcriptase gene by using probes optimized to function together in a reverse-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2'F-ANA antisense oligo #8, to elicit RNase H degradation of target RNA.
                                                                             Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme; detection; mutation; anti-HIV drug resistance; polymorphism; resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                       HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 17 BP; 6 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 25; 117pp; English.
                                                                                                                                                          Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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                                                                                                                                                                                                                                                                                                                                      11-JAN-2001; 2001EP-00870005.
20-APR-2001; 2001EP-00870085.
24-APR-2001; 2001US-0286102P.
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31-JAN-2003 (first entry)
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                                                                                                                                  degradation of target RNA. This sequence is used in the exemplification
They are useful for selectively preventing gene expression in a sequence-specific manner, for hybridising to complementary RNA such as cellular mRNA or viral RNA, to hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is an antisense oligo used to elicit human RMsse (ribonuclease)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/note= "aases 9 and 10 are linked by a butanediol linker
which is represented as B in page 49 and X in page 60,
Fig 3 and 4 of the specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          decreasing translation, reverse transcription and/or replication of a target RNA in a system, comprises a modified deoxyribonucleotide.
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAT antisense oligo #2, to elicit RNase H degradation of target RNA
                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                             10.3%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 1.46+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Min K;
                                                                                                                                                                                         Seguence 17 BP; 2 A; 4 C; 0 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parniak MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mangos MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Fig 3; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD56443 standard; DNA; 17 BP.
                                                                                                                                                                                                                                                                                                        1348 GGGGAAGAAAATAT 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29~OCT-2002; 2002WO-CA001628.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                  14; Conservative
                                                                                                                                                                                                                                                                                                                                           GGGAAAGAAAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viazovkina E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-421516/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYMC-) UNIV MCGILL
                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                        the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003037909-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antisense; ss
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                                                                                                                                                                                                                             Query Match
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The present invention describes a method for detecting mutations associated with anti-HIV drug resistance in a patient by detecting at associated with anti-HIV drug resistance in a patient by detecting at least one of the mutations K103N/R, V106A/I/L, Y181C/I, M184V/I, Y18BL, C G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT) of HIV strains in a biological sample using a specific set of probes optimised to function together in a reverse-hybridisation assay. The method and the nucleic acid sequences used in the method are useful for determining viral mutations and/or polymorphisms in the HIV RT gene associated with resistance. The probes are useful for the genetic detection, preferably in viro detection of the mutations K103N/R, C106A/I/L, Y181C/I, Q151M/L, M184V/I, Y18BL, G190A/S/R and/or C151SY/F/D/S/A in the RT of HIV strains in a biological sample, where the mutation is associated with anti-HIV drug resistance. The method provides a rapid, reliable and precise assay or determination and monitoring of a rapid, reliable and precise assay or determination and monitoring of a rapid, reliable such are used in the exemplification of the present exemplification of the present
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sequence is an antisense oligo used to elicit human RNase (ribonuclease) H degradation of target RNA. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting mutations associated with anti-HIV drug resistance comprises detecting at least one of the mutations in the HIV reverse transcriptase gene by using probes optimized to function together in a reverse-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme; detection; mutation; anti-HIV drug resistance; polymorphism; resistance;
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:358.
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                                                                                                                             10.3%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 1.4e+02; tive 0; Mismatches 1; Indels
                                                                                          Sequence 17 BP; 2 A; 4 C; 0 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 25; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus 1.
                                                                                                                                                                                                               1348 GGGGAAGAAAATAT 1362
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20-APR-2001; 2001EP-00870085.
24-APR-2001; 2001US-0286102P.
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                                                                                                                                                                                                                                                                                                                                                        ABZ34116 standard; DNA; 18
                                                                                                                                                                                                                                                     17 GGGAAAGAAAATAT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                         Query Match
Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stuyver L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-590680/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hybridization assay.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probe, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                ABZ34116;
                                                                                                                                                                                                                                                                                                                RESULT 37
                                                                                                                                                                                                                                                                                                                                       ABZ34116
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AAT80036-T80041 represent amplification primers for the alpha2 integrin coding sequence. The primers represented in AAT80030-T80035 are used for the amplification of the alpha1 integrin coding sequence. These sequences can be used in the method of the invention. The method of the invention of a mammal having, or at risk of devaloping, is for the identification of a mammal having, or at risk of devaloping, and and a contain cells expressing integrin RNA or protein for integrin subunit expression. The integrin subunit expression in the ample is then compared with a control tissue sample, where altered integrin subunit expression is correlated with glomerulopathy. The method can be modified to identify a mammal with diabetes who has, or is at risk of developing, secondary pathological changes associated with diabetes. An increase in alpha1 expression is diagnostic of increased risk of nephropathy. The methods can be used to determine if patients are likely to develop severe nephropathy and to monitor progress of disease during treatment protocols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detection of nephropathy in mammals - by comparing integrin subunit expression in a tissue sample compared to a control tissue sample.
                                                                                                                                                                                                                                                                                                                                                                                        PCR; polymerase chain reaction; primer; amplify; alphal integrin; alpha2 integrin; glomerulopathy; diabetes; nephropathy; ss.
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                                              Query Match 10.3%; Score 13.4; DB 1; Length 18; Best Local Similarity 93.3%; Pred. No. 1.5e+02; Matches 14; Conservative 0; Mismatches 1; Indels
              Sequence 18 BP; 6 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 BP; 3 A; 4 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mauer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Setty S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 6; Page 35; 73pp; English.
                                                                                                                                                                                                                                              ВР.
                                                                                                                    1441 ATACATGGAAGATGG 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0001387P.
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AAT80036 standard; cDNA; 18
                                                                                                                                                       4 ATACATGGACGATGG 18
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                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                    Alpha2 integrin primer #1.
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02-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                AAT80036;
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The invention provides a new method for identifying and characterising cells. The method for determining the genetic proximity of a first cell and a second cell comprises: (a) obtaining the first cell and the second cell; (b) determining in the first cell and the second cell; (b) determining in the first cell and the second cell; (b) determining in the first cell and (c) calculating a cell; (b) determining a specified formula. The methods can be used for characterising cells, e.g. for determining the origin of a cell; its characterising cells, e.g. for determining the origin of a cell; its cransformed. They can be used for determining the origin of a selected treatment on a test cell. They can also be used for effect of a selected treatment on a test cell. They can also be used for obtaining cells capable of expressing an homeobox related desired property. The method uses reverse transcriptase polymerase chain reaction (RT-PCR) for determining the pattern of gene expression in a selected con the RT-PCR reactions to determine the pattern of gene expression. The gene family can be selected from a set of homeobox genes, kinase genes, protein phosphatase genes, P450 enazyme genes, steroid receptor protein phosphatase genes, P450 enazyme genes, steroid receptor con protein phosphatase genes, P450 enazyme genes, steroid receptor
                                                                                                                                                                                                                                                             Genetic proximity; gene expression; cell characterisation; homeobox gene; genetic defect; reverse transcriptase polymerase chain reaction; RT-PCR; kinase gene; protein phosphatase; P450; steroid receptor; cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying and characterizing cells by comparing the pattern of gene expression in a selected gene family.
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                                                                                                                                                                                                                      RT-PCR primer specific for homeobox gene groups.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 30; 102pp; English.
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18 CAGACATCAACATGGATG 1
                                                                                                 AAZ17884 standard; DNA; 18 BP
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98IL-00126627.
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                                                                                                                                                                              11-OCT-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                          primer; 88
                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                        AAZ17884;
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Best Local Similarity

Matches

Query Match

1434 CAGACATATACATGGAAG 1451

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Genetic proximity, gene expression; cell characterisation; homeobox gene; genetic defect; reverse transcriptase polymerase chain reaction; RT-PCR; kinase gene; protein phosphatase; P450; steroid receptor; cadherin;

98WO-IL000625 97IL-00122793. 98IL-00126627.

28-DEC-1998; 29-DEC-1997; 16-OCT-1998;

WO9934016-A2. Homo sapiens

primer; ss. Synthetic. 08-JUL-1999

RT-PCR primer specific for homeobox gene groups.

11-OCT-1999 (first entry)

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Genetic proximity, gene expression, cell characterisation, homeobox gene, genetic defect, reverse transcriptase polymerase chain reaction, RT-PCR, kinase gene, protein phosphatase, P450, steroid receptor, cadherin,
                                                                                                                                                                                                                                                                         Identifying and characterizing cells by comparing the pattern of expression in a selected gene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 5 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
                                                          CNX embryonic gene OTX b specific primer.
                                                                                                                                                                                                                                                                                                  Claim 4; Page 39; 102pp; English
         AAZ18050 standard; DNA; 18 BP
                                                                                                                                                                              98WO-IL000625.
                                                                                                                                                                                              97IL-00122793
98IL-00126627
                                         (first entry)
                                                                                                                                                                                                                                                        WPI; 1999-419113/35.
                                                                                                                                                                                                                       (GENE-) GENENA LTD
                                                                                                                             Homo sapiens.
                                         11-OCT-1999
                                                                                                                                                                                            29-DEC-1997;
16-OCT-1998;
                                                                                                                                            WO9934016-A2
                                                                                                                                                                              28-DEC-1998;
                                                                                                                                                            08-JUL-1999
                                                                                                    primer; ss.
                                                                                                                   Synthetic
                         AAZ18050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                        Vider B;
AAZ18050
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The invention provides a new method for identifying and characterising

Claim 4; Page 29; 102pp; English

Identifying and characterizing cells by comparing the pattern of gene expression in a selected gene family.

WPI; 1999-419113/35.

(GENE-) GENENA LTD.

Vider B;

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cells. The method for determining the genetic proximity of a first cell and a descond cell comprises: (a) obtaining the first cell and the second cell; (b) determining in the first cell and the second cell; (b) determining in the first cell and the second cell; (b) determining the second cell the pattern of expression of genes in a selected gene family; and (c) calculating a proximity index using a specified formula. The methods can be used for characterising cells, e.g. for determining the origin of a cell; its genetic status, whether it carries a genetic defect, or whether it is can individual, e.g. a fetus. They can also be used for determining the effect of a selected treatment on a test cell. They can also be used for obtaining cells capable of expressing an homeobox related desired of superior (RT-PCR) for determining the pattern of gene expression in a selected con the RT-PCR reactions to determine the pattern of gene expression. The gene family. Sequences AAZ17803-Z18342 represent primers that can be used to the teamily can be selected from a set of homeobox genes, kinase genes, protein phosphatase genes, P450 enzyme genes, strong cenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13.2; DB 1; Length 18;
Pred. No. 1.7e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 18 BP; 5 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               superfamily genes or cadherin superfamily genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1430 TATGCAGACATATACATG 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TATCCGGACATATTCATG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ18048 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 83.3
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ18048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides a new method for identifying and characterising cells. The method for determining the genetic proximity of a first cell and a second cell comprises: (a) obtaining the first cell and the second cell the pattern cell; (b) determining in the first cell and the second cell the pattern of expression of genes in a selected gene family; and (c) calculating a proximity index using a specified formula. The methods can be used for characterising cells, e.g. for determining the method expression of genetic status, whether it carries a genetic defect, or whether it is cannot cannot not be used for determining the an individual, e.g. a fetus. They can also be used for determining the effect of a selected treatment on a test cell. They can also be used for obtaining cells capable of expressing an homeobox related desired property. The method uses reverse transcriptuses polymerase chain reaction (RT-PCR) for determining the pattern of gene expression in a selected gene family. Sequences AAZ17803-Z18342 represent primers that can be used to the RF-PCR reactions to determine the pattern of gene expression. The gene family can be selected from a set of homeobox spenses, kinase genes, protein phosphatase genes, P450 enzyme genes, steroid receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.2; DB 1; Length 18; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.2%;
83.3%;
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Matches 15; Conservative
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Gaps

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CNX embryonic gene OTX a specific primer.

11-OCT-1999 (first entry)

AAZ17882 standard; DNA; 18 BP.

RESULT 41 AAZ17882

ð g AAZ17882;

98WO-IL000625 97IL-00122793 98IL-00126627

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Integrin beta 3; human endothelial glycoprotein; GP3A; GPINa; ITGB3; CD61; platelet glycoprotein 3a; cellular adhesion; vitronectin receptor; fibronectin receptor; expression inhibition; antisense; tumour formation;
                                                                                                                                                                                                                          Identifying and characterizing cells by comparing the pattern of gene expression in a selected gene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human integrin beta 3 antisense oligonucleotide, SEQ ID NO:37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 BP; 5 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    protein phosphatase genes, P450 enzyme genes, st
superfamily genes or cadherin superfamily genes
                                                                                                                                                                                                                                                       Claim 4; Page 39; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1430 TATGCAGACATATACATG 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TATCCGGACATATTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA07064 standard; DNA; 18
                                                                                                                                                                                                        WPI; 1999-419113/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                  (GENE-) GENENA LTD
                                                                                                                       28-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUL-2000
                                                                Homo sapiens
                                                                                                                                        39-DEC-1997;
                                                                                                                                                 16-OCT-1998;
                                                                                 WO9934016-A2
                                                                                                    08-JUL-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                      primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA07064;
                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
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the human integrin beta 3 gene, which inhibit its expression. The attiseme obligonucleotides were designed to target different regions of the human integrin beta 3 RNA, and were analysed for their effect on integrin beta 3 RNA, and were analysed for their effect on integrin beta 3 RNA levels were measured as a control.

CG (glyceraldehyde-3-phosphate) RNA levels were measured as a control.

CI Integrins constitute one of four call migration, cell anchorage to and play an important role in cell migration, cell anchorage to cation-dependent membrane algoniting pathways. They are heterodimeric cation-dependent membrane (algorithms continuity in the grin beta 3 (sinck known as human endothelial glycoprotein, cation-dependent membrane (algorithms to beta subunit partner of the members of the beta-3 subfamily of integrins.

CT his family consists of the virronectin receptor (alpha-V-beta-3) and the fibronectin receptor (alpha-IIb-beta-3). Cells expressing this class of integrin can adhere to various matrix proteins and participate in various cycoadhesion-driven cellular responses. Integrin beta 3 is implicated in conditions such as vascular restenosis, excessive bone resorption, and conditions such as vascular restenosis, excessive bone resorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences AAA07035-A07074 represent antisense oligonucleotides targetted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  angiogenesis (in melanoma), tumour invasion, platelet aggregation and Glanzmann's thrombasthenia. The oligonucleotides of the invention are useful for diagnosis, prevention and treatment of conditions associated with integrin beta 3 expression, such as tumour formation, inflammation infections and the diseases mentioned above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense compound that inhibits human integrin beta3, useful e.g. for treating or preventing infection, inflammation and tumors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13.2; DB 1; Length 18;
Pred. No. 1.7e+02;
0; Mismatches 3; Indels
cancer invasion; bleeding disorder; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 BP; 6 A; 3 C; 2 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                            Monia BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 15; Col 40; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1410 TTAATGATGACCAGTCGT 1427
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                            Cowsert LM,
                                                                                                                                                                                                                                                                                                                                       (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-246189/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                       Homo sapiens.
                                                                                                                                                                                                                           25-JUN-1999;
                                                                                                                                                                                                                                                                                25-JUN-1999;
                                                                                                               US6037176-A.
                                                                                                                                                                                                                                                                                                                                                                                            Bennett CF,
                                                                                                                                                                      14-MAR-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides a new method for identifying and characterising cells. The method for determining the genetic proximity of a first cell and a second cell comprises: (a) obtaining the first cell and the second cell comprises: (a) obtaining the first cell and the second cell the pattern of expression of genes in a selected gene family; and (c) calculating a proximity index using a specified formula. The methods can be used for characterising cells, e.g. for determining the origin of a cell, its genetic status, whether it carries a genetic defect, or whether it is transformed. They can be used for detecting a selected genetic defect in an individual, e.g. a fetus. They can also be used for determining the effect of a selected treatment on a test cell. They can also be used for obtaining cells capable of expressing an homeobox related desired property. The method uses reverse transcriptase polymerase chain reaction property. The method uses reverse transcriptase polymerase chain reaction cylone family. Sequences AA217803-Z18342 represent primers that can be used in the RT-PCR reactions to determine the pattern of gene expression. The
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                       Genetic proximity, gene expression, cell characterisation, homeobox gene, genetic defect, reverse transcriptase polymerase chain reaction, RT-PCR, kinase gene, protein phosphatase, P450; steroid receptor, cadherin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene family can be selected from a set of homeobox genes, kinase genes, protein phosphatase genes, P450 enzyme genes, steroid receptor
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Gaps

3; Indels

0; Mismatches

83.3%;

Conservative

18

BP.

(first entry)

Homo sapiens

schultz911-3.rng

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Sequence 13 BP; 6 A; 3 C; 1 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2001; 2001WO-IB000713.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1356 AAATATTCCACG 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABF73482 standard; DNA; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-657177/75.
WPI; 2001-657177/75
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200177384-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABF73482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             olek A,
                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligoners described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                       of oligonuclectides, useful for diagnosis and cell typing, is igned to detect single-nuclectide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide SEQ ID NO 173480 for detecting SNP TSC0043213.
                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 237046; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.0%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13 BP; 6 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. .v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                            Berlin K;
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                                                                                                                                                                                                                                                                        methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cortral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 173480; 29pp + Sequence Listing; German.
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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 -ABC9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI0010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_per_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 1.2e+02;
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100.0%; Pred. No. ...
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ABH37068
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The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDF). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                  Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
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Pred. No. 1.7e+02;
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100.0%; Pred. No. 1...
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                                                                                     AAF03083 standard; DNA; 17 BP
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10.0%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels

13; Conservative

Query Match Best Local Similarity Matches 13; Conserva

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The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, ERR3/COUP-TF-1, the GATA transcription factor gene, IRR-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropojetin, granulocyte colony stimulating factor protein and interferon alpha
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 useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
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Pred. No. 1.7e+02;
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                                            Claim 37; Page 87; 164pp; English
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Best Local Similarity
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Matches 13; Conserv
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AAF03079/c
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                                                                                                                                                                                                                                                                                                                                                                               factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoletin, granulocyte colony stimulating factor protein and interferon alpha
                                                                                                                                                                                                                                                Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                                                                                                                                                                                                                                                                                                    The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
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Pred. No. 1.7e+02;
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100.0%; Prev
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Best Local Similarity 100.
Matches 13; Conservative
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               Homo sapiens
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                                                                      19-0CT-2000
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interferon alpha; ss.
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                                                                                                                                                                                                                                                                 WPI; 2000-647423/62
                                                                WO200061729-A2
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                               Homo sapiens
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                                                                                                 19-OCT-2000.
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                                                                                                                                                                                                                                Blatt L,
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ACC51406
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                                                                                                                                                                                                                                                                                 Ribozyme; erythropoietin; granulocyte colony stimulating factor;
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Pred. No. 1.7e+02;
0; Mismatches 0; Indels
 Indels
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Mismatches
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100.0%; Pre
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                               1350 GGAAGAAAATAT 1362
                                                                                                                                                AAF03080 standard; DNA; 17
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 Conservative
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                                                              17 GGAAGAAAATAT
                                                                                                                                                                                                                                                                                                  interferon alpha; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zwick M,
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Best Local Similarity
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Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha
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                                                                                                                                                                                                                                                                                                                 Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
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                                                                                                                                                                                             Mcswidgen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human tumour suppressor sequence #173.
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11-APR-2000; 2000WO-US009721.
                                                               99US-0129390P.
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                                                                                                                           (RIBO-) RIBOZYME PHARM INC
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Best Local Similarity 100.
Matches 13; Conservative
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Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
target; substrate; catalyst; modulation; expression; Raf gene; delivery;
screening; identification; synthesis; deprotection; purification; cancer;
inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
restenosis; rheumatoid arthritis; ss.
           New nucleic acid sequences associated with tumor suppression, regression, apoptosis or virus resistance are useful to diagnose and treat viral disease, development of tumor cells and cell degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying new catalytic nucleic acid that modulates selected processes especially ribozymes that cleave Raf RNA for treating cancer, restences, and also new ribozymes and modified nucleoside triphosphates used as antiviral agents and synthons.
                                                                                                                with tumour suppression or regression, apoptosis or virus resistence. invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration
                                                                                                   sequence represents an isolated nucleic acid sequence associated
                                                                                                                                                                                                                                                        Length 17;
                                                                                                                                                                                                                                                                                      0; Indels
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1gen JA, Karpeisky A,
1dry A, Sweedler D;
                                                                                                                                                                                                                        Sequence 17 BP; 9 A; 2 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                        Score 13; DB 1; Le
Pred. No. 1.7e+02;
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I, Workman CT, Beaudry A,
                                                                                                                                                                                                                                           10.0%; Scc...
100.0%; Pre
                                                                     Claim 1; Page 80; 798pp; French
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97US-0049002P.
97US-0051718P.
97US-0056808P.
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97US-0068212P.
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                                                                                                                                                                                                                                                                                      13; Conservative
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Thompson J,
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02-OCT-1997
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Best Local S
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Bellon L;

Burgin A;

Claim 177; Page 147; 259pp; English

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Gaps

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Comprises: (a) introducing into the system. The method capable of modulating a process in a biological system. The method capable of modulating a process in a biological system. The method capable of introducing into the system a random library of nucleic acid catalysts (NAC) having a substrate binding domain (BD), comprising a random sequence, and a catalytic domain (CD); and (b) identifying NAC in systems where modulation has occurred and/or determining the sequence of at least part of the SBDB in such systems. Nucleic acid molecules with endonuclease activity and catalytic activity, from the present invention, are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases caused by specific acid, particularly for treating systemic diseases caused by specific acid, particularly for treating systemic diseases caused by specific acid, particularly for treating systemic diseases caused by specific acid, particularly for treations in diseased calls and to determine or araf RNA. Specifically NACs with RNA-cleaving activity that modulate expression of the Raf gene, are used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or consition associated with the level of c-raf. Introduction of sugar/phosphate modifications increases stability against nuclease and activity. AAV99922 to AAV93877 repression of a Raf gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRR-2 and/or the CART Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF03157
g
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Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human teetis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.

Human HTPL scanning oligonucleotide SEQ ID 1130.

(first entry)

03-JAN-2003

; 0

ABV79884;

BP

ABV79884 standard; DNA; 17

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Genotypic classification of bacteria, useful e.g. for diagnosis, based on variations in the sequence of the gyr and par genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel method for genotypic classification of genes gyra, and is based on the sequences of parts of at least one of the genes gyra, gyrB, parc and parE, and comparison with known sequences of these genes. The method is used to identify bacteria, including differentiation between subspecies, for analytical or diagnostic dussification, e.g. in epidemiological studies and for detection of quinolone-resistance mutations. The specified genes are (almost) universally present in bacteria; show stable sequences variations; are identical within a given strain; show smaller variations between strains of a species than between species; contain species-specific variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genotypic classification; gyrB; gyrB; parC; parE; diagnosis; detection;
epidemiology; quinolone-resistance mutant; ds.
                                                                                                                                                                                                                                                                      Gaps
granulocyte colony stimulating factor protein and
                                                                                                                                                                                                                                                                      ·.
                                                                                                                                                                             Query Match 9.8%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 1.8e+02; Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                               T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17 BP; 6 A; 3 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MERL-) MERLIN GES MIKROBIOLOGISCHE DIAGNOSTIKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterobacter sp gyrB PCR primer gyrB3 #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 46; 54pp; German.
                                                                                                            Sequence 17 BP; 10 A; 1 C; 2 G; 4
                                                                                                                                                                                                                                                                                                                                1353 AGAAAATATTCCACG 1368
                                                                                                                                                                                                                                                                                                                                                                                                         1 AGAAAAATATTTCAAG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-APR-2000; 2000WO-EP003187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-APR-1999; 99DE-01016227.
19-AUG-1999; 99EP-00116340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC82073 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fuchs-Gomez Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and are highly conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-665142/64.
                                          interferon alpha
       erythropoietin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200061796-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heisig P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC82073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRESULT 57
ID AAC82073/X
XX AAC82
XX AAC8
XX AAC8
XX Geno
XX Synti
XX Geno
XX Synti
XX Heis.
XX Heis.
XX Geno
PP Heis.
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PP Heis.
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XX AGNO
PT YARI
XX A
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2001WO-US000669. 2001WO-US000669. 2001WO-US000669. 2001US-00864761. 2001US-0327898P.

30-JAN-2001; 30-JAN-2001; 30-JAN-2001;

23-MAY-2001; 09-OCT-2001;

2001WO-US000664.

30-JAN-2001; 30-JAN-2001;

30-JAN-2001;

28-JAN-2002; 2002EP-00001167

07-AUG-2002

Homo sapiens EP1229046-A2

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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall structure organisation with the Patched protein. The shares an overall structure organisation with the Patched protein. The cothat of Patched, and is a potential tumour suppressor. HTPL gene was important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome 10pl2.1. HTPL and in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, seletal muscle or colon function. HTPL proteins and nucleic acids are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cally useful diagnostic markers and potental therapeutic agents for infertility and cancer. The present oligonucleotide was used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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0
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87.5%; Pred. No. 1.8e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 4 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clinically useful diagnostic markers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 211; 718pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1458 TGATCAAGCAAATAGG 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 rgarcgagcaaarggg 2
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Matches 14; Conserv
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Gaps

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9.8%; Score 12.8; DB 1; Length 17; 87.5%; Pred. No. 1.8e+02; live 0; Mismatches 2; Indels

1400 GGTAAATTGTTAATG 1415

14; Conservative

Local Similarity

Best Loca Matches

Query Match

17 GGTAAATTCTTAACG 2

g ò

Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL.

WPI; 2002-676582/73.

(AEOM-) AEOMICA INC

Zhan J;

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Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL.
                                                                                         Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Parched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
                                                                         Human HTPL scanning oligonucleotide SEQ ID 1132.
                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 212; 718pp; English.
                                                                                                                                                                                                                           2001WO-US000664.
2001WO-US000667.
2001WO-US000667.
2001WO-US000668.
2001WO-US000668.
                ABV79886 standard; DNA; 17 BP.
                                                                                                                                                                                                28-JAN-2002; 2002EP-00001167
                                                                                                                                                                                                                                                                                     2001US-0327898P
                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                           WPI; 2002-676582/73.
                                                                                                                                                                                                                                                                                                        (AEOM-) AEOMICA INC.
                                                                                                                                                                                                                                                        30-JAN-2001;
30-JAN-2001;
23-MAY-2001;
                                                                                                                                                           EP1229046-A2.
                                                                                                                                                                                                                             30-JAN-2001;
                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                   30-JAN-2001;
                                                                                                                                                                                                                                               30-JAN-2001;
                                                                                                                                                                                                                                                                                     09-OCT-2001;
                                                     03-JAN-2003
                                                                                                                                                                              07-AUG-2002.
                                   ABV79886;
                                                                                                                                                                                                                                                                                                                         Zhan J;
RESULT 59
        ABV79886/
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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is mapped to human chromosome 10pl2.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17 BP; 4 A; 5 C; 2 G; 6 T; 0 U; 0 Other;
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Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;
                                                                                                                                                                                                                                                                                                                                                          Randi AM;
                                                                                                        Human ERG hammerhead ribozyme target sequence, Seq ID No 36.
                                                                                                                                                                                                                                                                                                                                                          Mcswiggen JA, Mclaughlin F,
                                               ABK17389 standard; RNA; 17 BP
                                                                                                                                                                                                                                                                                      16-MAY-2001; 2001WO-US015866.
                                                                                                                                                                                                                                                                                                         16-MAY-2000; 2000US-00572021.
                                                                                                                                                                                                                                                                                                                                                          Von Carlowitz I,
                                                                                                                                                                                                                                                                                                                            (RIBO-) RIBOZYME PHARM INC. (GLAX ) GLAXO GROUP LTD.
                                                                                       (first entry)
16 TIGATCGAGCAAATGG
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-082995/11.
                                                                                                                                                                                                                                                 WO200188124-A2.
                                                                                                                                                                                                                             Homo sapiens.
                                                                                      09-APR-2002
                                                                                                                                                                                                                                                                   22-NOV-2001
                                                                                                                                                                                                                                                                                                                                                        Jarvie T,
                                                                                                                                                                                                           amberzyme.
                                                                   ABK17389;
                            RESULT 60
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The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's saccoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, tumour angiogenesis, diabetic retinopathy, macular degeneration, cundurangle and the stains, Sturge neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca cunder syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more therapies the treatment. The method comprises the use of one or more therapies conditions suitable for the treatment in conditions suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (I) to the patient in conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of of the the cell with (I). (I) is useful for reducing ERG activity in a cell, by contacting (I) with RNA, in the presence of advalent confice the presence of ERG RNA in a cell. (I) is useful for specifically cated to the expression of ERG fusion genes. ARK1314-ABK2219 represent nucleic acide, including antisense and cargamatic nucleic acide molecules which regulate expression of ERG, and cargamatic nucleic acide molecules which regulate expression of ERG, and cargamatic nucleic acide invention

Novel polynucleotide which down regulates expression of Ets-related gene, useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.

Claim 4; Page 59; 149pp; English.

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Gaps

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Score 12.8; DB 1; Length 17; Pred. No. 1.8e+02; 0; Mismatches 2; Indels

1457 TTGATCAAGCAAATAG 1472

Query Match
Best Local Similarity 87.5%;
Matches 14; Conservative

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Gaps

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The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, the covascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca unigaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge wulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge wulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge weber syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. Leukaemia or tumour conjunction with one or more of other therapies such as radiation or cell, by contacting (I) is useful for reducing ERG activity in a cell of its useful for sequence of a divadent confice such as Mg2+. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotide which down regulates expression of Ets-related gene, useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, hammerhead ribozyme, cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Ewing's sarcoma; melanom; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; encovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port. wine stain; wound healing; sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; osler-weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
   9.8%; Score 12.8; DB 1; Length 17; 56.2%; Pred. No. 1.8e+02; ive 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ERG DNAzyme target sequence Seq ID No 1391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mcswiggen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 90; 149pp; English.
                                                                                                                                                      1418 GACCAGTCGTTCTATG 1433
                                                                                                                                                                                                                                                                                                                                                                                                                       ABK18744 standard; RNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAY-2001; 2001WO-US015866.
                                                                                                                                                                                             2 GACCAGUCGUUGUUG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAY-2000; 2000US-00572021.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RIBO-) RIBOZYME PHARM INC. (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-082995/11.
Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200188124-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK18744;
                                                                                                                                                                                                                                                                                                                                                RESULT 61
                                                                                                                                                                                                                                                                                                                                                                                ABK18744

XX ABK1
XX ABK1
XX ABK1
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XX O9-1-
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The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu Syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more therapies under conditions suitable for the treatment cleukaemia or tumour angiogenesis is treated by administering (I) to the patient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; veruca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fuelon genes. ABK17354-ABK22719 represent nucleic acids, including antisense and enzymatic nucleic acid molecules which regulate expression of ERG, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Von Carlowitz I, Mcswiggen JA, Mclaughlin F, Randi AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotide which down regulates expression of Ets-related
                                                                                                                                                                                                           ö
                                                                                                                                                                 Length 17;
                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ERG DNAzyme target sequence Seq ID No 1575.
                                                                                                                      Sequence 17 BP; 3 A; 3 C; 5 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                 Score 12.8; DB 1;
Pred. No. 1.8e+02;
                                                                                                                                                                                                         5; Mismatches
                                                                                  related PCR primers of the invention
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                                                                                                                                         Query Match
Best Local Similarity 56.2.
Best Sy Conservative
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οĘ conjunction with one or more of other therapies such as radiation or chemotherapy treatment. (1) is useful for reducing ERG activity in a cell, by contacting the cell with (1). (1) is useful for cleaving RNA or soft gene, by contacting (1) with RNA, in the presence of a dividing diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (1) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes. ABK17354-ABK22719 represent nucleic acids, including antisense and related PCR primers of the invention

Sequence 17 BP; 4 A; 3 C; 7 G; 0 T; 3 U; 0 Other;

; 0 9.8%; Score 12.8; DB 1; Length 17; 88.8%; Pred. No. 1.8e+02; ve 3; Mismatches 2; Indels 1412 AATGATGACCAGTCGT 1427 68.88; Best Local Similarity 68.8 Matches 11; Conservative Query Match ò

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Gaps

2 AgudAggaccagucgu 17

ABK18743 standard; RNA; 17 RESULT 63 ABK18743

ABK18743;

(first entry) 09-APR-2002

Human ERG DNAzyme target sequence Seq ID No 1390.

Human; hammerhead ribozyme, cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; oeteopathic; vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme; amberzyme

Homo sapiens.

WO200188124-A2.

22-NOV-2001.

16-MAY-2001; 2001WO-US015866.

16-MAY-2000; 2000US-00572021.

(RIBO-) RIBOZYME PHARM INC. (GLAX) GLAXO GROUP LID.

Randi AM; Von Carlowitz I, Mcswiggen JA, Mclaughlin F, WPI; 2002-082995/11. Jarvis T,

Novel polynucleotide which down regulates expression of Ets-related gene, useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.

Claim 4; Page 90; 149pp; English.

The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, tumour angiogenesis, diabetic retinopathy macular degeneration neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge

gradrome, leukaemia, Osteoprosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more therapies under conditions suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (I) to the patient in conjunction with one or more of other therapies such as radiation or chemotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting the cell with (I). (I) is useful for cleaving RNA of ERG gene, by contacting (I) with RNA, in the presence of a divalent cation such as Mg2+. (I) is useful for diagnosis of conditions and isseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically cargeting genes that share homology with ERG gene or ERG fusion genes. ABR17354-ABK2779 represent nucleic acids, including antisense and conjunction and the expression of ERG, and called the expression of ERG, and Osler-Weber-rendu syndrome, Kippel-Trenaunay-Weber syndrome, related PCR primers of the invention

Sequence 17 BP; 3 A; 3 C; 6 G; 0 T; 5 U; 0 Other;

Gaps ö Length 17; 2; Indels 9.8%; Score 12.8; DB 1; 62.5%; Pred. No. 1.8e+02; iive 4; Mismatches 2; Query Match Best Local Similarity 62.5° Matches 10, Conservative

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ò 셤 ACC53240/

ACC53240 standard; DNA; 17 BP.

ACC53240;

27-JUN-2003 (first entry)

Human tumour suppressor sequence #2007.

ss; tumour suppressor; antitumour; cytostatic; tumour suppression; tumour regression; apoptosis; virus resistance; diagnosis; cellular degeneration.

Homo sapiens.

FR2826373-A1.

27-DEC-2002

20-JUN-2001; 2001FR-00008139.

20-JUN-2001; 2001FR-00008139.

SA. (MOLE-) MOLECULAR ENGINES LAB Tuijnder M, Telerman A, Amson R;

WPI; 2003-250498/25.

New nucleic acid sequences associated with tumor suppression, regression, apoptosis or virus resistance are useful to diagnose and treat viral disease, development of tumor cells and cell degeneration.

Claim 1; Page 503; 798pp; French.

The This sequence represents an isolated nucleic acid sequence associated with tumour suppression or regression, apoptosis or virus resistance. invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease ö

Gaps

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9.8%; Score 12.8; DB 1; Length 17; ilarity 87.5%; Pred. No. 1.8e+02; Conservative 0; Mismatches 2; Indels

1438 CATATACATGGAAGAT 1453

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Local Similarity Les 14; Conserv

Query Match Best Loca Matches 17 CATATACAGTGAAGAT

ABT37232 standard; DNA; 17 BP.

RESULT 66 ABT37232/

Sequence 17 BP; 4 A; 3 C; 3 G; 7 T; 0 U; 0 Other;

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The invention relates to a novel isolated 17 mer nucleic acid sequence, a given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence that other or the corresponding RNA. The novel isolated nucleic component of them, or the corresponding RNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, dentifying advorantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti) sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, concaining the ucclost of parameterization of parameterization of parameterization of parameterization of parameterization of parameterization of pharmaceuticals for prevention and/or treatment of viral degeneration, specifically cancer but also Alzheimer's disease and component of parameterization of pharmaceuticals for prevention and/or treatment of viral degeneration, specifically cancer but also Alzheimer's disease and components and parameterization of the expression of the 17 mer nucleic acids in parameter the polypeptides can also be used to generate antibodies, and components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polymuleotide sequence represents a tumour suppression context.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytostatic, virucide, neuroprotective, nootropic, neuroleptic, gene chip, antisense, sense, tumour, cell degeneration, cancer, Alzheimer's disease, schizophrenia, protein chip, gene therapy, tumour suppression, human fukutin, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
characterized by development of tumour cells or cellular degeneration
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                                                                           Length 17;
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                                    Sequence 17 BP; 4 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
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9.8%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 2;
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Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds.

Tuijnder M;

relerman A, Amson R, WPI; 2003-313353/30.

(MOLE-) MOLECULAR ENGINES LAB

17-SEP-2002; 2002WO-IB004208. 17-SEP-2001; 2001FR-00011978.

WO2003025175-A2. Homo sapiens

27-MAR-2003

Tumour suppression related human fukutin oligo SEQ ID No 2869.

(first entry)

12-JUN-2003

ABT37232;

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New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
                                                                                                         Disclosure; Page 368; 720pp; French.
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The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence that calignment, at least 80 % identity to the 17 mer sequence that lybridizes to them under highly stringent conditions, or the complement of alignment, or the corresponding RNA. The novel isolated nucleic caries of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti) sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the polypeptides, vectors containing the nucleic acids, cells are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and correspondent of Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression character are characy.

Sequence 17 BP; 4 A; 4 C; 1 G; 8 T; 0 U; 0 Other;

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ABT37359

ABT37359/ RESULT

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38

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The present invention relates to murine oligonucleotides (ACC62754-ACC68806), which are associated with tumour suppression, tumour reversion, apoptoesis and virus resistence. The oligonucleotides are useful as (1) as probes and primers for detecting, identifying quantifying and/or amplifying nucleic acid, e.g. as one component of a gene chip; in vitro as (anti) sense reagents; and (2) for production of recombinant polypeptides. The oligonucleotides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
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                                                                                                                                                                                                                                                                                                                                                                          Murine oligonucleotide associated with tumour supression, SEQ ID 3255
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                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds.
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9.8%; Score 12.8; DB 1;
87.5%; Pred. No. 1.8e+02;
tive 0; Mismatches 2;
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                                                                                                1396 AGGAGGTAAATTGTT 1411
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relerman A, Amson R,

WPI; 2003-441574/41.

(MOLE-) MOLECULAR ENGINES LAB

17-SEP-2001; 2001FR-00011981.

17-SEP-2002; 2002WO-IB004219.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to murine oligonucleotides (ACC62754-ACC68806), which are associated with tumour suppression, tumour reversion, apoptorsis and Virus resistence. The oligonucleotides are useful as (1) as probes and primers for detecting, identifying, quantifying and/or amplifying nucleic acid, e.g. as one component of a gene othly, in vitro as (anti) sense reagents; and (2) for production of recombinant polypeptides. The oligonucleotides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer; probe; tumour suppression; tumour reversion; apoptosis;
virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid, useful for treating vizal diseases associated with tumors and cell degeneration, also related polypeptides, antibodies
                                           Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine; tumour suppression; tumour reversion; apoptosis; virus resistance; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; ss.
               Murine oligonucleotide associated with tumour supression, SEQ ID 2064.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiviral; neuroprotective; nootropic; neuroleptic; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specifically cancer but also Alzheimer's disease and schizophrenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumour suppression/reversion associated nucleotide #2951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 BP; 6 A; 1 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 272; 738pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1390 GATCAAAGGAGGTAAA 1405
                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR ENGINES LAB
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                                                                                                                                                                                                                                                        17-SEP-2001; 2001FR-00011979.
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                                                                                                                                                                                                                                                                                                                                                                                                                     and transfected cells.
                                                                                                                                                                                                                                                                                                                        Telerman A, Amson R,
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Best Local Similarity
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                                                                                                                                                           WO2003025176-A2
                                                                                                                           Mus musculus.
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04-DEC-2003
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The invention relates to the isolation of 6327 nucleotide sequences, fragments of at least 18 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides, or the complement, or corresponding RNA, of the conclectides. The nucleotides are used as probes or primers for detecting, identifying, quantifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour cuprension or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and calls containing the vectors), the encoded polypetides and antibodies (Ab) against the polypeptide are useful for prevention and/or treatment of viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

Analysis of the expression of the nucleotides and polypeptides can and or proposes and polypeptides and and polypeptides and and probabile and and an analysis of the expression of the nucleotides can be used for diagnosis and or prognosis of these diseases. The nucleotides and polypeptides can
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                                                                                                                                                                                                              New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          potentially useful for treating diseases associated with abnormal expression of the nucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used to screen for their specific interactive molecules
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                          Disclosure; Page 377; 771pp; French.
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hes 14; Conserv
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04-DEC-2003
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Analysis of the expression of the nucleotides can be used for diagnosis and only proprides can also he was and polypeptides can also he was and polypetides can also he was also because the expression of the model of the containing the was the containing the cont
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                                                                                                                                                            New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
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                                                                                                                                                                                                                                                 Disclosure; Page 364; 771pp; French
                                                                                Tuijnder M;
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                                       (MOLE-) MOLECULAR ENGINES LAB.
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ID ADB42671 standard; DNA; 17 BP.
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17-SEP-2001; 2001FR-00011981
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(first entry)
                                                                                Amson R,
                                                                                                                       WPI; 2003-441574/41
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                                                                                Telerman A,
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04-DEC-2003
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fragments of at least 15 consecutive nucleotides of these nucleotides, a fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, or the complement, or corresponding RNA, of the nucleotides. The nucleotides are used as probes or primers for detecting, identifying, quantifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour suppression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies of viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

Analysis of the expression of the nucleotides can be used for diagnosis and be used to screen for their specific interactive molecules, containing the useful for treating diseases associated with abnormal
                                                                                     New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
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87.5%; Pred. No. 1.8e+02;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human biallelic polymorphic marker downstream primer #184.
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                                                                                                                                                                                                     Disclosure; Page 382; 771pp; French.
Tuijnder M;
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Matches 14; Conservative
Telerman A, Amson R,
                                                  WPI; 2003-441574/41.
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                                                                                                                                                                                                                                                               isolation of various biallelic polymorphic markers found in the human genome (represented in AAX10269-X12917). These primers can be used in a genome (represented in AAX10269-X12917). These primers can be used in a genome for decermining polymorphic forms in an individual for use in e.g. forensics, paternity testing pot for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular Cydrophy, Wiskott-AHdrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, uberous sclerosis, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such system, infection by pathogenic microorganisms, and characteristics such endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid conventing and such or such to produce medicaments for the treatment or encounty.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expressing a heterologous protein of interest in a double haploid homozygous transgenic Nicotiana tabacum plant silenced for Ntp303, useful
                                                                                                                                                                                                                                         AAX09121-X10268 are allele-specific oligonucleotide primers used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                      New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.8%; Score 12.8; DB 1; Length 18; 37.5%; Pred. No. 2e+02; ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 BP; 5 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                               Claim 16; Page 68; 310pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Firefly luciferase PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1452 ATGGGTTGATCAAGCA 1467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-OCT-2001; 2001EP-00203772.
05-OCT-2001; 2001US-0327003P.
19-APR-2002; 2002EP-00076593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prophylaxis of such diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Best Local Similarity 87.5
Matches 14; Conservative
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WPI; 1998-286974/25.
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The invention describes a method of expressing a protein of interest in a plant. The method comprises providing a nucleic acid construct having a sequence that is at least 14 identical to a 173 base pair sequence, given in the specification, operably linked to a second sequence encoding a polypeptide of interest, contacting a plant with the construct, and subjecting the plant to express polypeptide, and optionally recovering the polypeptide. The method is useful for regulating translation of a second nucleotide sequence encoding a protein or polypeptide of interest, the second nucleotide sequence operably linked to the first nucleotide sequence. The methods and compositions can be used in the propagation, sexual reproduction and harvesting of transgenic N. tabacum plant. This sequence represents a primer used to isolate firstfy luciferase (luc+) for use as a reporter gene used to determine what cis-acting elements in the start of the sequence o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of isolated gene transcripts - useful for developing products for the diagnosis, prognosis and treatment of cancers, particularly colon and pancreatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX30947-31815 represent tag sequences of transcripts that are differentially expressed in colorectal cancer, in pancreatic cancer, or in both. The tag sequences can be used to identify genes by matching the tag to a gen data base member, or by using the tag sequences as probes to isolate unidentified genes from cDNA libraries. The tag sequences can also be used in a method for diagnosing colon or pancreatic cancer in a sample suspected of being neoplastic. The method comprises comparing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
for propagating, reproducing and harvesting of the transgenic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tag sequence; colorectal cancer; pancreatic cancer; colon cancer; diagnosis; prognosis; treatment; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tag sequence of a transcript increased in pancreatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12.8; DB 1; Length 18; Pred. No. 2e+02; 0; Mismatches 2; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 BP; 6 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
                                                                   24; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation regulation of the gene
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Best Local Similarity 87.5'
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-070161/06.
                                                                Disclosure; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAY-1998;
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AAV95372

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level of at least one transcript in a first sample of a tissue to a second sample, where the first sample is a colonic tissue suspected of being neoplastic and the second sample is a normal human colonic tissue. The transcript is identified by a tag selected from AAX30947-31815. The methods of the invention can be used in the diagnosis, prognosis and
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag; serial analysis of gene expression; diagnostic; prognostic; probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human nucleic acid containing specific SAGE tags, useful diagnostic markers for cancer, also derived probes.
                                                                                                                                              9.5%; Score 12.4; DB 1; Length 15; larity 92.9%; Pred. No. 1.8e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.5%; Score 12.4; DB 1; Length 15; larity 92.9%; Pred. No. 1.8e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                   Sequence 15 BP; 4 A; 1 C; 6 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Human pancreatic cancer SAGE tag #79.
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                                                                                    treatment of cancer
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                             Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer marker; ss.
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                                                                                                                                                                                                                                                                                               RESULT 76
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                                                                                                                         Human, c-fos, hammerhead ribozyme, hairpin ribozyme, target site, cancer, oncogene, leukaemia, neuroblastoma, diagnosis, genetic drift, mutation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an enzymatic nucleic acid molecule which specifically cleaves RNA derived from a c-fos gene. AAV95401 to AAV95541 to AAV95541 to Paryses tresent hammerhead ribozymes and hairpin ribozymes, respectively, which specifically cleave human c-fos. AAV95261 to AAV95400 and AAV95585 to AAV95628 represent human c-fos target sequences. The enzymatic nucleic acid molecules can be used for treating cancer associated with elevated levels of c-fos oncogene, especially leukaemias, neuroblastomas and lung, breast and colon cancers. The ribozymes may also be used as diagnostic tools to examine genetic drift and mutations within diseased cells, or to detect the presence of c-fos RNA in a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; c-fos; hammerhead ribozyme; hairpin ribozyme; target site; cancer; oncogene; leukaemia; neuroblastoma; diagnosis; genetic drift; mutation; diseased cell; ss.
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                                                                                             Human c-fos target sequence nucleotide position 1048.
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                                                                                                                                                                                                                                                                                                                                                                                                  Jarvis T, Mcswiggen JA, Stinchcomb DT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 51; 72pp; English.
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AAV95372 standard; RNA; 17
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                                                                                                                                                                                                                                                                                                                                                                  (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -fos, especially cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-427942/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                          diseased cell; ss.
                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                      WO9832846-A2
                                                                                                                                                                                                                                                                                      20-JAN-1998;
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                                                             24-FEB-1999
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Matches
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Enzymatic nucleic acid molecules which specifically cleave RNA derived from a c-fos gene - useful for treating conditions related to levels of c-fos, especially cancer.
                                                                                                                                                      The present invention describes an enzymatic nucleic acid molecule which specifically cleaves RNA derived from a c-fos gene. AAV95401 to AAV95540 and AAV95541 to AAV95544 represent hammerhead ribozymes and hairpin ribozymes, respectively, which specifically cleave human c-fos. AAV95261 to AAV95685 to AAV95628 represent human c-fos target sequences. The enzymatic nucleic acid molecules can be used for treating cancer associated with elevated levels of c-fos oncogene, especially leukaemias, neuroblastomas and lung, breast and colon cancers. The ribozymes may also be used as diagnostic tools to examine genetic drift and mutations within diseased cells, or to detect the presence of c-fos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRR-2 and/or the CAATI Displacement Protein (CPP). Inhibition of the repressors removes prevents inhibition (and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ribozyme; erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.
                                                                                                                                                                                                                                                                                                                                                                            9.5%; Score 12.4; DB 1; Length 17; 57.1%; Pred. No. 2.2e+02; tive 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                 Seguence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mcswiggen J;
   Ę,
   Stinchcomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hammerhead ribozyme substrate #1306.
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                                                                                                                            Claim 2; Page 51; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-2000; 2000WO-US009721.
                                                                                                                                                                                                                                                                                                                                                                                                                                           1423 GTCGTTCTATGCAG 1436
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF03011 standard; DNA; 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
   Mcswiggen JA,
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-647423/62.
                               WPI; 1998-427942/36
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                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 8; Conserv
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   Jarvis I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF03011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blatt L,
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                                                                                                                                                                                                                                                                  Enzymatic nucleic acid molecules which specifically cleave RNA derived from a c-fos gene - useful for treating conditions related to levels of \boldsymbol{c}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, c-fos, hammerhead ribozyme, hairpin ribozyme, target site; cancer, oncogene, leukaemia, neuroblastoma, diagnosis, genetic drift; mutation, diseased cell; ss.
                                                                                                                                                                                                                                                                                                                                                         The present invention describes an enzymatic nucleic acid molecule which specifically cleaves RNA derived from a c-fos gene. AAV95401 to AAV95540 and AAV95541 to AAV95564 represent hammerhead ribozymes and hairpin ribozymes, respectively, which specifically cleave human c-fos. AAV95261 to AAV95400 and AAV95585 to AAV95628 represent human c-fos target sequences. The enzymatic nucleic acid molecules can be used for treating cancer associated with elevated levels of c-fos oncogene, especially leukaemias, neuroblastomas and lung, breast and colon cancers. The ribozymes may also be used as diagnostic tools to examine genetic drift and mutations within diseased cells, or to detect the presence of c-fos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human c-fos target sequence nucleotide position 1051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 2 A; 5 C; 5 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                       Stinchcomb DT;
                                                                                                                                                                                                                                                                                                                             Claim 2; Page 51; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV95374 standard; RNA; 17 BP
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                                                                                         98WO-US001017
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                                                                                                                                                                        (RIBO-) RIBOZYME PHARM INC
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GUCCUUCUAUGCAG 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                     Mcswiggen JA,
                                                                                                                                                                                                                                                                                                 -fos, especially cancer.
                                                                                                                                                                                                                                     WPI; 1998-427942/36.
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Les 8; Conserv
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24-DEC-1997;
 Homo sapiens
                               WO9832846-A2
                                                                                           20-JAN-1998;
                                                                                                                         23-JAN-1997;
24-DEC-1997;
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                                                            30-JUL-1998
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                                                                                                                                                                                                     Jarvis T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV95374;
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The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoletin, granulocyte colony stimulating factor protein and interferon alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                                                                                                 Ribozyme; erythropoietin; granulocyte colony stímulating factor; interferon alpha; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erythropoietin; granulocyte colony stimulating factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.5%; Score 12.4; DB 1; Length 17; 92.9%; Pred. No. 2.2e+02; rive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 8 A; 4 C; 1 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                   Mcswiggen J;
                                                                                               Hammerhead ribozyme substrate #2256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hammerhead ribozyme substrate #1307.
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                                                            (first entry)
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interferon alpha, ss.
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                                                                                                                                                                                          Homo sapiens.
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                                                          16-FEB-2001
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                       AAF04740;
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AAF03012
ID AAF03
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consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, ERR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDF). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropojetin, granulocyte colony stimulating factor protein and interferon alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
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                                                                                                            Query Match

9.5%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels
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                                                                             Sequence 17 BP; 3 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mcswiggen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                Hammerhead ribozyme substrate #1808.
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AAF04740
ID AAF04740 standard; DNA; 17 BP.
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                                                                                                                                                                                        1382 CGTCTTCTGATCAA 1395
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Best Local Similarity 92.9
Matches 13, Conservative
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WPI; 2002-676582/73
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30-JAN-2001;
30-JAN-2001;
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09-OCT-2001;
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                                                                                                                                      The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/Or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated human testis expressed Patched like protein (HTPL), useful
                                                                             Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protein; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Human HTPL scanning oligonucleotide SEQ ID 1134.
                                                                                                                                                                                                                                                                          0; Mismatches
                                       Mcswiggen J;
                                                                                                                     Claim 37; Page 85; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                    ABV79888 standard; DNA; 17 BP
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30-JAN-2001; 2001WO-US000668.
30-JAN-2001; 2001WO-US000663.
23-MAY-2001; 2001US-00864761.
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99US-0129390P
                                      Pavco P,
                                                                                                                                                                                                                                                                                              1382 CGTCTTCTGATCAA 1395
                   (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                   CTTCTTCTGATCAA 16
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                           13; Conservative
                                                          WPI; 2000-647423/62.
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                                                                                                                                                                                                                                                                 Local Similarity
                                      Zwick M,
                                                                                                                                                                                                                interferon alpha
12-APR-1999;
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                                      Blatt L,
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specific binding partners, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                              The present invention relates to human testis expressed Patched like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17 BP; 4 A; 3 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human HTPL scanning oligonucleotide SEQ ID 1133.
identifying agonist and antagonist and sprtreating subjects having defects in HTPL.
                                                                                                                                                     Example 2; Page 212; 718pp; English
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2001WO-US000667.
2001WO-US000668.
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2001US-0327898P
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2001WO-US000664
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Best Local Similarity 92.9'
Matches 13; Conservative
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Hepatitis C virus.
                         RESULT 86
                         ACD57592
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MCSWIGGEN J. MORRISSEY D. PAVCO P. LEE P. DRAPER K. ROBERTS E MACEJAK Blatt L, M Draper K, (PAVC/) (LEEP/) (DRAP/) (ROBE/) (MORR/) %XCCCCCCCCCCCCCXXXLLLXXBXLLXXBABBBB The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two isoforms, with a few single base pair differences a premature stop codon in HTPL-5 (S for short) compared to HTPL-1 (L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall structure organisation with the Patched protein. The shares an overall structure organisation with the Patched protein. The cot that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was cappered to human chromosome lopi2.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorders associated with decreased expression or activity of human CHTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skelteal muscle or colon function. HTPL proteins and mucleic agents for male infertility and cancer. The present oligonucleotide was used in an accompletion of male infertility and cancer. The present oligonucleotide was used in an accompanian and more and the such in an accompletion of the sample from the invention . 0 Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL. Gaps .. Score 12.4; DB 1; Length 17; Pred. No. 2.2e+02; 0; Mismatches 1; Indels Seguence 17 BP; 4 A; 4 C; 2 G; 7 T; 0 U; 0 Other; Example 2; Page 212; 718pp; English. 9.5%;

1457 TTGATCAAGCAAAT 1470 15 TTGATCGAGCAAAT 2 Matches 13; Conservative Query Match Best Local Similarity

HCV DNAzyme substrate sequence #402. ACD57592 standard; RNA; 17 BP (first entry) 23-SEP-2003 ACD57592;

Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV; RNA stability; RNA expression; RNA synthesis; antisonse; enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; viral replication; degenerative, disease state; HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinmea; hepatotropic; cytostatic; virucide; antiinflammatory; substrate; ss.

08-JUN-2001; 2001US-00877478. 08-JUN-2001; 2001US-0296876P. 24-DCT-2001; 2001US-0335059P. 05-DEC-2001; 2001US-0337055P. 26-MAR-2001; 2001US-00817879. 26-MAR-2002; 2002WO-US009187 WO200281494-A1. 17-OCT-2002

(RIBO-) RIBOZYME PHARM INC. (BLAI/) BLAIT L.

The present invention relates to nucleic acid molecules which modulate
the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
Hepatitis B virus (HBV) RNN. The nucleic acid molecules include antisense
and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
c inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
are nucleic acid decoy molecules and aptamers that bind to HBV reverse
transcriptuse and/or HBV reverse transcriptuse primer sequences, as well
as oligonucleotides that specifically bind the Enhancer I region of HBV
DNA. The nucleic acids may be used to modulate the expression of HBV
compounds and/or potential therapies directed against HBV, and compounds
compounds and/or potential therapies directed against HBV, and compounds
c that modulate the expression and/or replication of HCV. The compounds and
methods of the invention are useful for the treatment of degenerative and
disease states related to HBV and HCV infection, replication and gene
disease states related to HBV and HCV infection, replication and gene
c expression such as cirrhosis, liver failure, and happatocallular
controlled and the property of the present of the present of the property of the p ö carcinoma. The present sequence represents a substrate for one of the HCV DNAzyme or minus strand DNAzyme sequences disclosed in the present Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus infection. Gaps <u>ب</u> Lee ; 0 9.5%; Score 12.4; DB 1; Length 17; 64.3%; Pred. No. 2.2e+02; ative 4; Mismatches 1; Indels Pavco P, Sequence 17 BP; 5 A; 5 C; 2 G; 0 T; 5 U; 0 Other; Morrissey D, Mcswiggen J, Claim 1; Page 241; 387pp; English. Local Similarity 64.3 les 9; Conservative Macejak D, Roberts E; WPI; 2003-229207/22. invention Query Match Matches

1426 GTTCTATGCAGACA 1439

ACD57593 standard; RNA; 17

RESULT 87 ACD57593

ò 셤 03-OCT-2003 (first entry)

ACD57593;

Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV; RNA stability; RNA expression; RNA synthesis; antisense; enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptemer; HBV reverse transcriptase; Enhancer I region; viral replication; degenerative; disease state; HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic; virucide; antilnflammatory; substrate; ss. HCV DNAzyme substrate sequence #403. Hepatitis C virus.

WO200281494-A1. 17-0CT-2002.

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The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HRV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes, inozymes, zinzymes, amberzymes, anderzymes, anderzymes, anderzymes, anderzymes, and stability and G-cleaver ribozymes. Also disclosed are nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase and/or HBV reverse transcriptase primer sequences, as wells as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV compounds and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies discused against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents a substrate for one of the HCV praction or minus strand DNAzyme sequences disclosed in the present
                                                                                                                                                                                                                                                                                                                                                                           Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
                                                                                                                                                                                                                                                                                                 Mcswiggen J, Morrissey D, Pavco P, Lee P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HCV minus strand DNAzyme substrate sequence #1876.
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                                       26-MAR-2001; 2001US-00817879.
08-JUN-2001; 2001US-00877478.
08-JUN-2001; 2001US-0296876P.
24-OCT-2001; 2001US-0335059P.
05-DEC-2001; 2001US-03370559P.
             26-MAR-2002; 2002WO-US009187
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ID ACD65077 standard; RNA; 17
                                                                                                                                      RIBOZYME PHARM INC.
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| GUUCUAUGCACACA 15
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MCSWIGGEN J.
MORRISSEY D.
PAVCO P.
                                                                                                                                                                                                                                                                                                              Roberts E;
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Best Local Similarity
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                                                                                                                                                                                                                                                                  ROBERTS E.
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DRAPER K.
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                                                                                                                                                                                                                                                                                                                                                                                                            infection.
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                                                                                                                                     (RIBO-)
(BLAT/)
(MACE/)
(MCSW/)
                                                                                                                                                                                                (MORR/)
(PAVC/)
(LEEP/)
                                                                                                                                                                                                                                              (DRAP/)
(ROBE/)
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                                        9.5%; Score 12.4; DB 1; Length 17; 64.3%; Pred. No. 2.2e+02; tive 4; Mismatches 1; Indels
Sequence 17 BP; 4 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
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Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV; RNA stability; RNA expression; RNA synthesis; antisense; enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
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amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; viral replication; degenerative; disease state; HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic; virucide; antiinflammatory; substrate; ss. <u>й</u> Lee Mcswiggen J, Morrissey D, Pavco P, 26-MAR-2001; 2001US-00817879. 08-JUN-2001; 2001US-00877478. 08-JUN-2001; 2001US-0296876P. 24-OCT-2001; 2001US-0337059P. 05-DEC-2001; 2001US-0337055P. 26-MAR-2002; 2002WO-US009187 RIBOZYME PHARM INC. Macejak D, Roberts E; BLATT L.
MACEJAK D.
MCSWIGGEN J.
MORRISSEY D.
PAVCO P. Hepatitis C virus ROBERTS E. DRAPER K. WO200281494-A1 17-0CT-2002. Blatt L, N Draper K, (ROBE/) (RIBO-) DRAP/) LEEP/) (PAVC/) (MCSM) MORR/ BLAT/ (MACE/

Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus WPI; 2003-229207/22.

Claim 1; Page 308; 387pp; English. infection.

The present invention relates to nucleic acid molecules which modulate the gravitesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes, inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed are nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV genes and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene carcinoma. The present sequence sequences disclosed in the present invention

Gaps .. 0 9.5%; Score 12.4; DB 1; Length 17; 92.9%; Pred. No. 2.2e+02; ive 0; Mismatches 1; Indels Sequence 17 BP; 5 A; 3 C; 5 G; 0 T; 4 U; 0 Other; 1426 GTTCTATGCAGACA 1439 Griciardcaca 2 Best Local Similarity 92.9 Matches 13; Conservative 15 Query Match ò 셤

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RESULT 89 ACD65076/c

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carcinoma. The present sequence represents a substrate for one of the HCV DNAzyme or minus strand DNAzyme sequences disclosed in the present
                                                                                                                                                 Invention
                                                                 RIBO-)
                                                                   (BLAT/)
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                                                                                  Nucleic acid molecule, Hepatitis C virus, HCV; Hepatitis B virus; HBV; RNA stability; RNA expression; RNA synthesis; antisense; enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; viral replication; degenerative, disease state; HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic; virucide; antiinflammatory; substrate; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pavco P,
                                                                 HCV minus strand DNAzyme substrate sequence #1875.
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ВЪ.
                                                                                                                                                                                                                                                                                 26-MAR-2001; 2001US-00817879.
08-UUN-2001; 2001US-00877478.
08-UUN-2001; 2001US-0296876P.
24-OCT-2001; 2001US-0335059P.
05-DEC-2001; 2001US-03370559P.
                                                                                                                                                                                                                                                             26-MAR-2002; 2002WO-US009187
ACD65076 standard; RNA; 17
                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                     RIBOZYME PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roberts E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macejak D,
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MACEJAK D.
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ROBERTS E.
                                                                                                                                                                                         Hepatitis C virus.
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                                                                                                                                                                                                                 WO200281494-A1.
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                                            30-SEP-2003
                                                                                                                                                                                                                                      17-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blatt L, N
Draper K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection.
                      ACD65076;
                                                                                                                                                                                                                                                                                                                                                                                      (MCSW/) P
(MORR/) P
(PAVC/) P
(LEEP/) P
(DRAP/) P
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The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as harmerhead ribozymes, DNAzymes, inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed are uncleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV compounds and/or potential theraphse directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and the invention are useful for the treatment of degenerative and disease states related to HBV and HV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular Claim 1; Page 308; 387pp; English.

Sequence 17 BP; 5 A; 4 C; 4 G; 0 T; 4 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic, antiviral, neuroprotective, nootropic, neuroleptic, ss, primer, probe, tumour suppression, tumour reversion, apoptosis; virus resistance, transgenic animals, Alzheimer's disease, schizophrenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
                                               Gaps
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Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                           Tumour suppression/reversion associated nucleotide #2714.
                                               Indels
  9.5%; Score 12.4; DB 1;
92.9%; Pred. No. 2.2e+02;
iive 0; Mismatches 1;
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                                                                                                                                                                                                                                                    ADB42391 standard; DNA; 17 BP.
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                                                                                           1426 GTTCTATGCAGACA 1439
                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                 13; Conservative
                                                                                                                            17 GTTCTATGCACACA
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  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis.
                                                                                                                                                                                                                                                                                                 ADB42391;
                                                 Matches
                                                                                                                                                                                                       RESULT 90
                                                                                                                                                                                                                             ADB42391
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The invention relates to the isolation of 6327 nucleotide sequences, fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides, or the complement, or corresponding RNA, of the nucleotides, rate used as probes or primers for detecting, identifying, quantifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour supression or reversion, apotosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and experimental models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies (Ab) against the polypeptide are useful for prevention and/or treatment of viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

Analysis of the expression of the nucleotides and polypeptides can and/or prognosis of these diseases. The nucleotides and polypeptides can be used to screen for their specific interactive molecules, potentially useful for treating diseases associated with abnormal expression of the nucleotides associated with abnormal Length 17; Sequence 17 BP; 3 A; 5 C; 2 G; 7 T; 0 U; 0 Other; 9.5%; Score 12.4; DB 1; 92.9%; Pred. No. 2.2e+02; tive 0; Mismatches 1; Query Match
Best Local Similarity 92.9
Matches 13; Conservative

Disclosure; Page 349; 771pp; French.

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Gaps

.. 0

1; Indels

14 AAGATGGGTGGATC 1

g

RESULT 92

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The invention relates to the isolation of 6327 nucleotide sequences, fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides, or the complement, or corresponding RNA, of the nucleotides or the under stringent conditions with incleotides. The nucleotides are used as probes or primers for detecting, identifying, quantifying and/or amplifying nucleic acids, as in vitro suppression or reversion, apoptosis and or viral resistence, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies (Ab) against the polypeptide are useful for prevention and/or treatment of viral infections or diseases characterized by development of tumours
                                                                                                                                                                                                                                                                                                                                                     primer; probe; tumour suppression; tumour reversion; apoptosis; virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and/or prognosis of these diseases. The nucleotides and polypeptides can also be used to screen for their specific interactive molecules, potentially useful for treating diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
Analysis of the expression of the nucleotides can be used for diagnosis
and/or prognosis of these diseases. The nucleotides and polypeptides can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
                                                                                                                                                                                                                                                                                                                                    cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.5%; Score 12.4; DB 1; Length 17; Best Local Similarity 92.9%; Pred. No. 2.2e+02; Matches 13; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                        Tumour suppression/reversion associated nucleotide #1879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 251; 771pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression of the nucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULAR ENGINES LAB.
                                                                                                                                             踞
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1379 GATCGTCTTCTGAT 1392
                                                                                                                                             ADB41556 standard; DNA; 17
                                    1 GATCCTCTTCTGAT 14
                                                                                                                                                                                                                             (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amson R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-441574/41
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Telerman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis.
                                                                                                                                                                                    ADB41556;
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                                                                                                      RESULT 91
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Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (WEGF). A patient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour anglogenesis, ocular diseases, psoriasis and rheumarcid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75722 represent specific examples of nucleic acid molecules from the present invention
                                                                                                                                     Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenessis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor; foetal liver kinase 1; ss.
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                                                                                                            Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escobedo J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 4 A; 3 C; 2 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 12.2; DB 1;
Pred. No. 2.3e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 140; 218pp; English.
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              BP.
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              AAX73104 standard; RNA; 17
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                                                                            28-JUL-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mcswiggen J,
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                                                                                                                                                                                                                                                                     WO9715662-A2.
                                                                                                                                                                                                                                                                                                                                    25-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                  26-OCT-1995;
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                                            AAX73104;
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AAX73104/c
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Gaps

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Mcswiggen JA;

Coeshott C,

Jarvis T,

99WO-US006507. 98US-0079678P

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Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors.
                                                                                                                                                                                                                                                                      Claim 54; Page 241; 305pp; English.
                                                                                                                                                (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                           Roberts E,
                                                                                                                                                                                                     WPI; 1999-591315/50
              Homo sapiens.
                                      WO9950403-A2
                                                                                            24-MAR-1999;
                                                                                                                    27-MAR-1998;
                                                                  07-OCT-1999,
                                                                                                                                                                           Pavco PA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGP). A patient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (fll-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour anglogenesis, coular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention
                      Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor; foetal liver kinase 1; ss.
                                                                                                                                                                                                                                                                                                                                                      expression or mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriaais; veruca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                    Nucleic acid molecule modulating VEGF receptor(s) gene expression or stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
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 Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.4%; Score 12.2; DB 1; Length 17; 70.6%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Integrin subunit beta 3 substrate sequence SEQ ID NO:5995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                   Escobedo J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 6 A; 4 C; 4 G; 0 T; 3 U; 0 Other;
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                                                                                                                                                                                                                                                                                                 Stinchcomb D,
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96US-00584040.
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                                                                                                                                                                                                                                                         RIBO-) RIBOZYME PHARM INC.
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                                                                                                                                                                                                                                                                                                                            WPI; 1997-259017/23.
                                                                                                                                                                                                                                                                        CHIRON CORP
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nes 12; Conserv
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                                                                                                                                                                                                                                                                                                 Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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The present invention describes enzymatic nuclear actual molecules with the procession describes enzymatic nuclear transporter (ARNY) gene, an integrin alpha 6 subunit gene, and AAA1761 to AAA1762 to AAA1768 to AAA1768 and AAA1984 to and AAA1766 to AAA1765 to AAA1768 to AAA1988 and AAA1988 to AAA1915 to AAA2180 to AAA2180 to AAA2180 to AAA2180 to AAA2180 to AAA2180 and AAA2180 to AAA2180 and AAA2180 to AAA2180 to AAA2180 and AAA2381 to AAA2180 to AAA2180 and AAA2382 to AAA2180 to AAA2180 and AAA2382 to AAA2180 to AAA2382 to AAA
present invention describes enzymatic nucleic acid molecules with RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            integrin subunit alpha-6, or integrin subunit beta-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 6 A; 0 C; 5 G; 0 T; 6 U; 0 Other;
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Human CD20 Inozyme #173
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MCSWIGGEN J.
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                                                                                             interferon alpha
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(BLAT/) 1
(MCSW/) 1
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                                                                                                                                                                                                                       RESULT 97
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                                                                                                                                                                                                                                        Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                                                                                                           Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                                                                                                                                                                     The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                          9.4%; Score 12.2; DB 1; Length 17;
llarity 52.9%; Pred. No. 2.36+02;
Conservative 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                         Sequence 17 BP; 9 A; 1 C; 2 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mcswiggen J;
                                                                                                        Mcswiggen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hammerhead ribozyme substrate #2883.
                                                                                                                                                                                   Claim 42; Page 127; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                  1400 GGTAAATTGTTAATGA 1416
                                                                                                                                                                                                                                                                                                                                                            ||:||||:|
GGUAAAUUCUAAAUAA 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-2000; 2000WO-US009721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0129390P
                                                 2000WO-US009721.
                                                                                                       Zwick M, Pavco P,
                                                                   99US-0129390P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                    AAF06086 standard; DNA; 17
                                                                                     (RIBO-) RIBOZYME PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interferon alpha; ss.
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Local 9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-647423/62.
                                                                                                                          WPI; 2000-647423/62.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200061729-A2
          WO200061729-A2
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                                                11-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                    12-APR-1999;
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                             19-0CT-2000
                                                                                                        Blatt L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF06086;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
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                                                                          The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; 8s; antisense therapy; cytostatic; antiinflammatory; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 12.2; DB 1; Length 17;
Pred. No. 2.3e+02;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17 BP; 5 A; 4 C; 3 G; 0 T; 5 U; 0 Other;
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Claim 42; Page 122; 164pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1439
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28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50....
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GUCUUCCUAUGCAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1423 GTCGTTCTATGCAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK03222 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-2002 (first entry)
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The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NGCO). The regulates expression of a neurite growth inhibitor goals (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a numberzyme (aleaving RNA with an NGN motif), a go-cleaving RNA with an NGN motif) proposessing an NGH motif), a G-cleaver (cleaving RNA with an NGN with a NGN motif) proposessing an NGH motif). The CD20-targetting nucleic acid is used to cleave RNA of the presence of a divalent cation that is preferably NGC of CD20 in the presence of a divalent cation that is preferably NGC the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more theory with a particular, the CD20 targetting nucleic acid may be used to treat lymphoma (NGL), immunocytoma (NML), lowlky low-grade or follicular NHL, lymphocytic lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, cleukaemia, and inflammatory arthropathy. The NOGO ene in the presence of a divalent cation that is preferably MG<sup>2</sup>+. Furthermore, the presence of a divalent cation that is preferably MG<sup>2</sup>+. Furthermore, the cargetting nucleic acid may be contacted with a cell to reduce NOGO gene in the cation that is preferably MG<sup>2</sup>+. Furthermore, the condition associated with the level of condition associated with the level of the caption system (NGS) injury and cereborovascular accident (CMA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral aclerosis (MS), parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob CG states which respond to the modulation of NOGO expression. The present captary is a particular, the involve disease, central response to the present captary of the captary and disease, ataxia, Huntington's disease, central particular of the present ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 4 A; 5 C; 2 G; 0 T; 6 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Chowrira BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 88; Page 87; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1388 CTGATCAAAGGAGGTAA 1404
                                                                                                                              11-FEB-2000; 2000US-0181797P.
28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
                                                                  09-FEB-2001; 2001WO-US004273.
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                                                                                                                                                                                                                                                                   RIBOZYME PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Blatt L, Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                  MCSWIGGEN J.
CHOWRIRA B M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-607195/69.
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                                                                                                                                                                                                                                                                                                      BLATT L.
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   16-AUG-2001
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(MCSW/)
                                                                                                                                                                                                                                                                   (RIBO-)
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                                          The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down control of a neurite growth inhibitor gene (NGO). The regulates expression of a neurite growth inhibitor gene (NGO). The nucleic acids (e.g. a ribozyme or a nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a mRN motif) proposessing an NCH motif), a G-cleaver (cleaving RNA with a m NCH with a NRN motif) proposessing an NCH motif), a G-cleaver (cleaving RNA with a m NGN motif) a zinzyme (cleaving RNA with a m NGN triple!), a zinzyme (cleaving RNA with a presence of a divalent cation that is preferably MG<sup>22</sup>+. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma (MLI), pulky low-grade or follicular non-flowing mucleic acid may be contacted with a cell to reduce NGO gene in the lymphoma (MLI), immunocytoma (IMC), small B-cell lymphocytic lymphoma, contacted with a cell to reduce NGO gene in the presence of a divalent cation that is preferably MG<sup>2</sup>+. Furthermore, the crucine cation that is preferably MG<sup>2</sup>+. Furthermore, the capted may be contacted with a cell to reduce NGO activity of the contacted may be contacted with a cell to reduce NGO activity of the contacted may be contacted with a cell to reduce NGO activity of the contacted with a cell to reduce NGO activity of the contacted with a contacted with a cell to reduce NGO activity of the contacted with a contacted with a cell to reduce NGO activity of the contacted with a contacted with a cell to reduce NGO activity of the contacted with a contacted with a cell to reduce NGO activity of the contacted with a contacted with a cell to reduce NGO activity of the contacted with a capted to the NGO activity of the contacted with a contacted with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 5 A; 5 C; 4 G; 0 T; 3 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence is an inozyme of the invention
Claim 30; Page 148; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1384 TCTTCTGATCAAAGGAG 1400
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Query Match

Best Loca Matches

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Gaps

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ABK18533 standard; RNA; 17

RESULT 99 ABK18533 ABK18533;

HXXX

WO200159103-A2.

sapiens.

12-MAR-2002 ABK01312;

ABK01312/

(first entry)

09-APR-2002

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Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel Trenaunay Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
Human ERG G-cleaver ribozyme target sequence Seq ID No 1180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amberzyme
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Homo sapiens.

WO200188124-A2.

22-NOV-2001.

16-MAY-2001; 2001WO-US015866.

16-MAY-2000; 2000US-00572021

(RIBO-) RIBOZYME PHARM INC. (GLAX) GLAXO GROUP LTD.

Randi AM; Mclaughlin F, Mcswiggen JA, Von Carlowitz I, Jarvis T,

WPI; 2002-082995/11.

Novel polynucleotide which down regulates expression of Ets-related gen useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.

Claim 4; Page 80; 149pp; English.

The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sacroma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, the conditions selected from cancer, lymphoma, Ewing's sacroma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, melanoma, cumigaris, angiotibroma of tuberous sclerosis, port-whose stains, Sturge Weber syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more therapies the treatment. The method comprises the use of one or more therapies conditions suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (I) to the patient in conjunction with one or more of other therapies such as radiation or chamotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting the cell with (I). (I) is useful for cleaving RNA of ERG gene, by contacting (I) with RNA, in the presence of a divalent cat diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically caractering genes that share homology with ERG gene or ERG fusion genes. ARX 7354-ABK22719 represent nucleic acids, including antisense and carymatic nucleic acid molecules which regulate expression of ERG, and carymatic nucleic acid molecules which regulate expression of ERG, and carymatic nucleic acid molecules which regulate expression of ERG, and carymatic nucleic acid molecules which regulate expression of ERG, and

Seguence 17 BP; 4 A; 2 C; 7 G; 0 T; 4 U; 0 Other;

; 0 9.4%; Score 12.2; DB 1; Length 17; 88.8%; Pred. No. 2.3e+02; ve 4; Mismatches 3; Indels 58.8%; Conservative Local Similarity les 10; Conserv Query Match Best Loca Matches

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Gaps

1407 TTGTTAATGATCCAG 1423 17 UNGUGAGUGAGGACCAG

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RESULT 100 **ABK19156**

ABK19156 standard; RNA; 17 BP

ABK19156;

(first entry) 09-APR-2002

Human ERG Amberzyme target sequence Seq ID No 1803.

ophthalmological; antiarthritis; antipsoriatis; virucide; osteopathic; vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme; cytostatic; antitumour; antidiabetic; Human; hammerhead ribozyme; amberzyme.

Homo sapiens.

WO200188124-A2.

22-NOV-2001.

16-MAY-2001; 2001WO-US015866.

16-MAY-2000; 2000US-00572021

(RIBO-) RIBOZYME PHARM I (GLAX) GLAXO GROUP LTD.

Randi AM; Mcswiggen JA, Mclaughlin F, Jarvis T, Von Carlowitz I,

WPI; 2002-082995/11.

Novel polynucleotide which down regulates expression of Ets-related gene, useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.

Claim 4; Page 121; 149pp; English.

The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, metanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, cundurates, angiofibroma of tuberous sclerosis, port wine stains, Sturge Weber syndrome, Rippel-Trenaunay-Weber syndrome, Osteoporosis and wound healing. (I) is useful for syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more therapies the treatment. The method comprises the use of one or more therapies or under conditions suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (I) to the patient in conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or cation such as Mg2+. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes. ABK17354-ABK22719 represent nucleic acids, including antisense and enzymatic nucleic acid molecules which regulate expression of ERG, and related PCR primers of the invention

Sequence 17 BP; 4 A; 3 C; 7 G; 0 T; 3 U; 0 Other;

Query Match

DB 1; Length 17; 9.4%; Score 12.2;

The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, tumour anglogenesis, diabetic retinopathy, macular degeneration, the acid of neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca rugoristis, angiofibrona of tuberous sclerosis, port wine stains, Sturge CV ungaris, angiofibrona of tuberous sclerosis, port wine stains, Sturge CV weber syndrome, Rippel-Trenaunay-Weber syndrome, Osler-Weber-rendu CC where yindrome, Hubbel Trenaunay-Meber syndrome, Osler-Weber-rendu CC weber string a partient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. Leukaemia or tumour conjunction with one or more of other therapies such as radiation or angiogenesis is treated by administering (I) to the patient in conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or call, by contacting (I) with RNA, in the presence of a divalent confice seamine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically crangeting genes that share homology with ERG gene or ERG fusion genes. 0 ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Ewing's Barcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; mecular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiotibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome; leukaemia; ss; Novel polynucleotide which down regulates expression of Ets-related genuseful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome. Gaps Randi AM; hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ö Mclaughlin F, Indels Human ERG Amberzyme target sequence Seq ID No 1802. No. 2.3e+02; 3; Mismatches Mcswiggen JA, Pred. Claim 4; Page 121; 149pp; English 1410 TTAATGATGACCAGTCG 1426 BP. 1 UGAGUGAGGACCAGUCG 17 16-MAY-2001; 2001WO-US015866 16-MAY-2000; 2000US-00572021 Von Carlowitz I, 64.78; (RIBO-) RIBOZYME PHARM INC. (GLAX) GLAXO GROUP LTD. ABK19155 standard; RNA; 17 (first entry) 11; Conservative WPI; 2002-082995/11. Best Local Similarity Matches 11; Conserv WO200188124-A2. Homo sapiens. 09-APR-2002 22-NOV-2001 Jarvis T, amberzyme. ABK19155; RESULT 101 **ABK19155** à dd

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ABK17354-ABK22719 represent nucleic acids, including antisense and enzymatic nucleic acid molecules which regulate expression of ERG, and related PCR primers of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with tuniour suppression or regression, apoptosis or virus resistance. invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration
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                                                                                                                           Gaps
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                                                             Sequence 17 BP; 4 A; 3 C; 7 G; 0 T; 3 U; 0 Other;
                                                                                       9.4%; Score 12.2; DB 1;
64.7%; Pred. No. 2.3e+02;
ative 3; Mismatches 3;
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Pred. No. 2.3e+02;
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                                                                                                         Local Similarity 64.7
hes 11; Conservative
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ID ACC519
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FR2826373-A1

27-DEC-2002

Tuijnder M,

Homo sapiens

27-JUN-2003

ACC51977;

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The invention describes an isolated nucleic acid encoding a G protein coupled receptor (GPCR), mutations of which cause cancer, comprising a 225 or 1921 base pair sequence, or their degenerate variants, encoding a 409 residue amino acid sequence, all given in the specification, with or without conservative amino acid substitutions, or complements of the sequence of them. The encoding nucleic acid is not more than 100 kbase in length. The methods and compositions of the present invention are useful for diagnosing, investigating and/or treating disorders associated with aberrant expression or activity of GPCR-A-1, such as tumours and cancers. This sequence represents an oligonucleotide used to analyse the gene encoding human G-protein coupled receptor GPCR-A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
                                                                                                                                                                     New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing, investigating and/or treating disorders associated with aberrant expression or activity of GPCR-A-1, such as tumors and cancers.
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Pred. No. 2.3e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                           Example 2; SEQ ID NO 226; 156pp; English.
                                        (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
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12-OCT-2001; 2001US-0329000P.
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nes 14; Conservative
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                                                                                                                              WPI; 2003-381720/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with tumour suppression or regression, apoptosis or virus resistance, invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration
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G-Protein-Agonist, G-Protein-Antagonist, gene therapy, cytostatic, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents an isolated nucleic acid sequence associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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tumour regression; apoptosis; virus resistance; diagnosis;
cellular degeneration.
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82.4%; Pred. No. 2.3e+02;
iive 0; Mismatches 3; Indels
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Homo sapiens

17-APR-2003

28-JUL-2003

ACA99709

Query Match

Matches

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Gaps

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The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, component of a gene chip, in vitro as (anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, colypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for propagation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell casenserion, specifically cancer but also Alzheimer's disease and scharacterised by development of tumours or cell categorients amples is useful for disponsis and/or prognosis of these contained better the polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies and or prognosis of these contained between the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression contained buman fukutin oligonucleotide of the invention

Sequence 17 BP; 4 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

ö Gaps .. 0 9.4%; Score 12.2; DB 1; Length 17; 82.4%; Pred. No. 2.3e+02; Indels 0; Mismatches Query Match
Best Local Similarity 82.4
Matches 14; Conservative

1379 GATCGTCTTCTGATCAA 1395 1 darccrerrcreadcaa 17 ò

ABT38096 standard; DNA; 17 BP. ABT38096; RESULT 106

12-JUN-2003 (first entry)

Tumour suppression related human fukutin oligo SEQ ID No 3733.

Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds.

Homo sapiens.

WO2003025175-A2.

27-MAR-2003

17-SEP-2002; 2002WO-IB004208.

(MOLE-) MOLECULAR ENGINES LAB. 17-SEP-2001; 2001FR-00011978.

Tuijnder M; Telerman A, Amson R,

WPI; 2003-313353/30.

associated antibodies New isolated nucleic acid, useful for treating viral diseases with tumors and cell degeneration, also related polypeptides, and transfected cells.

Disclosure; Page 470; 720pp; French

The invention relates to a novel isolated 17 mer nucleic acid sequence,

MCSWIGGEN J. DRAPER K G.

Dispersion of the sequence, a signment, at least 80 % identity to the 17 mer sequence, a sequence that alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated mucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying and or amplifying and or a sequence, and for component of a gene chip, in vitro as (anti) sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, colls containing the component of recombinant polypeptides. Any of the nucleic acids, colls containing the vector or antibodise directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or call degeneration, specifically cancer but also Alzheimer's disease and captient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and coth the polypeptides and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polymucleotide sequence represents a tumour suppression created human fukutin oligonucleotide of the invention. ö in the specification, a sequence containing at least 15 consecutive Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme; clastycancy; amberzyme; cancer; REL-A activity; breast cancer; human; lung cancer; prostate cancer; colorectal cancer; prostate cancer; colorectal cancer; pancreatic cancer; oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer; cervical acncer; melanoma; lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate; chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate; gencitabine; radiation therapy; inflammatory disease; asthma; diabetes; rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia; gene therapy; aucoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic airway inflammatory bowel disease; infection; ss. ; 9.4%; Score 12.2; DB 1; Length 17; 32.4%; Pred. No. 2.3e+02; 3; Indels Sequence 17 BP; 10 A; 1 C; 5 G; 1 T; 0 U; 0 Other; NFKB sub-unit modulating inozyme substrate #652. 0; Mismatches 1390 GATCAAAGGAGGTAAAA 1406 1 GATCAAAGAAGAAGA 17 94US-00245466. 94US-00291932. 23-MAY-2001; 2001US-00864785 92US-00987132 96US-00777916 82.4%; ACA06833 standard; RNA; 17 (first entry) Local Similarity 82.4 es 14; Conservative STINCHCOMB D T. US2002177568-A1. 03-JUN-2003 Homo sapiens 07-DEC-1992; 18-MAY-1994; 15-AUG-1994; 23-DEC-1996; 28-NOV-2002. ACA06833; Query Match (STIN/) S (MCSW/) N (DRAP/) I Matches RESULT 107 ACA06833/c В ð

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Wed Apr

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The invention describes an enzymatic nucleic acid molecule (I) which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B (NFRM), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially MG^2+. The enzymatic and nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, ossophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer. The method involves use of other drug the treations such as monoclonal antibodies, stomach, stomach, and thotrexate, chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edarrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, catrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, and antisense nucleic acid molecules are also useful for treating inflammatory disease such as the method mandered arthrities, restensed them. The mandered arthrities are also useful for treating inflammatory arthrities are also useful for mandered arthrities are also useful for mandered arthrities.
                                                                                                                                                                                                                                                        enzymatic nucleic acid molecules which down regulates expression of
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                                                                                                                                                                                                                                                                                                                   a sequence encoding a subunit of nuclear factor kappa B useful streating cancer, inflammatory disorders and autoimmune diseases
      Draper KG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 36; 72pp; English
      Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid molecule
                                                                                                                                  WPI; 2003-340953/32.
Stinchcomb DT,
                                                                                                                                                                                                                                                        Novel
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ö Gaps ö 9.4%; Score 12.2; DB 1; Length 17; 82.4%; Pred. No. 2.3e+02; Live 0; Mismatches 3; Indels Sequence 17 BP; 2 A; 7 C; 1 G; 0 T; 7 U; 0 Other; 1456 GTTGATCAAGCAAATAG 1472 Conservative Similarity Mar Local St... 14; Query Match Matches à

ABZ60049 standard; RNA; 17 ABZ60049; RESULT 108

GTTGAGCAAGGAAGAG

17

a

Human K-Ras DNAzyme substrate #161. (first entry) 21-MAR-2003

Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras; enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV; anti-rheumatic; cancer; AIDS; ss. Homo sapiens.

2001US-0294140P. 2001US-0296249P. 2001US-0318471P. WO200297114-A2 29-MAY-2001; 06-JUN-2001; 10-SEP-2001; 29-MAY-2002; 05-DEC-2002

acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytostatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ55889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ65524, ABZ65520 - ABZ65520 - ABZ65524, ABZ65520 - ABZ65520 - ABZ65520, A invention relates to a novel short interfering RNA (siRNA) nucleic Novel short interfering RNA and enzymatic nucleic acid useful for treating cancer, modulates the expression of a nucleic acid encoding HBR2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences. Claim 58; Page 88; 185pp; English (RIBO-) RIBOZYME PHARM INC. ribozymes of the invention WPI; 2003-140484/13. Mcswiggen J;

Gaps ö 9.4%; Score 12.2; DB 1; Length 17; 76.5%; Pred. No. 2.3e+02; tive 1; Mismatches 3; Indels 1390 GATCAAAGGAGGTAAAA 1406 1 GAGCAAAGAUGGUAAAA 17 Query Match
Best Local Similarity 76.5
Matches 13; Conservative ð 셤

BP

ACC67934 standard; DNA; 17

RESULT 109 ACC67934/ ACC67934;

Sequence 17 BP; 9 A; 1 C; 5 G; 0 T; 2 U; 0 Other;

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Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine; tumour suppression; tumour reversion; apoptosis; virus resistance; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease; Murine oligonucleotide associated with tumour supression, SEQ ID 5181. 01-JUL-2003 (first entry) schizophrenia; ss

(MOLE-) MOLECULAR ENGINES LAB 17-SEP-2002; 2002WO-IB004210. 17-SEP-2001; 2001FR-00011979. Telerman A, Amson R, WO2003025176-A2. Mus musculus 27-MAR-2003.

Disclosure; Page 636; 738pp; French

New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.

WPI; 2003-333167/31.

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The present invention relates to murine oligonucleotides (ACC62754-ACC68806), which are associated with tumour suppression, tumour reversion, apoptosis and virus resistance. The oligonucleotides are useful as (1) as probes and primers for detecting, identifying, quadrofor amplifying nucleotides are detecting, identifying appearance of a gene chip; in vitro as (anti) sense reagents; and (2) for production of recombinant polypeptides. The oligonucleotides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia
      8833333333333888
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Sequence 17 BP; 6 A; 2 C; 1 G; 8 T; 0 U; 0 Other;

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Score 12.2; DB 1; Length 17;
Pred. No. 2.3e+02;
0; Mismatches 3; Indels
                                                                               1405 AATTGTTAATGATGACC 1421
Query Match
Best Local Similarity 82.4%;
Matches 14; Conservative (
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Gaps . 0

> 17 AATTATTAAAGATGATC 1 d

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BP
   ACC64079 standard; DNA; 17
         (first entry)
         01-JUL-2003
      ACC64079;
RESULT 110
 ACC64079
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Murine oligonucleotide associated with tumour supression, SEQ ID 1326.

Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine; tumour suppression; tumour reversion; apoptosis; virus resistance; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease; SS schizophrenia;

Mus musculus.

WO2003025176-A2.

27-MAR-2003.

17-SEP-2002; 2002WO-IB004210.

17-SEP-2001; 2001FR-00011979.

(MOLE-) MOLECULAR ENGINES LAB

Tuijnder M; Amson R, Telerman A,

WPI; 2003-333167/31.

New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.

Disclosure, Page 186; 738pp; French

The present invention relates to murine oligonucleotides (ACC62754-ACC68006), which are associated with tumour suppression, tumour reversion, apoptosis and virus resistance. The oligonucleotides are useful as (1) as probes and primers for detecting, identifying, quantifying and/or amplifying nucleic acid, e.g. as one component of a gene chip; in vitro as (anti) sense reagents; and (2) for production of recombinant polypeptides. The oligonucleotides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia

Sequence 17 BP; 8 A; 1 C; 5 G; 3 T; 0 U; 0 Other;

DB 1; Length 17;

9.4%; Score 12.2;

Query Match

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The invention relates to the isolation of 6327 nucleotide sequences, fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides. The nucleotides are used as probes or primers for detecting, ct annifying, quantifying and/or amplifying nucleic acids, as in vitro curespond antisense sequences, of nucleotides involved in tumour cuppression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and calls containing the vectors), the encoded polypeptides and antibodies (Ab) against the polypeptide are useful for prevention and/or treatment or viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

Canalysis of the expression of the nucleotides can be used for diagnosis and/or prognosis of these diseases. The nucleotides can be used to screen for their specific interactive molecules, can be used to screen for their specific interactive molecules.

Ce expression of the nucleotides as and polypeptides can be used to screen for their specific interactive molecules.
                                                                                                                                                                                                                                                                                                                                                                    cytostatic, antiviral, neuroprotective, nootropic, neuroleptic; ss, primer, probe; tumour suppression, tumour reversion; apoptosis; virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
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                    Gaps
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                                                                                                                                                                                                                                                                                                                                 Tumour suppression/reversion associated nucleotide #2330.
                    Indels
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Pred. No. 2.3e+02;
); Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 304; 771pp; French.
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                                                                                             1 GATCTGAGGAGATAAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-2002; 2002WO-IB004219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-SEP-2001; 2001FR-00011981.
Best Local Similarity 82.4%;
Matches 14; Conservative
                                                        1390 GATCAAAGGAGGTAAAA
                                                                                                                                                                                            ADB42007 standard; DNA; 17
                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Telerman A, Amson R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003040369-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis.
                                                                                                                                                                                                                                  ADB42007;
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                                                                                                                                                       RESULT 111
                                                                                                                                                                           ADB42007
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1390 GATCAAAGGAGGTAAAA 1406

à

cytostatic, antiviral, neuroprotective, nootropic, neuroleptic, ss; primer, probe, tumour suppression, tumour reversion, apoptosis, virus resistance, transgenic animals, Alzheimer's disease; schizophrenia,

Tumour suppression/reversion associated nucleotide #3933.

(revised)
(first entry)

18-DEC-2003 04-DEC-2003

ADB43610;

BP.

ADB43610 standard; DNA; 17

RESULT 113

ADB43610

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The invention relates to the isolation of 6327 nucleotide sequences, fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides, or the complement, or corresponding RNA, of the nucleotides. The nucleotides are used as probes or primers for detecting, identifying quantifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour suppression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies (Ab) against the polypeptide are useful for prevention and/or treatment of viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

Analysis of the expression of the nucleotides can be used for diagnosis and/or prognosis of these diseases. The nucleotides and polypeptides can allow be used to screen for their specific interactive molecules, the molecules of the expression of the nucleotides and polypeptides can be used to screen for their specific interactive molecules.
                                                                                                                                                                                                                                                                                                                   primer; probe; tumour suppression; tumour reversion; apoptosis; virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
                                                                                                                                                                                                                                                                                               cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.4%; Score 12.2; DB 1; Length 17; 82.4%; Pred. No. 2.3e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                        Tumour suppression/reversion associated nucleotide #1731.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tuijnder M;
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    GATCAAAGAAGGAAAGA 17
                                                                                                          ADB41408 standard; DNA; 17 BP.
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                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amson R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-441574/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003040369-A2.
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                           18-DEC-2003
04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                               diagnosis.
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                                                                                                                                                  ADB41408;
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                                                                   RESULT 112
                                                                                       ADB41408
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New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.

Ξ

Tuijnder

Telerman A, Amson R, WPI; 2003-441574/41.

(MOLE-) MOLECULAR ENGINES LAB.

17-SEP-2002; 2002WO-IB004219. 17-SEP-2001; 2001FR-00011981.

WO2003040369-A2. Homo sapiens.

diagnosis.

15-MAY-2003

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The invention relates to the isolation of 6327 nucleotide sequences, fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 08% identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides, or the complement, or corresponding RNA, of the nucleotides. The nucleotides are used as probes or primers for detecting, identifying, quantifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour cupression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transganic animals, as experimental models. The nucleotides (also vectors containing them and calls containing the vectors), the encoded polypeptides and antibodies (Ab) against the polypeptide are useful for prevention and/or treatment of viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

Analysis of the expression of the nucleotides can be used for diagnosis and be not be used for diagnosis and or prognosis of these diseases. The nucleotides and polypeptides can be not be used for diagnosis and be not accounted to the capture of the containing the proposition of the nucleotides and polypeptides can be not be used for diagnosis and polyperides.
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molecules,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 7 A; 6 C; 3 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 491; 771pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1377 GCGATCGTCTTCTGATC 1393
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Best Local Similarity 82.4
Matches 14; Conservative
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17 gegriesigingiane à g

RESULT 114

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Gaps

; 0

1356 AAAATATTCCACGCATC 1372

Conservative

Local Similarity es 14; Conserv

Best Loca Matches

17 AAAATAATGCACGGATC 1

plant growth; plant growth trait modulation; Brassicaceae; Arabidopsis; Brassica; Zea; Oryza; Triticum; Hordeum; Lolium; Sorghum; Glycine; Medicago; Helianthus; Lactuca; Beta; Vitis; Solanum; Lycopersicon; Capsicum; Gossypium; Hevea; Linum; Prunus; Citrus; Populus; Pinus;

Plant growth associated polynucleotide seg id 110.

(first entry)

29-JAN-2004

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                                                                                                                                                                                                                             primer; probe; tumour suppression; tumour reversion; apoptosis;
virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
Analysis of the expression of the nucleotides can be used for diagnosis
and/or prognosis of these diseases. The nucleotides and polypeptides can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
                                                                                                                                                                                                      cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
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                                                                                                                                                       Tumour suppression/reversion associated nucleotide #5321.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tuijnder M;
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                           ADB44998 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-SEP-2002; 2002WO-IB004219
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                                                                                                                  (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                  18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                       15-MAY-2003
                                                                     ADB44998;
      ADB44998
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New isolated or recombinant polypeptide for use in modulating a plant growth trait in a flowering plant e.g. in Arabidopsis, Brassica, Zea, or

Buckler ES;

(LYNX-) LYNX THERAPEUTICS INC.

Bowen BA, Haudenschild CD,

WPI; 2003-803305/75.

07-JAN-2003; 2003US-00338777. 09-JAN-2002; 2002US-0347288P.

US2003188343-A1. Magnoliophyta.

02-OCT-2003.

Quercus; ss.

Example 2; SEQ ID NO 110; 81pp; English.

Oryza.

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The invention describes an isolated or recombinant polypeptide (1) comprising a sequence: (a) comprising 1 of 30 sequences (51), as given in the specification, or a conservative variant; (b) encoded by 1 of 30 sequences ($2), as given in the specification, or a conservative variant; (c) encoded by a sequence that hybridises under stringent conditions to $2; and (d) encoded by a sequence 70 % identical to $2. The expression or activity of (I) is modulated to modulate a plant growth trait in a flowering plant, of the family Brassicaceae, preferably in a plant that is Arabidopsis, Brasslea, Zea, Oryza, Triticum, Hordeum, Lolium, Sorghum, Lycopersicon, Capsicum, Gossypium, Hevea, Linum, Prunus, Citrus, Populus, Plants, or Quercus. A new method is used to detect genes for a plant plant growth trait. This sequence represents a polymucleotide isolated from the plant growth associated genes of the invention that can be used a grown to the control of the contro
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1390 GATCAAAGGAGGTAAAA 1406

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Matches

17

GATCAAAGGAGAAACAA

ADE25135 standard; DNA; 17 BP

RESULT 115 ADE25135 ADE25135;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                             oligonuclectides, useful for diagnosis and cell typing, is to detect single-nuclectide polymorphisms and cytosine
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                                                                                                                                     Claim 1; SEQ ID NO 275206; 29pp + Sequence Listing; German
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Berlin K;
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Matches 12; Conservative
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 Olek A, Piepenbrock C,
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                                WPI; 2001-657177/75
                                                                                                    methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABC0010-ABE99989, ABC0010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                          Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 358611; 29pp + Sequence Listing; German.
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Matches 12; Conservative
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                       Homo sapiens
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acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABR0010-ABB9989 and ABI0010-ABB9989 and ABB9989 and ABB998 and ABB998 and ABB998 and ABB9989 and ABB998 and ABB
oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fib. wipo.int/pub/published_pct_sequences
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designed to detect single-nucleotide polymorphisms and cytosine
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100.0%; Pred. No. 1.6e+02;
iive 0; Mismatches 0; Indels
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ABC95961/c
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9.2%; Score 12; DB 1; Length 13;

Query Match

Sequence 13 BP; 7 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Local Similarity 100.
                                                                             12 TTGTTAATGATG 1
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ABF73478/C
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ABF58579/c
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABF00010-ABF99889, ABF00010-ABF99889 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                 Oligonucleotide SEQ ID NO 173475 for detecting SNP TSC0043213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 173475; 29pp + Sequence Listing; German.
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Best Local Similarity 100.0%; Pred, No. 1.8
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                (first entry)
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPD at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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100.0%; Pred. No. 1.8e+02;
iive 0; Mismatches 0;
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Matches 12; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
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                                                                                              This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABF9989, ABH00010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                               Claim 1; SEQ ID NO 122875; 29pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.2%; Score 12; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 12; Conservative 0; Mismatches 0; Indels
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                        methylation status.
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represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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RESULT 126 ABH4502 ABH45026;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The coligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010 ABC99989, ABF00010-ABF9989, ABH00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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100.0%; Pre-
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Best Local Similarity 100.6
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                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG.
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                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                              Olek A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                      Oligonucleotide SEQ ID NO 245003 for detecting SNP TSC0059825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       claim 1; SEQ ID NO 245003; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.2%; Score 12; DB 1; Length 13; 100.0%; Pred. No. 1.8e+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABF42023 standard; DNA; 13 BP.
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                  GGGGAAGAAAAA 13
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Best Local Similarity
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Gaps

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06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173.

Oligonucleotide SEQ ID NO 142020 for detecting SNP TSC0035574.

(first entry)

21-FEB-2002

XEXEXEX

ABF42023;

RESULT 127 ABF42023/c

Matches

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18-OCT-2001

Olek A,

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06-APR-2001; 2001WO-IB000713.
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Best Local Similarity luv..
Best Local 2; Conservative
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            Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG.
   (EPIG-) EPIGENOMICS AG
                    WPI; 2001-657177/75.
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                                                                                                                                                               RESULT 129
ABF22879/c
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine

WPI; 2001-657177/75.

methylation status.

Claim 1; SEQ ID NO 122876; 29pp + Sequence Listing; German

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This invention describes novel oligomucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically precreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE09989, ABF00010-ABE9989, ABH00010-ABE9989, and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH0010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                              Length 13;
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100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                            Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
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1es 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                         This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                        Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide SEQ ID NO 122876 for detecting SNP TSC0030713.
                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 245004; 29pp + Sequence Listing; German.
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100.0%; Pred. No. 1.8e+02;
live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Grouth Factor [IGF]-1 receptor, IGF binding protein [IGF]-1 receptor, IGF binding protein [IGF]-1 related to a standard cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense oligonucleotide which can be used to a sign the antisense oligonucleotide with a susful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, ineoplasias, seleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other selerotic disease, kidney disease, hyperproliferation of the inside of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a method for ameliorating the effects of
                                                                                                                                                Gaps
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                                                                9.2%; Score 12; DB 1; Length 13; 100.0%; Pred. No. 1.8e+02; Ive 0; Mismatches 0; Indels
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Sequence 13 BP; 7 A; 0 C; 1 G; 5 T; 0 U; 0 Other;
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                                                                                                          Similarity
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                                                                        Query Match
                                                                                                              Local
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AAF52309/C
ID AAF52309/C
XX AAF52309/C
DT 30-MAR
XX BE IGF-I
XX ANTISE
KW SKIN GER bi
KW KETATO
KW HIGF bi
KW HYPETIN
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DB 1; Length 15;

2.2e+02;

9.2%; Score 12; .00.0%; Pred. No.

100.08;

Best Local Similarity

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonuclectide, (for Insulin-like Growth Factor [IGF] receptor, IGF binding protein [IGFBP] -2 or IGFBPB), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonuclectide which can be used to design the antisense oligonuclectide which can be used to design the antisense oligonuclectides of the present invention (see AAF45151 and AAF45153 - F45161). The method is useful for ameliorating the effects of psortasis, ichthyosis, pityriasis, ruba, pilaris, serbornhoea, keloids, keratosis, neoplasis, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina,
                                                                                                                                                                                                                                                                                      Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFB-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.2%; Score 12; DB 1; Length 15;
100.0%; Pred. No. 2.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 BP; 5 A; 4 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Edmondson SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 8; Page 82; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUN-2000; 2000WO-AU000693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0140345P
                                                                                                                                                                                                                                                           IGF-I oligonucleotide #3267.
1413 ATGATGACCAGT 1424
                                                                                                                                        AAF52307 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1413 ATGATGACCAGT 1424
                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Werther GA,
                                   13 ATGATGACCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-041421/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200078341-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUN-1999;
                                                                                                                                                                                                                   30-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wraight CJ,
                                                                                                                                                                             AAF52307;
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                                                                                                  RESULT 132
                                                                                                                     AAF52307
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15 ATGATGACCAGT

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Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keartosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasis; kidney disease; neoblation; the retina; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MURD-) MURDOCH CHILDRENS RES INST.
                                                                AAF52310 standard; DNA; 15 BP
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                                                                                                                                                                                                                                                                          oligonucleotide #3270.
                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-041421/05.
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                                                                                                                                     AAF52310;
RESULT 133
AAF52310/c
ID AAF52310/c
XXX
AC AAF523
DDT 30-MAR
XXX
BE IGF-I
XXX
BRID GR bi
KW BIGF bi
KW BRID GR
KW BR
KW B
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Edmondson SR;

The present invention relates to a method for ameliorating the effects of antisense oligonucleotide, (for Insulin-like Growth Factor [IGF] receptor, IGF binding protein [IGRBP] - 2 or IGFBB3), which is capable of inhibiting or reducing protein [IGRBP] - 2 or IGFBB3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide so f the present invention (see AAF4151 and AAF45153 oligonucleotides of the present invention (see AAF4151 and AAF45153 ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or Example 8; Page 82; 201pp; English.

vessels or any other hyperplasia

Sequence 15 BP; 4 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

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; 0 9.2%; Score 12; DB 1; Length 15; 100.0%; Pred. No. 2.2e+02; ve 0; Mismatches 0; Indels 9.2°; 100.0%; FIU Query Match Best Local Similarity 100.0 **** Conservative

1413 ATGATGACCAGT 1424 ATGATGACCAGT 1

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RESULT 134

AAD32444 standard; DNA; 15 BP.

RESULT 135

AAD32444

AAD32444;

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1413 ATGATGACCAGT 1424

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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 creceptor, IGF binding protein [IGFBP], which is capable of inhibiting or reducing growth factor mediated cell proliferation, collgonucleotide which can be used to design the antisense collgonucleotide so the present invention the antisense collgonucleotides of the present invention (F45161). The method is useful for ameliorating the effects of psoriasis, colthhyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, conthyosis, pityriasis, ruba, pilaris, serborrhoea, caloids, keratosis, contendated malignancies, condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
                                                                                                                                                           Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; shi discorder; Insulin-like Growth Factor. I receptor; IGFP: pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neophasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplesia; kidney disease; neobascular condition; hyperplesia; kidney disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 BP; 4 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match
Local Similarity 100.0%; Pred. NO. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Edmondson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 8; Page 82; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vessels or any other hyperplasia
308/c
AAF52308 standard; DNA; 15 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUN-2000; 2000WO-AU000693
                                                                                                                               IGF-I oligonucleotide #3268
                                                                                            30-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wraight CJ, Werther GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-041421/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammation.
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUN-1999;
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                                                       AAF52308;
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The present invention relates to an isolated human olfactory receptor, family 1, subfamily G, member 1, (OR.G1) polymucleotide comprising a sequence which is a polymucrbic variant for a reference sequence for the OR.G1 game or its fragment, or a polymorphic variant of a reference sequence for a OR.G1 cDNA or its fragment. OR.G1 is useful in studying the expression and function of OR.G1 and in expressing OR.G1 protein for use in screening for candidate drugs to treat diseases related to OR.G1 activity. OR.G1 is useful for therapeutic purposes. The invention is useful for studying expression of the OR.G1 isogenes in vivo, for in vivo screening and testing of drugs targetted against OR.G1 protein, and for testing the efficacy of therapeutic agents and compounds for olfactory sensory deficitle, in a blotogical system. The invention is useful in gene therapy and is located on the . The present sequence is human OR.G1 gene polymorphism detecting ASO (allele specific oligomucleotide) probe
                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated human olfactory receptor, family 1, subfamily G, member 1 polymucleotide, for therapeutic purposes, for studying expression and function of the polymucleotide and for expressing receptor protein.
                                                                             Human, olfactory receptor family 1 subfamily G member 1; OR1G1; therapy; polymorphism; drug screening; olfactory sensory deficit; gene therapy; chromosome 17p13.3; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               erythropoietin; granulocyte colony stimulating factor;
                                                Human OR1G1 gene polymorphism detecting ASO probe #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15 BP; 6 A; 1 C; 4 G; 3 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hammerhead ribozyme substrate #25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 16; Page 13; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF01730 standard; DNA; 17 BP
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                                                                                                                                                                                                                                                                 03-AUG-2001; 2001WO-US024478.
                                                                                                                                                                                                                                                                                                  03-AUG-2000; 2000US-0222755P.
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Best Local Similarity 85.75
                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                        Messer C,
                                                                                                                                                                                                                                                                                                                                     (GENA-) GENAISSANCE
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-269097/31.
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                    18-JUN-2002
                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                              14-FEB-2002.
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                                                                                                                                                                                                                                                                                                                                                                        Kazemi A,
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Tanguay DA;

PHARM INC.

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The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                                                                                                                              Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ribozyme; erythropoietin; granulocyte colony stimulating factor; interferon alpha; 88.
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                                                                                                                                                                                                                                                                                                                                                                                            Length 17;
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                                                                                                                                                                                                                                                                                                                                                                              9.2%; Score 12; DB 1; Ler
100.0%; Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                Sequence 17 BP; 0 A; 6 C; 3 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blatt L, Zwick M, Pavco P, Mcswiggen J;
                                                                                                                Mcswiggen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 37; Page 56; 164pp; English
                                                                                                                                                                                                                        Claim 37; Page 56; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hammerhead ribozyme substrate #23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-2000; 2000WO-US009721.
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                                                              99US-0129390P
                                                                                                                  Pavco P,
                                     11-APR-2000; 2000WO-US009721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1347 AGGGGAAGAAA 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF01728 standard; DNA; 17
                                                                                      (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                         WPI; 2000-647423/62.
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hes 12; Conserv
                                                                                                                  Zwick M,
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                                                              12-APR-1999;
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           19-OCT-2000
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                                                                                                                  Blatt L,
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Matches
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Gaps

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9.2%; Score 12; DB 1; Length 15; 15.7%; Pred. No. 2.2e+02; ve 1; Mismatches 1; Indels

85.7%;

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            The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of represor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribozyme; erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.
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                                                                                                                                                                                                  / Match 9.2%; Score 12; DB 1; Length 17; Local Similarity 100.0%; Pred. No. 2.5e+02; nes 12; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                  Sequence 17 BP; 1 A; 5 C; 4 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hammerhead ribozyme substrate #1628.
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                                                                                                                                                                                                                                                                                                                                                                                          AAF03333 standard; DNA; 17
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The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRR-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha
                                                                                                                                                                                                                                                                                                                                                                     Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
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                                                                                                                   Ribozyme; erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.
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100.0%; Pred. No. 2.5e+02;
.ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                      Mcswiggen J;
                                                                                           Hammerhead ribozyme substrate #1379.
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100.0%; Pre-
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            AAF03084 standard; DNA; 17
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nes 12, Conserv
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AAF03084,
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Query Match
9.2%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels

1355 AAAATATTCCA 1366

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Claim 37; Page 93; 164pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                                                                                              Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
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                                                                                             Mcswiggen J;
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                                                        99US-0129390P
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                                                                          (RIBO-) RIBOZYME PHARM INC
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                                                                                                                                                                                                                                                          interferon alpha
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                                                                                             Blatt L,
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Best Local &
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The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRR-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoletin, granulocyte colony stimulating factor protein and interferon alpha
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100.0%; Pred. No. 2.5e+02;
iive 0; Mismatches 0;
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The present invention relates to murine oligonucleotides (ACC62754-ACC68806), which are associated with tumour suppression, tumour reversion, apoptosis and virus resistence. The oligonucleotides are useful as (1) as probes and primers for detecting, identifying, quantifying and/or amplifying nucleic acid, e.g. as one component of a gene chip; in vitro as (anti) sense reagents; and (2) for production of recombinant polypeptides. The oligonucleotides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
                                                                                                                                                   Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine; tumour suppression; tumour reversion; apoptosis; virus resistance; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; ss.
                                                                                                                       Murine oligonucleotide associated with tumour supression, SEQ ID 1141.
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                BP.
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                ACC63894 standard; DNA; 17
                                                                                    (first entry)
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      100.0%; Pred. ...
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tes 12; Conserv
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AAT54301 standard; RNA; 15 BP. (first entry) (revised) 25-MAR-2003 24-MAR-1997 AAT54301; RESULT 144 AAT54301 XXXEEX8

Human IL-5 hammerhead ribozyme target sequence (nt. position 580).

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gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; INF-alpha; respiratory syncytial virus; RSV; bor-abl; oncogene; translocation; chromic myelogenous leukaemia; CML; cancer; philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; heumatoid arthritis; psoriasis; myocardial ischaemia; Kawaeasi disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
trans cleavage; inhibition;
Enzymatic nucleic acid; ribozyme;
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94US-00291433.
94US-00292620.
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94US-00303039.
94US-00311486.
94US-00311749.
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94US-00316771.
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94US-00334847.
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94US-00357577.
94US-00363233.
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94US-0022795.
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94US-00245736.
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                                                                                                                                                                                                                                                                                                                                                            95WO-IB000156
                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-APR-1994;
15-APR-1994;
15-APR-1994;
18-MAY-1994;
06-JUL-1994;
15-AUG-1994;
                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                              WO9523225-A2
                                                                                                                                                                                                                                                                                                                                                            23-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-1994;
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10-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAR-1994
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b DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW; Karpeisky A, Kieich K, Matulic-Adamic J, Mcswiggen JA; Parco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD; Usman N, Wincott FE, Woolf T; Stinchcomb DT, Grimm S, Modak A, Tracz D,

(RIBO-) RIBOZYME PHARM INC.

WPI; 1995-351090/45.

Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes

Claim 2; Page 215; 407pp; English.

The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-5) mRNA at the nucleotide base position indicated in the DB line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the IL-5 target sequences and thereby inhibit IL-5 expression, making them useful for treating chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes and preventing the recruitment and activation of eosinophils. The

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Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                       Antisense therapy, antiproliferative, antinflammatory, antipsoriatic, cytostatic, dermatological, cardiant, virucide, ophthalmological, keloid, skin disorder, Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFB-2; IGFBP3; inflammation; psoriasis; pilaris, growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba, keartosis; neoplasis; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasis, kidney disease; neovascular condition of the retina; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUN-2000; 2000WO-AU000693.
                                                                                                                                                                             IGF-I oligonucleotide #1368.
                                                                               AAF50408 standard; DNA; 15
                                                                                                                                             30-MAR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammation.
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wraight CJ,
                                                                                                               AAF50408;
                                                 RESULT 146
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                                                                  AAF50408
                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use of isolated gene transcripts - useful for developing products for the diagnosis, prognosis and treatment of cancers, particularly colon and pancreatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX30947-31815 represent tag sequences of transcripts that are differentially expressed in colorectal cancer, in pancreatic cancer, or in both. The tag sequences can be used to identify genes by matching the tag to a gen data base member, or by using the tag sequences as probes to isolate unidentified genes from cDNA libraries. The tag sequences can also be used in a method for diagnosing colon or pancreatic cancer in a sample suspected of being neoplastic. The method comprises comparing the level of at least one transcript in a first sample of a tissue to a second sample, where the first sample is a colonic tissue suspected of being neoplastic and the second sample is a normal human colonic tissue. The transcript is identified by a tag selected from AAX30947-11815. The methods of the invention can be used in the diagnosis, prognosis and
ribozymes can also be used to treat eosinophilia (related to parasitic infection or with pulmonary infiltration) and L-tryptophan-associated eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 Tag sequence; colorectal cancer; pancreatic cancer; colon cancer; diagnosis; prognosis; treatment; ss.
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0
                                                                                                                                                                                                                                                                                                                                                                                    Tag sequence of a transcript increased in colorectal cancer.
                                                                                                            9.1%; Score 11.8; DB 1; Length 15; 60.0%; Pred. No. 2.3e+02; iive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;
                                                                            15 BP; 6 A; 2 C; 2 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 36; 120pp; English.
                                                                                                                                                                                                                                                                                         AAX31212 standard; DNA; 15 BP
                                                                                                                                                                             1357 AAATATTCCACGCAT 1371
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                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                              Query Match
Best Local Similarity 60.0.
Best Local 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9853319-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAY-1998;
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                                                                                                                                                                                                                                                                                                                       AAX31212;
                                                                                 Sequence
                                                 field.
                                                                                                                                                                                                                                                         RESULT 145
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Edmondson SR

Werther GA,

99US-0140345P

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                                                             The present invention relates to a method for ameliorating the effects of
                                                                                   skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP], which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 2.3e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 8 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
Example 8; Page 69; 201pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vessels or any other hyperplasia
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nes 13; Conservative
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Gaps

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Indels

Match 9.1%; Score 11.8; DB 1; Length 15; Local Similarity 86.7%; Pred. No. 2.3e+02; les 13; Conservative 0; Mismatches 2; Indels

Query Match

Matches

1433 GCAGACATATACATG 1447

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Antisense therapy, antiproliferative, antinflammatory, antipsoriatic; cytostatic, dermatological, cardiant, viucide, ophthalmological, keloid; skin disorder, Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pitais; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.

IGF-I oligonucleotide #1367.

30-MAR-2001 (first entry)

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The present invention relates to a method for ameliorating the effects of artisens edisorders. The method comprises contacting the skin with an antisense oligomuclectide, (for Insulin-like Growth Factor [IGF]) receptor, IGF binding protein [IGFBP]-2 or IGFBB], which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligomuclectide which can be used to design the antisense oligomuclectides of the present invention (see AAF4151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, inchthyosis, pityriasis, ruba, pitaris, serborrhoea, Keloids, keratosis, theoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
                                                                                                                                                                          Antisense therapy; antiproliferative; antinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin discorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBPB; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplama; kidney disease; neoblation of the retina; s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 BP; 6 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Edmondson SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 6; Page 43; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vessels or any other hyperplasia
                     AAF46528 standard; DNA; 15 BP
                                                                                                                                             IGFBP2 oligonucleotide #1367.
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                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-041421/05
                                                                                                                                                                                                                                                                                                                                                                                                                     WO200078341-A1.
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wraight CJ,
                                                                                                    30-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-DEC-2000.
                                                               AAF46528;
AAF46528
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Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Edmondson SR;

Wraight CJ, Werther GA, WPI; 2001-041421/05.

(MURD-) MURDOCH CHILDRENS RES INST.

99US-0140345P

21-JUN-1999;

21-JUN-2000; 2000WO-AU000693.

WO200078341-A1

28-DEC-2000.

Homo sapiens.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP]), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense is oligonucleotide which can be used to a second to see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, karatosis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, karatosis, hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, hyperproliferation of the inside of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a method for ameliorating the effects of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 11.8; DB 1; Length 15;
Pred. No. 2.3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 15 BP; 8 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 8; Page 69; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vessels or any other hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF50406 standard; DNA; 15 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGF-I oligonucleotide #1366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TCAAAGCAGGGAAAA 15
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001
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Gaps

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9.1%; Score 11.8; DB 1; Length 15; larity 86.7%; Pred. No. 2.3e+02; Conservative 0; Mismatches 2; Indels

Query Match Best Local Similarity Matches 13; Conserv

1348 GGGGAAGAAAATAT 1362

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1 GGGGAAGAGAATTT 15

AAF50407 standard; DNA; 15 BP

RESULT 148 AAF50407 AAF50407

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin discorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; kearbosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neoblasia; sclerotic disease; neoblasia; schoolition; hyperplasia; kidney disease; (MURD-) MURDOCH CHILDRENS RES INST. Example 8; Page 69; 201pp; English 99US-0140345P. 21-JUN-2000; 2000WO-AU000693 Werther GA, WPI; 2001-041421/05. WO200078341-A1. inflammation. 21-JUN-1999; Homo sapiens Wraight CJ, SOURCE COURSE SERVICE STREET SERVICE S

Edmondson SR;

The present invention relates to a method for ameliorating the effects of antisense oligonucleotide, (for Insulan-like Growth Factor [IGF] receptor, IGF binding protein [IGFBB] -2 or IGFBB3, which is capable inhibiting or reducing protein [IGFBB] -2 or IGFBB3, which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders of present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF4151 and AAF45153 - F45161). The method is useful for ameliorating the effects of psoriasis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

Sequence 15 BP; 8 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

Query Match

9.1%; Score 11.8; DB 1; Length 15; 86.7%; Pred. No. 2.3e+02; tive 0; Mismatches 2; Indels 1391 ATCAAAGGAGGTAAA 1405 13; Conservative Local Similarity Matches ઠ

ATCAAAGCAGGGAAA 15

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AAF46529 standard; DNA; 15 AAF46529; RESULT 150 AAF46529 ID AAF4 M.W.K. S. S. K. S.

BP.

(first entry) 30-MAR-2001 IGFBP2 oligonucleotide #1368.

Antisense therapy, antiproliferative, antiinflammatory, antipsoriatic, cytostatic, dermatological, cardiant, virucide, ophthalmological, keloid, skin disorder, Insulin-like Growth Factor 1 receptor, IGF-1, pityriasis,

IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; seleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss. Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or Edmondson SR; (MURD-) MURDOCH CHILDRENS RES INST. 21-JUN-2000; 2000WO-AU000693. 99US-0140345P. Werther GA, WPI; 2001-041421/05. WO200078341-A1. 21-JUN-1999; Homo sapiens Wraight CJ, 28-DEC-2000

Example 6; Page 43; 201pp; English.

inflammation.

antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 acceptor, IGF binding protein [IGFBF]-2 or IGFBF]-3 in thick is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborthoea, keloids, keratosis, ichthyosis, pityriasis, ruba, pilaris, serborthoea, keloids, keratosis, hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, hyperproliferation of the inside of blood present invention relates to a method for ameliorating the effects of vessels or any other hyperplasia

Sequence 15 BP; 6 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Gaps ; 0 Length 15; Indels 9.1%; Score 11.8; DB 1; 16.7%; Pred. No. 2.3e+02; ve 0; Mismatches 2; 86.78; Local Similarity 86.7 nes 13; Conservative Query Match Matches

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1349 GGGAAGAAAATATT 1363 GGGAAGAGAATTTT 15

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Gaps ;

IGFBP3 oligonucleotide #1525. (first entry) 30-MAR-2001 AAF48105;

AAF48105 standard; DNA; 15

RESULT 151

AAF48105,

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityrlaais; IGF binding protenin; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease;

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The patent application claims a plasmid contg. a restriction site, (a promoter region), an RBS and a signal sequence. The plasmid when introduced into a Bacillus host is useful for determining the efficiency of functional element(s) in the prodn. of a peptide. (Updated on 03-OCT-2002 to add missing OS field.)
                                                                                                                                                                                                                                                                       The invention relates to an isolated, purified human nucleic acid (I) that has the same sequence as a mENA found in humans and is a SAGE (serial analysis of gene expression) tag comprising a single stranded probe containing at least 10 consecutive nucleotides. SAGE tags, are diagnostic and prognostic markers of cancer, especially of the colon and pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New plasmid capable of replication in Bacillus strains - useful in evaluating regulatory or signal sequences for expression of hybrid gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of domain comprising at least one restriction site in plasmid
                                                                                                                                                                              93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                          New human nucleic acid containing specific SAGE tags, useful diagnostic markers for cancer, also derived probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.1%; Score 11.8; DB 1;
86.7%; Pred. No. 2.3e+02;
vative 0; Mismatches 2;
                                                                                               3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              capable of replication in Bacillus strains.
                                                                                               Zhou
                                                                                               Kinzler KW, Zhang L,
                                                                                                                                                                                                                                         Disclosure; Col 32; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2A; p19; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1433 GCAGACATATACATG 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86EP-00201951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus expression plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85NL-00003074
                 98US-00081646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAN70234 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 gradacagaracard 1
                                                                                                                                                                                                                                                                                                                                                                                                       SAGE tags of the invention
                                                       (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huygens AV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1987-151763/22.
                                                                                                                                      WPI; 2002-153821/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                 Vogelstein B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-NOV-1985;
                 20-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-2002
15-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUN-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP224294-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vanee JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAN70234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for ameliorating the effects of artisens of antisens contacting the skin with an antisense oligonuclectide, (for Insulin-IRe Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBB]-2 or IGFBB], which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonuclectide which can be used to design the antisense oligonuclectide which can be used to design the antisense oligonuclectides of the present invention (see AAF4151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pitaris, serborrhoea, Keloids, Keratosis, leoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovacular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
                                                                                                                                                                                                                                                                                                                                                            Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colon cancer; colorectal cancer; pancreatic cancer; SAGE tag; analysis of gene expression; diagnostic; prognostic; probe; marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15 BP; 3 A; 2 C; 2 G; 8 T; 0 U; 0 Other;
neovascular condition of the retina; ss.
                                                                                                                                                                                                                                                                                    Edmondson SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 7; Page 54; 201pp; English.
                                                                                                                                                                                                                                            (MURD-) MURDOCH CHILDRENS RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human colon cancer SAGE tag #267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vessels or any other hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1432 TGCAGACATATACAT 1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-00081646.
                                                                                                                                                               21-JUN-2000; 2000WO-AU000693
                                                                                                                                                                                                     99US-0140345P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 rgaagacaraacar 1
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                    Werther GA,
                                                                                                                                                                                                                                                                                                                          WPI; 2001-041421/05.
                                                                                WO200078341-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                              inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS6333152-B1
                                            Homo sapiens.
                                                                                                                                                                                                     21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-2002
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                                                                                                                                                                                                                                                                                    Wraight CJ,
                                                                                                                         28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK32166;
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serial
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Gaps

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AAT36418-T36420 are a 5' primer, probe and 3' primer, respectively, used for the amplification and detection of human papillomavirus 34 (HPV34) E6 gene. The E6 gene product is implicated in human papillomavirus carcinogenesis and therefore should be present in all HPV related cervical carcinomas. The primers and probe are used in a PCR/ELISA method for the diagnosis of HPV34 in a sample. HPV34 is a low-risk oncogenic HPV type, detection of the E6 gene in a sample indicates only a low risk of cervical cancer development. Primers and probes for high-risk HPV types (HPV16, HPV18, HPV35, etc.) are also used in the same PCR/ELISA method for diagnosis of oncogenic potential of a cervical smear. The probes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gnosis of oncogenic potential of a cervical smear. The probes and are also useful for diagnosing cervical cancer and high grade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting high oncogenic potential human papilloma virus strains - by specific PCR of nucleic acid in cervical cells, reacting amplified prod. with specific probe and detecting bound probe by ELISA.
                                                                                                             Human papillomavirus; HPV; oncogene; cervical cancer; neoplasia; probe; detection amplification; diagnosis; prognosis; high risk; low risk; ELISA; enzyme-linked immunosorbent assay; PCR; primer; polymerase chain reaction; 8s.
                                                                            Human papillomavirus 34 (HPV34) E6 gene 3' primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16 BP; 6 A; 0 C; 3 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wright TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Page 21; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                          95US-00390684.
                                                                                                                                                                                                                                                                                                                                                                  96WO-US002130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABZ34141 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lungu 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 ATAAAATTATTCCAC
                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Silverstein SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                  16-FEB-1996;
                                                                                                                                                                                                                                                                               WO9625521-A1
                                                                                                                                                                                                                                                                                                                                                                                                             17-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
                                          15-APR-1997
                                                                                                                                                                                                                                                                                                                       22-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABZ34141;
  AAT36420;
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ABZ34141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of antisense c-jun, c-fos or jun-B nucleic acids - for preventing and treating neuronal injury, degeneration, cell death and/or neoplasms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense nucleic acid hybridising with an area of the mRNA and/or DNA comprising the genes c-jun, jun-B or c-fos, expression of which plays a causal role in neuronal injury, degeneration, call death and/or neoplasms, can be used to prevent and treat such conditions. c-jun antisense sequences are described in AAQ83267-321 and AAQ83440-43; jun-B for antisense sequences are described in AAQ83322-63 and AAQ83444-65; and c-for antisense sequences are described in AAQ83364-439 and AAQ8346-51. Preferably the antisense sequences are posphorothicate oligonucleotides since these are not described as fast by endogenous factors as naturally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             jun-B; neuronal injury; cell death; neoplasm; antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brysch W;
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     occuring molecules. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schlingensiepen R, Schlingensiepen K,
                                                              9.1%; Score 11.8; DB 1; Length 16; 86.7%; Pred. No. 2.5e+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 16 BP; 2 A; 3 C; 4 G; 7 T; 0 U; 0 Other
                          Sequence 16 BP; 5 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 45; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            jub-B antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1438 CATATACATGGAAGA 1452
                                                                                                                                                                                                                                                                                                            BP
                                                                                                                                                          1390 GATCAAAGGAGGTAA 1404
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                                                                                                                                                                                                                                                                                                            AAQ83356 standard; DNA; 16
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                                                                     Query Match
Best Local Similarity 86.73
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         c-jun; c-fos; jun-B;
phosphorothioate; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schlingensiepen G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9502051-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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Richart RM;

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                                                                                                                                                                                                                                                                     Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme; detection; mutation; anti-HIV drug resistance; polymorphism; resistance;
                            Gaps
                                                                                                                                                                                                                                          HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:383.
                            ;
0
9.1%; Score 11.8; DB 1; Length 16; 86.7%; Pred. No. 2.5e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus 1.
                                                                                                                                                            ВР.
                                                         1353 AGAAAATATTCCAC 1367
                                                                                                                                                                                                                                                                                                     probe; ss.
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AAT36420 standard; DNA; 16 BP

RESULT 155 AAT36420/ ID AAT3 XX

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18-JUL-2002

Synthetic.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                 of oligonucleotides, useful for diagnosis and cell typing, is igned to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.9%; Score 11.6; DB 1; Length 13; 91.7%; Pred. No. 2.1e+02; ative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 189699; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13 BP; 3 A; 0 C; 3 G; 6 T; 0 U; 1 Other;
                                                                                                                                                                                         Berlin K;
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                                             06-APR-2001; 2001WO-IB000713
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                                                                                                                                                                                                                                                                                                                                          methylation status.
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18-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for detecting mutations associated with anti-HIV drug resistance in a patient by detecting at associated with anti-HIV drug resistance in a patient by detecting at least one of the mutations K103N/R, V106A/I/L, V181C/I, M184V/I, Y18BL, C G190A/S/R, 721SY/FD/S/A and/or Q151M/L in the reverse transcriptase (RT) of HIV strains in a biological sample using a specific set of probes optimised to function together in a reverse-hybridisation assay. The method and the mucleic acid sequences used in the method are useful for determining viral mutations and/or polymorphisms in the HIV RT gene associated with resistance. The probes are useful for the genetic detection, preferably in vitro detection of the mutations K103N/R, C 715X/F/D/S/A in the RT of HIV strains in a biological sample, where the mutation is associated with anti-HIV drug resistance. The method provides a rapid, reliable and precise assay or determination and monitoring of a rapid, reliable and precise assay or determination and monitoring of a rapid, reliable mathem anti-HIV drug resistance of a rapid, reliable mathem and associated with drug resistance of a rapid, reliable and precise assay or determination and monitoring of a rapid, reliable mathem and an apple and probes which are used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting mutations associated with anti-HIV drug resistance comprises detecting at least one of the mutations in the HIV reverse transcriptase gene by using probes optimized to function together in a reverse-hybridization assay.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 26; 117pp; English.
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20-APR-2001; 2001EP-00870085.
24-APR-2001; 2001US-0286102P.
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ID ABF89702 standard; DNA; 13
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Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                             (INNO-) INNOGENETICS NV
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide SEQ ID NO 189700 for detecting SNP TSC0046671.
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WO200177384-A2

Homo sapiens

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
                                                                                           This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABE99989 and ABI00010-ABE99987 are present the oligomers described in the invention. NOTE: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                              Claim 1; SEQ ID NO 189700; 29pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                  Sequence 13 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 1 Other;
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Best Local Similarity
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABE99899 ABR00010-ABE99899 and ABI00010-ABE9003 represent the oligomers described in the invention. NOTE: The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/pub/lished_pct_sequences
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                  8.8%; Score 11.4; DB 1; Length 13; 92.3%; Pred. No. 2.38+02; tive 0; Mismatches 1; Indels
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                                                                                              Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 U; 0 Other;
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ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 92.33
Matches 12, Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, certral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                        Oligonucleotide SEQ ID NO 64463 for detecting SNP TSC0017001.
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                                                                                     ABC64446 standard; DNA; 13
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF0010-ABF9989, ABH0010-ABH99999 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 136992; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13 BP; 5 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was obtained in electronic format from WI
ftp.wipo.int/pub/published_pct_sequences
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les 12; Conservative
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                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                              methylation status.
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1; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of oligonucleotides, useful for diagnosis and cell typing, igned to detect single-nucleotide polymorphisms and cytosine
                                                                                                      Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             8.8%; Score 11.4; DB 1; Length 13; 92.3%; Pred. No. 2.3e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                         Claim 1; SEQ ID NO 138953; 29pp + Sequence Listing; German.
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                                             Berlin K;
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Best Local Similarity 92.3%
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                                             Piepenbrock C,
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             (EPIG-) EPIGENOMICS AG
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Claim 1; SEQ ID NO 172419; 29pp + Sequence Listing; German.

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 ABC99999, ABF00010-ABF99999 and ABI00010-ABI22073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPD at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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tes 12; Conservative
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                   Oligonucleotide SEQ ID NO 189806 for detecting SNP TSC0046704.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 189806; 29pp + Sequence Listing; German.
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 ABF89809 standard; DNA; 13
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                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG
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                           Score 11.4; DB 1; Length 13;
Pred. No. 2.3e+02;
0; Mismatches 1; Indels
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Seguence 13 BP; 9 A; 1 C; 0 G; 3 T; 0 U; 0 Other;
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                             Query Match
Best Local Similarity 92.3%;
Matches 12; Conservative
                                                                                      1352 AAGAAAATATTC 1364
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Best Local Similarity 92.3
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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1403 AAATTGTTAATG 1415

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AAAATTGTTTATG 13

RESULT 167

ABF89809

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                                                                                                                                                                                                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 92.3°
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                                                                                                                         Olek A, Piepenbrock C,
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                                                                                                   (EPIG-) EPIGENOMICS AG
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,
                                                                                                                                                                                                                                                                              acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF0010-ABF9989 and ABI0010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                       Claim 1; SEQ ID NO 137724; 29pp + Sequence Listing; German
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABE9989, ABF00010-ABE9989, ABF00010-ABE9989, ABF00010-ABE9989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989 and ABI00010-ABE99998 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fixed from but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                   8.8%; Score 11.4; DB 1; Length 13; 32.3%; Pred. No. 2.3e+02;
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                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                  Sequence 13 BP; 8 A; 1 C; 0 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                         1 AATAAAATATTC 13
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Matches 12; Conservative
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ABC99864
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABC0010-ABE09989, ABC0010-ABE99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                Oligonucleotide SEQ ID NO 221379 for detecting SNP TSC0053879.
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                                                                                                         ABH21402 standard; DNA; 13 BP
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1402 TAAATTGTTAAT 1414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
              Oligonucleotide SEQ ID NO 63940 for detecting SNP TSC0016878.
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ò Gaps ö 8.8%; Score 11.4; DB 1; Length 13; nilarity 92.3%; Pred. No. 2.3e+02; Conservative 0; Mismatches 1; Indels Sequence 13 BP; 7 A; 3 C; 0 G; 3 T; 0 U; 0 Other, 1407 TTGTTAATGATGA 1419 Local Similarity 12; Query Match Matches à

Oligonucleotide SEQ ID NO 145723 for detecting SNP TSC0036706. BP. ABF45726 standard; DNA; 13 (first entry) rrgrraargriga 1 21-FEB-2002 13 ABF45726: RESULT 174 ABF45726

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

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06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

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WPI; 2001-657177/75.

oligonucleotides, useful for diagnosis and cell typing, is to detect single-nucleotide polymorphisms and cytosine methylation status. φ

Claim 1; SEQ ID NO 145723; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fire.wipo.int/pub/published_pot_sequences

Sequence 13 BP; 5 A; 0 C; 3 G; 5 T; 0 U; 0 Other;

Gaps .. 0 Length 13; Indels Score 11.4; DB 1; Pred. No. 2.3e+02; 0; Mismatches 8.8%; 92.3%; Conservative Local Similarity ses 12; Conserv Query Match Matches

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1406 ATTGTTAATGATG 1418 1 ATTGTTAATGAAG

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ABF54798 standard; DNA; 13 BP. 21-FEB-2002 (first entry) ABF54798; RESULT 175 ABF54798/ ID ABF5 THE STATE OF THE S

Oligonucleotide SEQ ID NO 154795 for detecting SNP TSC0009515.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K; Piepenbrock C, Olek A,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABC0010-ABE99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
Claim 1; SEQ ID NO 154795; 29pp + Sequence Listing; German
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Query Match

8.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels Sequence 13 BP; 4 A; 0 C; 1 G; 8 T; 0 U; 0 Other; 1352 AAGAAAATATTC 1364 ଚ

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Gaps

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13 AATAAAAATATTC 1 d

ABF37376 standard; DNA; 13 BP. 21-FEB-2002 (first entry) ABF37376; RESULT 176

Oligonucleotide SEQ ID NO 137373 for detecting SNP TSC0034317.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2

18-0CT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 137373; 29pp + Sequence Listing; German.

acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989, ABH00010-ABE99989, ABH00010-ABE99989, ABE00010-ABE99989, ABE00010-ABE9989, AB This invention describes novel oligonucleotide primers or peptide nucleic

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Gaps

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Query Match

8.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels

1406 ATTGTTAATGATG 1418

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire vipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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92.3%;
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central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                         Oligonucleotide SEQ ID NO 171583 for detecting SNP TSC0042775.
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                                               ABF71586 standard; DNA; 13 BP
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8.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 1; Indels
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(EPIG-) EPIGENOMICS AG
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABH00010-ABH99989 and ABI00010-ABF99819, ABH00010-ABH99989 and ABI00010-ABF99810, ABF00010-ABH99989 and ABI00010-ABF99810, ABF00010-ABH99989 and ABI00010-ABF99810, ABF00010-ABH99989 and ABI00010-ABF99810, ABF00010-ABH99989 and ABI00010-ABF99810, ABF00010-ABF99810, ABF00010-ABF99810, ABF00010-ABH998980, ABF00010-ABH998980, ABF00010-ABF998980, ABF00010-ABH998980, ABH900010-ABH998980, ABH900010-ABH998980, ABH900010-ABH99880, ABH99880, 
and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coingomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABF9989 and ABI00010-ABF32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fup.wipo.int/pub/published_pct_sequences
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and extosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0001-ABC99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                        Oligonucleotide SEQ ID NO 173477 for detecting SNP TSC0043213.
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92.3%; Pred. No. 2.3e+02;
ive 0; Mismatches 1;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABH99999 and ABI00110-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010
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Set of oligonucleotides, useful for diagnosis and cell typing, addesigned to detect single-nucleotide polymorphisms and cytosine
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                                                                        Claim 1; SEQ ID NO 137374; 29pp + Sequence Listing; German.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABH00010-ABH99989 and ABI00010-ABIS2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NoTE: The sequence data for this partent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                     RESULT 188
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABR00010-ABH99989 and ABI00010-ABR92073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained, in electronic format from WIPO at
                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                      Oligonucleotide SEQ ID NO 138954 for detecting SNP TSC0034809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.8%; Score 11.4; DB 1; Length 13; 92.3%; Pred. No. 2.3e+02; vative 0; Mismatches 1; Indel8
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Best Local 12; Conservative
                                                                              ABF38957 standard; DNA; 13
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                                                                                                              ABF38957;
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Query Match 8.8%; Score 11.4; DB 1; Length 13; Best Local Similarity 92.3%; Pred. No. 2.3e+02; Matches 12; Conservative 0; Mismatches 1; Indels

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Berlin K;

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Olek A,

WPI; 2001-657177/75.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99889, ABH00010-ABH99889 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at they published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
                                                                                                                                                                                                                                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 151702; 29pp + Sequence Listing; German.
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Best Local Similarity 92.3%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9999, ABF00010-ABF9999 and ABI0010-ABF2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                       ber or oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                   Claim 1; SEQ ID NO 237050; 29pp + Sequence Listing; German.
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32.3%; Pred. No. 2.3e+02;
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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8.8%; Score 11.4; DB 1; Length 13; 92.3%; Pred. No. 2.3e+02; ive 0; Mismatches 1; Indels Sequence 13 BP; 5 A; 1 C; 0 G; 7 T; 0 U; 0 Other; 1402 TAAATTGTTAAT 1414 Query Match Best Local Similarity 92.38 Matches 12; Conservative

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TAAAATGTTAAT 1 13 ò 셤

ABC38138 standard; DNA; 13 BP. ABC38138; RESULT 193

Oligonucleotide SEQ ID NO 38155 for detecting SNP TSC0011826. (first entry) 20-FEB-2002

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 38155; 29pp + Sequence Listing; German.

ftp.wipo.int/pub/published_pct_sequences ABC38138/6

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1 AGGGGAAAAAAA 13

RESULT 195

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Query Match Best Local Similarity

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 2.3e+02;
0; Mismatches 1; Indels
                                         Length 13;
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          Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
                                         Score 11.4; DB 1;
Pred. No. 2.3e+02;
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ftp.wipo.int/pub/published_pct_sequences
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                                             Match 8.8%;
Local Similarity 92.3%;
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                                                                                                                   1361 ATTCCACGCATCA 1373
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ABH16258;

ABH16258

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99889, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire wipo.int/pub/published_pot_sequences
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Homo sapiens,
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                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                               Oligonucleotide SEQ ID NO 216235 for detecting SNP TSC0052586.
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Matches 12; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory. Central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC00010-ABC99999, ABF00010-ABP9999, ABF00010-ABP9999, ABF00010-ABC9010 ABC00010-ABC0010 ABC00010-ABC0010 ABC0010 ABC00010 ABC0010 ABC001
                        central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989 and ABI00010-ABF9989 and ABI00010-ABF9989 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at figuriar from the printed specification, but figuration. The sequences of the printed specification and figuration in the problem of the sequences.
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range of diseases including immune system, gastrointestinal, respiratory,
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                      acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastrointestinal, respiratory. Central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE09989, ABF00010-ABE09989, ABF00010-ABE9989, ABF00010-ABE9989, and ABI0010-ABE82073 tarpresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form par of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but the wibo.int/pub/published_pct_sequences
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                                                                                                       Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 83729; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABH00010-ABH99989, ABH00010-ABH99899 and ABI00010-ABH99808, ABH00010-ABH99898, Chance are also used for detecting cell type differentiation. ABC00010-ABE99898, ABH00010-ABH99989, ABH00010-ABH99898, ABH00010-ABH99898, ABH00010-ABH998989, ABH90010-ABH998989, ABH90010-ABH9989899, ABH90010-ABH998989, ABH90010-ABH998989, ABH90010-ABH998989, ABH90010-ABH998989, ABH90010-ABH998989, ABH90010-ABH998989, ABH90010-ABH998989, ABH90010-ABH998989, ABH998989, ABH900010-ABH998989, ABH900010-ABH998989, ABH900010-ABH998989, ABH900010-ABH998989, ABH900010-ABH998989, ABH900010-ABH998989, ABH900010-ABH9989899, ABH998989, ABH99899, ABH99899, ABH99899, ABH99899, ABH99899, ABH999899, ABH99899, ABH999899, ABH999899, ABH999899, ABH9998999, ABH999899, ABH999899, ABH999899, ABH999899, ABH999899, ABH9998
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                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                        Oligonucleotide SEQ ID NO 38156 for detecting SNP TSC0011826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berlin K;
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20-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                          1356 AAATATTCCACG 1368
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                      12; Conservative
                                                                                                                           13 ACAATATTCCACG 1
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
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Pred. No. 2.3e+02;
                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 63939; 29pp + Sequence Listing; German.
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               06-APR-2001; 2001WO-IB000713.
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                                                                                                             Olek A, Piepenbrock C,
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                                                                             (EPIG-) EPIGENOMICS
                                                                                                                                          WPI; 2001-657177/75
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Best Local Similarity
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABR00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                    Claim 1; SEQ ID NO 66953; 29pp + Sequence Listing; German.
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methylation status.
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ABF72423/c
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SNP, single nucleotide polymorphism, human; diagnosis, PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

WO200177384-A2.

18-OCT-2001.

Homo sapiens.

Oligonucleotide SEQ ID NO 216234 for detecting SNP TSC0052586.

ABH16257 standard; DNA; 13

ABH16257

ABH16257;

22-FEB-2002 (first entry)

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                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                              Oligonucleotide SEQ ID NO 150141 for detecting SNP TSC0037898.
                                                                           Query Match 8.8%; Score 11.4; DB 1; Length 13; Best Local Similarity 92.3%; Pred. No. 2.3e+02; Matches 12; Conservative 0; Mismatches 1; Indels
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                                                      Seguence 13 BP; 7 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                      13 ATTGTTAATGTTG 1
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Query Match 8.8%; Score 11.4; DB 1; Length 13; Best Local Similarity 92.3%; Pred. No. 2.3e+02; Matches 12; Conservative 0; Mismatches 1; Indels

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1352 AAGAAAATATTC 1364

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13 AAAAAAAATATTC 1

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Best Local Similarity 92.3
Matches 12; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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92.3%;
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Query Match

Best Local Similarity 92.5.,

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12; Conservative
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                                Piepenbrock C,
(EPIG-) EPIGENOMICS AG.
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peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
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Oligonucleotide SEQ ID NO 237019 for detecting SNP TSC0057824. ABH37042 standard; DNA; 13 BP. (first entry) 1 AAAATTGATAATG 13 22-FEB-2002 ABH37042; RESULT 210 ABH37042/ 셤

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173. WO200177384-A2 Homo sapiens 18-OCT-2001

Berlin K; Piepenbrock C, Olek A,

(EPIG-) EPIGENOMICS

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oligonuclectides, useful for diagnosis and cell typing, is ed to detect single-nuclectide polymorphisms and cytosine methylation status. Set of

Claim 1; SEQ ID NO 237019; 29pp + Sequence Listing; German

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Sequence 13 BP; 2 A; 1 C; 6 G; 4 T; 0 U; 0 Other;

ABF37726 standard; DNA; 13 BP.

RESULT 212

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                                                                                                                                                                                                                                                                                                                     SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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 Length 13;
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92.3%; Pred. No. 2.3e+02;
ive 0; Mismatches 1;
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Matches 12, Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                            Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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WO200177384-A2
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                                                                                                                                                                                                                                                                          olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                        Oligonucleotide SEQ ID NO 137723 for detecting SNP TSC0034420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.8%; Score 11.4; DB 1; Length 13; 92.3%; Pred. No. 2.3e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 137723; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berlin K;
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Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                       Oligonucleotide SEQ ID NO 231560 for detecting SNP TSC0056462.
                        8.8%; Score 11.4; DB 1; Length 13; 92.3%; Pred, No. 2.3e+02; ative 0; Mismatches 1; Indels
Sequence 13 BP; 0 A; 6 C; 0 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berlin K;
                                                                                                                                                                 BP.
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                                                                           1347 AGGGGAAGAAAA 1359
                                                                                                                                                               ABH31583 standard; DNA; 13
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                   Query Match
Best Local Similarity 92.3<sup>3</sup>
                                                                                                    13 AGGGGAAGGAAAA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-657177/75.
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Homo sapiens

RESULT 213

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schultz911-3.rng

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE9989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
          Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                     Claim 1; SEQ ID NO 231560; 29pp + Sequence Listing; German.
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Query Match 8.8%; Score 11.4; DB 1; Length 13; Best Local Similarity 92.3%; Pred. No. 2.3e+02; Matches 12; Conservative 0; Mismatches 1; Indels Sequence 13 BP; 4 A; 2 C; 0 G; 7 T; 0 U; 0 Other; 1403 AAAATTGTTAATG 1415 13 AAAATTGATAATG 1 ò g

215

ABH37071 standard; DNA; 13 ABH37071; RESULT 21: ABH37071/

BP

(first entry) 22-FEB-2002

Oligonucleotide SEQ ID NO 237048 for detecting SNP TSC0057828.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

EPIG-) EPIGENOMICS AG

ver or origonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. Berlin K; Olek A, Piepenbrock C, WPI; 2001-657177/75.

Claim 1; SEQ ID NO 237048; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The

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oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at flow this published pot_sequences
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Sequence 13 BP; 6 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

Gaps .; 0 8.8%; Score 11.4; DB 1; Length 13; 92.3%; Pred. No. 2.3e+02; ative 0; Mismatches 1; Indels Local Similarity 92.3 Query Match Matches

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1406 ATTGTTAATGATG 1418 13 Arrefreardard 1 à g

RESULT 216 ABH16256

ABH16256 standard; DNA; 13

BP.

ABH16256;

(first entry) 22-FEB-2002

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Gaps

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Oligonucleotide SEQ ID NO 216233 for detecting SNP TSC0052586.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Berlin K; ú Piepenbrock olek A,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 216233; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at

Seguence 13 BP; 6 A; 0 C; 3 G; 4 T; 0 U; 0 Other;

Gaps .; 0 8.8%; Score 11.4; DB 1; Length 13; 92.3%; Pred. No. 2.3e+02; 1; Indels 0; Mismatches Query Match
Best Local Similarity 92.3
Matches 12; Conservative

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABMO0010-ABH99989 and ABI00010-ABIS2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        set or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Oligonucleotide SEQ ID NO 99882 for detecting SNP TSC0024826.
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13 TAAATTTGTTAAT
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ABF61093/
        8X46466666666668X8X444448
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                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                ABH16259 standard; DNA; 13 BP.
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                                            AAATTGGTAATGA 13
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Best Local Similarity
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ABC99865/c
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RESULT 21:

XXX ABHIGES9/
XXX ABHIGES OLIGY
DT 22-F)
DE XXX XXX XXX
XXX YXX Cent.
XXX YXX Cent.
XXX YXX Cent.
XXX XXX Colaid
CC acid.
CC acid.
CC colaid
CC

SYSXEX

8 g

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Gaps

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1; Indels

Length 13;

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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                            Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                         Claim 1; SEQ ID NO 161090; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                        Sequence 13 BP; 6 A; 2 C; 0 G; 5 T; 0 U; 0 Other;
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     07-APR-2000; 2000DE-01019173.
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Matches 12; Conservative
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                                              Olek A, Piepenbrock C,
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                          (EPIG-) EPIGENOMICS AG
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
                                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine
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Claim 1; SEQ ID NO 237047; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                  Oligonucleotide SEQ ID NO 46249 for detecting SNP TSC0013388.
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                                             8.8%; Score 11.4; DB 1; Length 13; ilarity 92.3%; Pred. No. 2.3e+02; Conservative 0; Mismatches 1; Indels
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                      Sequence 13 BP; 4 A; 1 C; 3 G; 5 T; 0 U; 0 Other;
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ftp.wipo.int/pub/published_pct_sequences
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llarity 92.3%; Pred. No. 2.3e+02;
Conservative 0; Mismatches 1; Indels
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ABC97181 standard; DNA; 13
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Homo sapiens.

18-OCT-2001

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The
                                                                                                                                                                                                                       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABM00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                    Claim 1; SEQ ID NO 64464; 29pp + Sequence Listing; German.
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Berlin K;
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methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single-nuclectide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.8%; Score 11.4; DB 1; Length 13; Best Local Similarity 92.3%; Pred. No. 2.3e+02; Matches 12; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 85504; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13 BP; 6 A; 2 C; 0 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                            07-APR-2000; 2000DE-01019173
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                                                                                      WO200177384-A2.
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Homo sapiens

ABC64447;

RESULT 225

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Gaps

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide SEQ ID NO 223955 for detecting SNP TSC0054559
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                                                                                                                                                                                                                                               Length 13;
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                                                                                                                                                                                                         Sequence 13 BP; 6 A; 4 C; 1 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                             8.8%; Score 11.4; DB 1;
92.3%; Pred. No. 2.3e+02;
live 0; Mismatches 1;
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Best Local Similarity 92.3
Matches 12; Conservative
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8.8%; Score 11.4; DB 1; Length 13;

Query Match

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                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13 BP; 5 A; 0 C; 2 G; 6 T; 0 U; 0 Other;
Pred. No. 2.3e+02;
0; Mismatches 1;
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Pred. No. 2.3e+02;
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                                             1355 AAAAATATTCCAC 1367
                                                                                                                                                        ABF51704 standard; DNA; 13
                                                                                                                                                                                                                      21-FEB-2002 (first entry)
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Local Similarity 92.3
nes 12; Conservative
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                                                                           13 AAAAATATTCTAC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   designed to detect amethylation status.
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                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                Matches
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95WO-US016000.
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                                                                                                                                                              RIBOZYME PHARM
                                                                                                                                                                              (WARN ) WARNER LAMBERT
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              Homo sapiens.
                                           WO9620279-A1.
                                                                                                    11-DEC-1995;
                                                                                                                                  23-DEC-1994;
                                                                      04-JUL-1996
                                                                                                                                                                                                           Couture L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the isolation of seepweed (Suaeda liaotungensis kitag) choline monooxygenase (CMO), and the polynucleotide sequence encoding it. The present invention may be used in gene conversion to reach the aim of raising a plant's salt tolerance, low temperature resistance, and drought tolerance. The present sequence represents a reverse transcriptase (RT)-PCR primer used in the examples of the present invention. (Updated on 27-OCT-2003 to standardise OS
                                                                                 Seepweed; choline monooxygenase; CMO; gene conversion; salt tolerance; low temperature resistance; drought tolerance; reverse transcriptase-PCR; RT-PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                           RT-PCR primer for cDNA encoding seepweed choline monooxygenase (CMO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suaeda liaotungensis kitag chloine monoxygenase gene and its cloning
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                                                                                                                                                                                                                                         /note= "Optionally modified by p (not defined)"
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Pred. No. 2.5e+02;
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                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                  *tag= a
mod base= OTHER
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92.3%;
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                                                                                                                                                      Suaeda liaotungensis; kitag.
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                     (revised)
(first entry)
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nes 12; Conservative
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                                                                                                                                                                                     Key
modified_base
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                     27-OCT-2003
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Li Q,

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AAT49608-T49863 represent target sequences for the human cholesterol
cetter transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
cetter transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
CC T50137) CETP is a 74 kD glycoprotein that facilitates neutral lipid
cransfer between plasma lipoproteins. The numbering of the targets refers
cc to the position of the cleaveds site in full length CETP. The ribozyme
cc binds to 5 nucleotides either side of this site, provided the sequence UH
cs immediately upstream. The ribozymes are able to cleave mRNA from the
cc gene encoding CETP, thereby blocking synthesis and/or expression of the
can be inhibited (or eliminated) thereby preventing the reduction in size
can be inhibited (or eliminated) thereby preventing the reduction in size
cdensity of the high density lipoproteins (HDL), prolonging HDL half life,
and therefore increasing HDL levels The ribozymes can be used to treat
conditions associated with abnormal levels of CETP, specifically familial
cc conditions associated with abnormal levels of HDL, and low
cc conditions laterons of diabetes, transplant, atherectomy and
congipatric restenosis. By inhibiting CETP, the levels of HDL and low
cc angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
density lipoproteins (LDL), and the HDL.LDL ratio are favourably altered
can density lipoproteins (LDL), and a corresponding increase in HDL levels.
cc The HH ribozymes can also be used diagnostically to study genetic drift
cribozymes target specific regions of the CETP gene, they have low non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage; neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy; reverse cholesterol transport; high density lipoprotein; therapy; CETP; familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
                                                                                                                                                                                New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA useful for preventing or treating initial development, progression or regression of vascular diseases, esp. familial hypercholesterolaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
Bisgaier C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15 BP; 3 A; 0 C; 7 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.8%; Score 11.4; DB 1;
31.5%; Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human CETP HH ribozyme target sequence #670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
     Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 32; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
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AAT49821;

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RESULT 230

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AAT49821

Query Match

Matches

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AAT49608-T49863 represent target sequences for the human cholesterol
ceter transfer protein (CETP) hammerhead (HH) ribozymes (see AAT49881-
150137) CETP is a 74 kD glycoprotein that facilitates neutral lipid
transfer between plasma lipoproteins. The numbering of the targets refers
to the position of the cleavage site in full length CETP. The ribozyme
binds to 5 nucleotides either side of this site, provided the sequence UH
is immediately upstream. The ribozymes are able to cleave mRNA from the
gene encoding CETP, thereby blocking synthesis and/or expression of the
mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
can be inhibited (or eliminated) thereby preventing the reduction in size
density of the high density lipoproteins (HDL), prolonging HDL half life,
and therefore increasing HDL levels. The ribozymes can be used to treat
conditions associated with abnormal levels of CETP, specifically familial
hypercholesterolaemia, hypoalphalipoproteinaemia, dyslipidaemia,
hypercholesterolaemia, hypoalphalipoproteinaemia, dyslipidaemia,
angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
density lipoproteins (LDL), and the HDL.LDL ratio are favourably altered
the decrease in LDL levels, and a corresponding increase in HDL levels.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The HH ribozymes can also be used diagnostically to study genetic drift and mutations in diseased cells, and to detect CETP mRNA. As the HH ribozymes target specific regions of the CETP gene, they have low non-
peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor; angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for preventing or treating initial development, progression or regression of vascular diseases, esp. familial hypercholesterolaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.8%; Score 11.4; DB 1; Length 15; Best Local Similarity 76.9%; Pred. No. 2.8e+02; Matches 10; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                           Pape
                                                                                                                                                                                                                                                                                                                                                           Bisgaier C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 BP; 4 A; 3 C; 6 G; 0 T; 2 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe 184w25 for wild type HIV RT gene Q182M184.
                                                                                                                                                                                                                                                                                                                                                           Couture L, Stinchcomb D, Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 30; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT98966 standard; DNA; 15
                                                                                                                                                                                                                                                                                            (RIBO-) RIBOZYME PHARM INC. (WARN ) WARNER LAMBERT CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specific activity
                                                                                      Homo sapiens.
                                                                                                                             WO9620279-A1
                                                                                                                                                                                                              11-DEC-1995;
                                                                                                                                                                       04-JUL-1996
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                                             LDL; ss.
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This sequence represents a probe for a wild type HIV reverse
transcriptase (RT) gene fragment. This sequence can be used in the method
cr transcriptase (RT) gene fragment. This sequence can be used in the method
cr viruses which contain RT genes and are present in a biological sample. It
comprises: (1) releasing, isolating or concentrating the polymucleic
caids present in a sample; (2) amplifying the relevant part of the RT
genes present with at least one suitable primer pair; (3) hybridising the
copyrucleic acids of step (1) or (2) with at least two RT gene probes,
the probes being applied to known locations on a solid support, and are
capable of simultaneously hybridising to their respective target regions
under appropriate hybridisation and wash condition allowing the detection
cunder appropriate hybridisation and wash condition allowing the detection
cof homologous targets, or with the probes hybridising specifically with a
sequence complementary to any of the target sequences; (4) detecting the
hybrids formed in step (3); and (4) inferring the nucleotide sequence at
the codons of interest (codons 38-44, 47-53, 65-72, 73-7), 148-154, 180-
cof viral isolates involved from the differential hybridisation signals
cof viral isolates involved from the differential hybridisation signals
cof viral strains of viruses containing RT genes, especially HIV
corrections of the method can also be used for
                                                                                                                                                                                                                                                                                                                                                                               Determining susceptibility to antiviral drugs of reverse transcriptase containing viruses - useful for genotyping HIV RT and detecting antiviral resistant HIV.
virus susceptibility; antiviral drug resistant viral strain; retrovirus;
Hepadnaviridae; HIV RT genotyping; probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
8.8%; Score 11.4; DB 1;
Best Local Similarity 92.3%; Pred. No. 2.8e+02;
Matches 12; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pSM700 CBS 668.95 ribosome binding site.
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                                                                                                                                                                                                                                                                                                                          Rossau
                                                                        Human immunodeficiency virus 1.
                                                                                                                                                                                                                           96EP-00870005.
96EP-00870081.
                                                                                                                                                                                        97WO-EP000211
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(first entry)
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                                                                                                                                                                                                                                                                                                                        Louwagie J,
                                                                                                                                                                                                                                                                                  (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-393716/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genotyping HIV RT
                                                                                                                                                                                                                             26-JAN-1996;
                                                                                                               WO9727332-A1
                                                                                                                                                                                        17-JAN-1997;
                                                                                                                                                                                                                                                 25-JUN-1996;
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04-FEB-1998
                                                                                                                                                     31-JUL-1997
                                                                                                                                                                                                                                                                                                                        Stuyver L,
                                                      Synthetic.
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98WO-US010277. 97US-0047352P.

20-MAY-1998; 21-MAY-1997;

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carbamoylase; D alpha amino acid; pharmaceutical intermediate; penicillin; cephalosporin; pesticide; fluvanilate; sweetener; ss
                                                                                                                                                                                                                    Query Match
Best Local Similarity 92.3<sup>†</sup>
Matches 12, Conservative
                                                              (ENIE ) ENIRICERCHE SPA
                                                                                  WPI; 1997-283101/26.
                                                                        Grifantini R,
                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                               26-NOV-1998
                                                     23-NOV-1995;
                                            31-OCT-1996;
                         EP775748-A2
                                   28-MAY-1997
                                                                                                                                                                                                                                                                                  AAX31805;
                Synthetic.
                                                                                                                                                                                                                                                               RESULT
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differentially expressent tag sequences of transcripts that are differentially expressed in colorectal cancer, in pancreatic cancer, or in both. The tag sequences can be used to identify genes by matching the tag to a gen data base member, or by using the tag sequences as probes to isolate unidentified genes from CDNA libraries. The tag sequences can also be used in a method for diagnosing colon or pancreatic cancer in a sample suspected of being neoplastic. The method comparises comparing the level of at least one transcript in a first sample of a tissue to a second sample, where the first sample is a colonic tissue suspected of being neoplastic and the second sample is a colonic tissue suspected of the transcript is identified by a tag selected from AAX30947-31815. The methods of the invention can be used in the diagnosis, prognosis and
                                                                                                                                                                                                    Use of isolated gene transcripts - useful for developing products for the diagnosis, prognosis and treatment of cancers, particularly colon and pancreatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tag sequence; colorectal cancer; pancreatic cancer; colon cancer; diagnosis; prognosis; treatment; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tag sequence of a transcript increased in colorectal cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.8%; Score 11.4; DB 1; Length 15; 92.3%; Pred. No. 2.8e+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15 BP; 2 A; 6 C; 1 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                      Disclosure; Page 79; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bb.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1395 AAGGAGGTAAAAT 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX31143 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNINGO HOLVING (OLYU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vogelstein B, Kinzler KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                    (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                     Kinzler KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 AAGGAGGTAACAT 2
                                                                                                                                                                                WPI; 1999-070161/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                     Vogelstein B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-NOV-199B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A process for the production of D-alpha-amino acids has been improved.

The process is effected by stereoselective conversion of racemic 5-
substituted hydantoins with an enzyme system produced by a microorganism,
which is obtained by: (a) constructing plasmid psM700 (CBS 668.95), which
contains a carbamoylase-hydantoinase operon under the control of a
constitutive promoter, where the region comprising the ribosome binding
constitutive promoter, where the region comprising the ribosome binding
constitutive promoter, where the region comprising the ribosome binding
constitutive promoter, where the region comprising the ribosome binding
constitutive promoter, where the region comprising the ribosome binding
conficultion and acroorganism with the plasmid, and (c) culturing the
microorganism in an aqueous medium containing assimilable sources of
carbon and nitrogen, cations, anions and optionally vitamins under
carbon and nitrogen, cations, anions and optionally vitamins under
carbon and nitrogen, cations, anions and optionally vitamins and
caphalosporins), pesticides (e.g. fluvanilate) or sweeteners. A single
conversion kinetics. E. coli swc37 gives higher yields than the
conversion kinetics. E. coli swc37 gives higher yields than the
currently used strain swc305. (Updated on 25-MAR-2003 to correct PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               Production of D-alpha-amino acid from racemic 5-substituted hydantoin - using recombinant microorganism expressing hydantoinase and carbamoylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcript tag sequence increased in pancreatic and colorectal cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tag sequence; colorectal cancer; pancreatic cancer; colon cancer; diagnosis; prognosis; treatment; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15 BP; 9 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                          Carpani G;
                                                                                                                                                                                                                                                                                                                                                             Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 10; 16pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX31805 standard; DNA; 15 BP.
                                                                                                                                                                                                                     96EP-00117455.
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Gaps

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the

Use of isolated gene transcripts - useful for developing products for diagnosis, prognosis and treatment of cancers, particularly colon and pancreatic cancer.

WPI; 1999-070161/06.

Page 111

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treatment of cancer
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differentially expressed in colorectal cancer, in parcreatic cancer, or in both. The tag sequences can be used to identify genes by matching the tag to a gen data base member, or by using the tag sequences as probes to isolate unidentified genes from cDNA libraries. The tag sequences can also be used in a method for diagnosing colon or pancreatic cancer in a sample suspected of being neoplastic. The method comprises comparing the level of at least one transcript in a first sample of a tissue to a second sample, where the first sample is a colonic tissue suspected of being neoplastic and the second sample is a normal human colonic tissue. The transcript is identified by a tag, selected from AAX30947-31815. The methods of the invention can be used in the diagnosis, prognosis and
                                                                                                                  AAX30947-31815 represent tag sequences of transcripts that are
Claim 2; Page 32; 120pp; English.
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Score 11.4; DB 1; Length 15; Pred. No. 2.8e+02; 0; Mismatches 1; Indels Sequence 15 BP; 4 A; 1 C; 7 G; 3 T; 0 U; 0 Other; 8.8%; 92.3%; CATGGAAGATGGG 1456 CATGGAAGATGTG 13 12; Conservative Query Match Best Local Similarity 1444 Matches g ₹

AAX31156 standard; DNA; 15 AAX31156; RESULT 236

Tag sequence, colorectal cancer; pancreatic cancer; colon cancer; tagnosis; prognosis; treatment; ss. Tag sequence of a transcript increased in colorectal cancer. (first entry) WO9853319-A2 Homo sapiens 21-MAY-1999

diagnosis; prognosis; treatment; 97US-0047352P. 98WO-US010277 20-MAY-1998; 21-MAY-1997; 26-NOV-1998

SNING HOLVING (OLYU)

Kinzler KW; Vogelstein B,

WPI; 1999-070161/06.

AAX30947-31815 represent tag sequences of transcripts that are differentially expressed in colorectal cancer, in pancreatic cancer, or in both. The tag sequences can be used to identify games by matching the tag to a gen data base member, or by using the tag sequences as probes to isolate unidentified genes from cDNA libraries. The tag sequences can also be used in a method for diagnosing colon or pancreatic cancer in a sample suspected of being neoplastic. The method comprises comparing the level of at least one transcript in a first sample of a tissue to a second sample, where the first sample is a colonic tissue suspected of being neoplastic and the second sample is a normal human colonic tissue. use or isolated gene transcripts - useful for developing products for diagnosis, prognosis and treatment of cancers, particularly colon and pancreatic cancer. Claim 2; Page 33; 120pp; English.

The transcript is identified by a tag selected from AAX30947-31815. $^{\circ}$ methods of the invention can be used in the diagnosis, prognosis and treatment of cancer 8 X C C C

G; 6 T; 0 U; 0 Other; Sequence 15 BP; 2 A; 6 C; 1

Gaps ö Length 15; Indels Score 11.4; DB 1; Pred. No. 2.8e+02; 0; Mismatches Query Match 8.8%; Best Local Similarity 92.3%; Matches 12; Conservative

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1395 AAGGAGGTAAAAT 1407 2 AAGGAGGTAACAT 14 셤 à

AAV93864 standard; RNA; 15 RESULT 237 AAV93864

BP.

AAV93864;

(first entry) 18-FEB-1999

; 0

Gaps

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Human, c-raf, A-raf, B-raf, hammerhead ribozyme; hairpin ribozyme; target; substrate; catalyst; modulation; expression; Raf gene; delivery; screening; identification; synthesis; deprotection; purification; cancer; inflammation; psoriasis; non-hepatic ascites; infection; genetic drift; restenosis; rheumatoid arthritis; ss.

Target sequence with sequence homology to c-raf and B-raf position 1806.

Homo sapiens

WO9850530-A2

12-NOV-1998

97US-0046059P. 97US-0049002P. 97US-0056808P. 97US-0061321P. 97US-0061324P. 97US-0061324P. 98WO-US009249 05-MAY-1998; 1997-YUL-60 09-MAY-1997; 03-JUL-1997

97US-0068212P 22-AUG-1997; 02-OCT-1997; 02-OCT-1997 05-NOV-1997 19-DEC-1997

(RIBO-) RIBOZYME PHARM INC

Bellon L; Burgin A; Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Thompson J, Workman CT, Beaudry A, Sweedler D;

WPI; 1999-009494/01.

the

Identifying new catalytic nucleic acid that modulates selected processes - especially ribozymes that cleave Raf RNA for treating cancer, restenosis, and also new ribozymes and modified nucleoside triphosphates used as antiviral agents and synthons.

Claim 180; Page 177; 259pp; English.

capable of modulating a process in a biological system. The method comprises: (a) introducing into the system a random library of nucleic acid catalysts (MaC) having a substrate binding domain (SBD), comprising a random sequence, and a catalytic domain (CD); and (b) identifying NAC in systems where modulation has occurred and/or determining the sequence of at least part of the SBDs in such systems. Nucleic acid molecules with endonuclease activity and catalytic activity, from the present invention, are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases method has been developed for the identification of a nucleic acid

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme; target; substrate; catalyst; modulation; expression; Raf gene; delivery; screening; identification; synthesis; deprotection; purification; cancer; inflammation; psoriasis; non-hepatic ascites; infection; genetic drift; restenosis; rheumatoid arthritis; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying new catalytic nucleic acid that modulates selected processes - especially ribozymes that cleave Raf RNA for treating cancer, restenosis, and also new ribozymes and modified nucleoside triphosphates
caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic ascites and infection. They may also be used to detect genetic drift and mutations in diseased cells and to determine c-raf RNA. Specifically NACS with RNA-cleaving activity that modulate expression of the Raf gene, used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or generally any condition associated with the level of c-raf. Introduction of sugar/phosphate modifications increases stability against nuclease and activity. ANY99022 to AAV9387 represent NACS that can be used in the method, specifically for modulating the expression of a Raf gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Target sequence with sequence homology to c-raf and B-raf position 1804.
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Sweedler D;
                                                                                                                                                           Sequence 15 BP; 5 A; 2 C; 0 G; 0 T; 8 U; 0 Other;
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F, Beigelman L, Mcswiggen JA,
on J, Workman CT, Beaudry A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restenosis, and also new ribozymes and
used as antiviral agents and synthons
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97US - 0051718P
97US - 0051321P
97US - 0061321P
97US - 0064866P
97US - 00648212P
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                                                                                                                                                                                                                                                                                                                                                                               AAV93863 standard; RNA; 15
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Thompson J, Workman CT,
                                                                                                                                                                                                                                                                                             13 GAAGAAATATATT 1
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05-NOV-1997
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A method has been developed for the identification of a nucleic acid capable of modulating a process in a biological system. The method comprises: (a) introducing into the system a random library of nucleic acid catalysts (NAC) having a substrate binding domain (SBD), comprising

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a random sequence, and a catalytic domain (CD); and (b) identifying NAC in systems where modulation has occurred and/or determining the sequence of at least part of the SBDs in such systems. Nucleic acid molecules with endounclease activity and catalytic activity, from the present invention, are used to modulate gene expression in plant and mammalian cells and to are used to modulate gene expression in plant and mammalian cells and to caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-happic ascites and infection. They may also be used to detect genetic drift and ascites and infection. They may also be used to detect genetic drift and with RNA-cleaving activity that modulate expression of the Raf gene, are used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or generally any condition associated with the level of craft. Introduction of squary/phosphate modifications increases stability against nuclease and activity. AAV90922 to AAV93877 represent NACs that can be used in the cativity. AAV90622 to method, specifically for modulating the expression of a Raf gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
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Best Local Similarity 92.3
Matches 12; Conservative
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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, infilammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-
inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, inthyyosis, pityriasis, ruba, pilaris, serborrhoea, kelodis, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperpoliferation of the inside of blood vessels or any other hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated call proliferation; ichthytosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 6 A; 0 C; 7 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Conservative
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Best Local Similarity
Matches 12; Conserv
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AAP46526
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           ichthyosis, pityriaais, ruba, pilaris, serborrhea, Keloida, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated, purified human nucleic acid (I) that has the same sequence as a mRNA found in humans and is a SAGE (serial analysis of gene expression) tag comprising a single stranded probe containing at least 10 consecutive nucleotides. SAGE tags, are diagnostic and prognostic markers of cancer, especially of the colon and pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer SAGE tags of the invention
F45161). The method is useful for ameliorating the effects of psoriasis,
                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag
serial analysis of gene expression; diagnostic; prognostic; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human nucleic acid containing specific SAGE tags, useful as
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                                                                                                                                                           Length 15;
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                                                                                                                           Sequence 15 BP; 7 A; 0 C; 7 G; 1 T; 0 U; 0 Other;
                                                                                                                                                        Score 11.4; DB 1;
Pred. No. 2.8e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Human colon cancer SAGE tag #197.
                                                                                               vessels or any other hyperplasia
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                                                                                                                                                                                                                      1348 GGGGAAGAAAT 1360
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                                                                                                                                                                                          12; Conservative
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Best Local Similarity
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Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer marker; ss.
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ABK32109;

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New protocadherin 2 (PCDH2) polymorphic variants and encoding genes, useful in expressing PCDH2 protein for screening candidate drugs to treat diseases related to PCDH2 activity.
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                                                                                                                                                                                                                                                                            The invention relates to an isolated, purified human nucleic acid (I) that has the same sequence as a mRNA found in humans and is a SAGE (serial analysis of gene expression) tag comprising a single stranded probe containing at least 10 consecutive nucleotides. SAGE tags, are diagnostic and prognostic markers of cancer, especially of the colon and pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; PCDH2; protocadherin 2; haplotyping; polymorphic variant; SNP;
single nucleotide polymorphism; cytostatic; cancer; chromosome 5g31;
allele-specific oligonucleotide; ASO; probe; 88.
                                                                                                                                                                                          New human nucleic acid containing specific SAGE tags, useful as diagnostic markers for cancer, also derived probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 11.4; DB 1; Length 15;
Pred. No. 2.8e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 BP; 2 A; 6 C; 1 G; 6 T; 0 U; 0 Other;
                                                                                                                      Zhou W;
                                                                                                                        'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PCDH2 ASO probe SEQ ID NO 21.
                                                                                                                                                                                                                                                    Disclosure; Col 93; 161pp; English.
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                                                                                                                        Kinzler KW, Zhang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.8%;
92.3%;
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               98US-00081646.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABI99064 Btandard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                               SAGE tags of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-097928/13.
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               20-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated, purified human nucleic acid (I) that has the same sequence as a mRNA found in humans and is a SAGE (serial analysis of gene expression) tag comprising a single stranded probe containing at least 10 consecutive nucleotides. SAGE tags, are diagnostic and prognostic markers of cancer, especially of the colon and pancreas. ABR31900-ABR32770 represent human colon and pancreatic cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                         Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag; serial analysis of gene expression; diagnostic; prognostic; probe; cancer marker; ss.
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Pred. No. 2.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15 BP; 2 A; 6 C; 1 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhou W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Col 28; 161pp; English.
                                                                                                                                              Human colon cancer SAGE tag #210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK32759 standard; DNA; 15 BP.
                                    ABK32109 standard; DNA; 15 BP.
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Best Local Similarity 92.3%;
Matches 12; Conservative
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                                                                                                          (first entry)
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ABK32759;

RESULT 243

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Gaps

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G; 10 T; 0 U; 0 Other;

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Sequence 15 BP; 0 A;

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defines one or both copies of the individual's pCDH2 gene. The polymorphisms are within a 30244 base pair sequence (ABA05413), fully defined in the specification. The polymorphic variants are useful in studying the expression and function of PCDH2, in expressing PCDH2 protein for use in screening for candidate drugs to treat diseases such as cancer, related to PCDH2 activity, in studying the effect of the variation on the biological activity of PCDH2 and the binding affinity of candidate drugs targeting PCDH2. The haplotyping methods are useful in validating PCDH2 as a candidate target for treating a specific condition or disease predicted to be associated with PCDH2 activity or in the design of clinical trials of candidate drugs for treating a specific condition or disease associated with PCDH2 activity. The present sequence is that of a PCDH2 allele-specific oligonucleotide (ASO) probe of the
             5555555555555555555X&
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Seguence 15 BP; 6 A; 1 C; 4 G; 3 T; 0 U; 1 Other;

ö Gaps ô 8.8%; Score 11.4; DB 1; Length 15; 30.0%; Pred. No. 2.8e+02; ive 1; Mismatches 2; Indels 80.08; Conservative Local Similarity tes 12; Conserv Query Match Best Loca Matches

1455 GGTTGATCAAGCAAA 1469 GGTTGAAYATGCAAA 15 g ò

AAL54230 standard; DNA; 15 RESULT 245

AAL54230

ВР

RNAP recognition and target sequence spacer DNA, SEQ ID No 11.

(first entry)

Oligonucleotide primer, spacer sequence, intermediate duplex, phage-encoded RNA polymerase recognition sequence, ds.

WO200298895-A1.

12-DEC-2002.

07-JUN-2002; 2002WO-US018229.

07-JUN-2001; 2001US-0296812P. 15-FEB-2002; 2002US-00077383.

(SAIG-) SAIGENE CORP

WPI; 2003-148649/14.

U'ren J;

Haydock PV,

New oligonucleotide primer having phage-encoded RNA polymerase recognition sequences, spacer sequences and target complementary sequences, useful in nucleic acid amplification procedures or for copying target nucleic acids.

Disclosure; Page 10; 69pp; English.

The invention relates to a novel oligonucleotide primer comprises in the following order, from 5' to 3': a phage-encoded RNA polymerase recognition sequence, a spacer sequence comprising a sequence of 12-21 nucleotides; and a target complementary sequence that can bind a segment of a target nucleic acid. The oligonucleotide primer is useful in amplifying a target nucleic acid. The primer is also useful in intermediate duplexes and target nucleic acid. The primer is also useful for copying intermediate duplexes and target nucleic acids. This polynucleotide represents an example of a spacer sequence between an RNA polymerase recognition and target sequence of the invention

that target NNMT, and for identifying associations between a trait and a NNMT genotype, haplotype or haplotype pair for one or more of the novel

8.8%; Score 11.4; DB 1; Length 15; 80.0%; Pred. No. 2.8e+02;

Query Match Best Local Similarity

Seguence 15 BP; 6 A; 1 C; 4 G; 3 T; 0 U; 1 Other;

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The present sequence is a preferred allele-specific oligonucleotide (ASO)

Compose for detecting the PS2 polymorphic site in the human nicotinamide Newethyltransferase (INMT) gene (see also ABV6204). The invention is based on the discovery of 3 novel polymorphic sites (PS1-PS3) in the NNMT gene.

Composition of 79 unrealated individuals self-identified as belonging to African descent, Asian, Caucasian and Hispanic/Latino population groups. The invention provides a method, composition and kit composition comprises a probe or primer designed to specifically the NNMT gene in an individual. A genotyping kit composition comprises a probe or primer designed to specifically hypridise to a target region containing, or adjacent to, one of the NNMT copy, and its complement, are both claimed. The invention also provides probe, and its complement, are both claimed. The invention also provides composited for happlotyping the NNMT gene. This is useful for improving the development of drugs metabolised by NNMT or drugs for treating diseases associated with NNMT activity, e.g. Parkinson's disease and cancer that it is the invention is also useful for scene and it is complement. The invention is also useful for sending compounds that it is not the NNMT activity, e.g. Parkinson's disease and cancer that it is not the NNMT and second is a possible for treating diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide having nicotinamide N-methyltransferase (NNMT) gene, useful for treating diseases associated with NNMT activity, e.g. Parkinson's disease and cancer cachexia.
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                           Human; nicotinamide N-methyltransferase; NNMT; enzyme; haplotyping; genotyping; Parkinson's disease; cachexia; antiparkinsonian; single nucleotide polymorphism; SNP; probe; ss.
                                                                                                                                                                                                                                                                                                                                          Nicotinamide N-methyltransferase gene PS2 allele-specific probe.
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8.8%; Score 11.4; DB 1; Length 15; 92.3%; Pred. No. 2.8e+02; cive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 31; Page 13; 57pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAY-2002; 2002WO-US014538.
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                                                                                1349 GGGAAGAAAATA 1361
                                                                                                                                                                                                                       ABV76208 standard; DNA; 15
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                                             Conservative
                                                                                                                    GGGAAGAAAAAA 3
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                    Local Similarity
les 12; Conserv
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    Query Match
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Matches
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1441 ATACATGGAAGAT 1453

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This sequence represents a probe for a wild type HIV reverse transcriptuse (RT) gene fragment. This sequence can be used in the method transcriptuse (RT) gene fragment. This sequence can be used in the method of the invention for determining the susceptibility to antiviral drugs of viruses which contain RT genes and are present in a biological sample. CC comprises: (1) releasing, isolating or concentrating the polymucleic acids present with at least one suitable primer pair; (3) hybridising the compress persent with at least one suitable primer pair; (3) hybridising the polymucleic acids of step (1) or (2) with at least two RT gene probes, the probes being applied to known locations on a solid support, and are capable of simultaneously hybridising to their respective target regions under appropriate hybridisation and wash condition allowing the detection of homologous targets, or with the probes hybridising specifically with a companies of interest (codons 38-44, 47-53, 65-72, 73-77, 148-154, 180-187, 212-216, and 211-220), and/or the maino acids of the codons of interest and/or antiviral drug resistance specifically used to detect antiviral drug resistant strains of viruses containing RT genes, especially HIV reteroviruses and Hepadnaviridae. The method can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determining susceptibility to antiviral drugs of reverse transcriptase containing viruses - useful for genotyping HIV RT and detecting antiviral
                                                                                                                                                                                                                                                                                                 Reverse transcriptase gene, HIV, RT gene, antiviral drug susceptibility, virus susceptibility; antiviral drug resistant viral strain; retrovirus; Hepadnaviridae; HIV RT genotyping; probe; ss.
Gaps
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 Indels
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 2.
                                                                                                                                                                                                                                                                   Probe 184w26 for wild type HIV RT gene Q182M184.
 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus 1.
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                                                                                                                                                               ВР
                                     1435 AGACATATACATGGA 1449
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                                                                      1 AGTCATAYAGATGGA 15
                                                                                                                                                             AAT98967 standard; DNA; 16
                                                                                                                                                                                                                                     (first entry)
   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 containing virresistant HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-1997;
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25-JUN-1996;
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                                                                                                                                                                                                                                     23-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-1997
     12;
                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                  AAT98967;
       Matches
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The invention relates to a randomised ribozyme gene vector library which consists introduced into a population of cells expressing negative selection marker gene operatively linked to viral nucleic acid acted on by cellular regulator of virus replication or expression (e.g. the human translation initiation factor 2B gamma subunit, eIRPagamma, and proteasome alpha subunit 1, PMRA1, acting on Hepatitis C virus, HCV, sequences) and a target recognition sequence of recovered ribozymes are sequenced to target recognition sequence of recovered ribozymes sequence tags, TST, derived from eIRPagamma and PMRA1, the ribozyme sequence tags, TST, derived from eIRPagamma and PMRA1, the ribozyme sequence tags, TST, derived from eIRPagamma and PMRA1, the ribozyme sequence tags, C TST, derived from a list of target genes given in the capturation with the cellular regulator. The methods are useful for interaction with the cellular regulator. The methods are useful for identifying a compound that modulates the activity of a viral cellular regulator, identifying a ribozyme reactive with a cellular regulator of virus replication or expression, and for treating an HCV infection by continiting the activity of a cellular regulator involved in HCV infection. The methods are used to reduce the severity of such an above screening methods are used to reduce the severity of such an infection. The methods allow rapid and efficient identification of infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cellular genes involved in the propagation or pathogenesis of infectious agents. The present sequence is a ribozyme target sequence tag of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying cellular regulators essential in pathogenesis of infectious agents, useful for treatment of infectious diseases preferably viral diseases especially hepatitis C virus (HCV).
                                                                                                                                                                                                                                                                                              Human; ss; translation initiation factor 2B gamma subunit; eIF2Bgamma; ribozyme sequence tag; RST; TST; target sequence tag; HCV; hepatitis C virus infection; virucide; hepatotropic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16 BP; 7 A; 2 C; 2 G; 0 T; 4 U; 1 Other;
                                                                                                                                                                                                                                                              Human eIF2Bgamma ribozyme target sequence tag #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 18; Page 17; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                   proteasome alpha subunit; PMSA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barber JR;
                                                                                                                                          ABK41364 standard; RNA; 16 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAY-2001; 2001WO-US014337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAY-2000; 2000US-00563794.
                                                                                                                                                                                                                         21-MAY-2002 (first entry)
                                    16
                                  4 ATACATGGACGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kruger M, Welch PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-034514/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMU-) IMMUSOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-2001.
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                                                                                                                                                                                   ABK41364;
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Gaps

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Score 11.4; DB 1; Length 16; Pred. No. 3e+02; 0; Mismatches 1; Indels

8.8%;

Query Match Best Local Similarity 92.3 Matches 12; Conservative

16

4 ATACATGGATGAT

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The present invention describes a method for detecting mutations associated with anti-HIV drug resistance in a patient by detecting at associated with anti-HIV drug resistance in a patient by detecting at least one of the mutations K103N/R, V106A/I/L, Y181CI, M184V/I, M18BL, G190A/S/R, T215Y/F/D/S/A and/Oro (151M/L in the reverse transcriptase (RT) of HIV strains in a biological sample using a specific set of probes optimised to function together in a reverse-hybridisation assay. The method and the nucleic acid sequences used in the method are useful for determining viral mutations and/or polymorphisms in the HIV RT gene associated with resistance. The probes are useful for the genetic detection, preferably in vitro detection of the mutations K103N/R, V106A/I/L, Y181CI, O151M/L, M184V/I, Y188L, G190A/S/R and/or C T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the mutation is associated with anti-HIV drug resistance. The method provides CC antiviral drug resistance or mutations associated with drug resistance of viruses containing RT genes. ABZ33759 to ABZ34642 represent HIV RT services and probes which are used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting mutations associated with anti-HIV drug resistance comprises detecting at least one of the mutations in the HIV reverse transcriptase gene by using probes optimized to function together in a reverse-hybridization assay.
                                                                                                                                                                                                                                                                                 Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme; detection; mutation; anti-HIV drug resistance; polymorphism; resistance;
                                                                                                                                                                                                                                             HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16 BP; 6 A; 2 C; 3 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 24; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus 1.
                                                                                                                                  ABZ34088 standard; DNA; 16 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JAN-2001; 2001EP-00870005.
20-APR-2001; 2001EP-00870085.
24-APR-2001; 2001US-0286102P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JAN-2002; 2002WO-EP000153.
1407 TIGITAAIGATGAC 1420
                                                                                                                                                                                                               (first entry)
                                    16 TTGTTAATGACNAC 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-590680/63.
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                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                 probe; ss.
                                                                                                                                                                            ABZ34088;
                                                                                                RESULT 249
                                                                                                                    ABZ34088
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The present invention describes a method for detecting mutations associated with anti-HIV drug resistance in a patient by detecting at least one of the mutations K103N/R, V106A/I/L, Y181C/L M184V/I, Y188L, CG 190A/S/R, T212Y/F/D/S/A and/D/Or Q151M/L in the reverse transcriptase (RT) of HIV strains in a biological sample using a specific set of probes optimised to function together in a reverse-hybridisation assay. The determining viral mutations and/or polymorphisms in the HIV RT gene associated with resistance. The probes are useful for the genetic determining viral mutations and/or polymorphisms in the HIV RT gene contention, preferably in vitro detection of the mutations K103N/R, CT 215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the mutation is associated with anti-HIV drug resistance. The method provides containing RT genes. ABZ33759 to ABZ34642 represent HIV RT containing ST genes. ABZ33759 to ABZ34642 represent HIV RT containing RT genes. ABZ33759 to ABZ34642 represent HIV RT containing RT genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting mutations associated with anti-HIV drug resistance comprises detecting at least one of the mutations in the HIV reverse transcriptase gene by using probes optimized to function together in a reverse-
                                                                                                                                                                        Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme; detection; mutation; anti-HIV drug resistance; polymorphism; resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                    HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16 BP; 6 A; 1 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 24; 117pp; English.
                                                                                                                                                                                                                                                     Human immunodeficiency virus 1.
                                ABZ34091 standard; DNA; 16 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                    11-JAN-2001; 2001EP-00870005.
20-APR-2001; 2001EP-00870085.
24-APR-2001; 2001US-0286102P.
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                                                                                                       31-JAN-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stuyver L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-590680/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene by using probes
hybridization assay.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                               WO200255741-A2.
                                                                                                                                                                                                                                                                                                                                                   18-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      De Smet K,
                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                    probe; ss.
                                                                      ABZ34091;
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RESULT 250
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2 ATACATGGATGAT 14

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Gaps

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Score 11.4; DB 1; Length 16; Pred. No. 3e+02; 0; Mismatches 1; Indels

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8.8%;

schultz911-3.rng

(first entry)

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Detecting mutations associated with anti-HIV drug resistance comprises detecting at least one of the mutations in the HIV reverse transcriptase gene by using probes optimized to function together in a reverse-hybridization assay.
                                                                                                                                                     Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme; detection; mutation; anti-HIV drug resistance; polymorphism; resistance;
                                                                                                           HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 25; 117pp; English.
                                                                                                                                                                                                                                                      Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JAN-2001; 2001EP-00870005.
20-APR-2001; 2001EP-00870085.
24-APR-2001; 2001US-0286102P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             De Smet K, Stuyver L;
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                                                                  31-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                         18-JUL-2002
                                                                                                                                                                                                        probe; ss.
                                                                                                                                                                                                                                                                                 Synthetic
                   ABZ34121;
The present invention describes a method for detecting mutations associated with anti-HIV drug resistance in a patient by detecting at associated with anti-HIV drug resistance in a patient by detecting at least one of the mutations K103N/R, V106A/I/L, Y181C/I, M184V/I, Y18BL, C190A/S/R, T215Y/F/D/S/A and/or OliMiL in the reverse transcriptase (RT) of HIV strains in a biological sample using a specific set of probes optimised to function together in a reverse-hybridisation assay. The method and the nucleic acid sequences used in the method are useful for determining viral mutations and/or polymorphisms in the HIV RT gene associated with resistance. The probes are useful for the genetic detection, preferably in vitro detection of the mutations K103N/R, V106A/I/L, Y181C/I, O151M/L, M184V/I, Y180L, G190A/S/R and/or C151SY/F/D/S/A in the RT of HIV strains in a biological sample, where the mutation is associated with anti-HIV drug resistance. The method provides a rapid, reliable and precise assay or determination and monitoring of antiviral drug resistance or mutations associated with drug resistance of viruses containing RT genes. ARZ34542 represent HIV RT sequences and probes which are used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting mutations associated with anti-HIV drug resistance comprises detecting at least one of the mutations in the HIV reverse transcriptase gene by using probes optimized to function together in a reverse-hybridization assay.
                                                                                                                                                                                                                                   Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme; detection; mutation; anti-HIV drug resistance; polymorphism; resistance;
                                                                                                                                                                                    HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:369,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.6%; Score 11.2; DB 1; Length 16; Best Local Similarity 81.2%; Pred. No. 3.2e+02; Matches 13; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 25; 117pp; English.
                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus 1.
                                                ABZ34127 standard; DNA; 16 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JAN-2001; 2001EP-00870005.
20-APR-2001; 2001EP-00870085.
24-APR-2001; 2001US-0286102P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JAN-2002; 2002WO-EP000153.
                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                    WO200255741-A2.
                                                                                                                                           31-JAN-2003
                                                                                                                                                                                                                                                                                         probe; ss.
                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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                                                                                               ABZ34127;
    RESULT 251
                               ABZ34127
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The present invention describes a method for detecting mutations associated with anti-HIV drug resistance in a patient by detecting at associated with anti-HIV drug resistance in a patient by detecting at least one of the mutations K1030/R, V106A/I/L, V181C/I, M184V/I, V188L, C G190A/S/R, T215Y/F/D/S/A and/or OlilM/L in the reverse transcriptase (RT) of HIV strains in a biological sample using a specific set of probes coptimized to function together in a reverse-hybridisation assay. The coptimized to function together in a reverse-hybridisation assay. The compact and mutations and/or polymorphisms in the HIV FT gene associated with resistance. The probes are useful for the genetic detection, preferably in vitro detection of the mutations K103N/R, C V106A/I/L, Y181C/I, O151M/L, M184V/I, Y188L, G190A/S/R and/or C T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the mutation is associated with anti-HIV drug resistance. The method provides a rapid, reliable and precise assay or determination and monitoring of a rapid, reliable and precise assay or determination and monitoring of a rapid, reliable and session as associated with drug resistance of viruses containing RT genes. ABZ34781 represent HIV RT contains associated and precise and probes which are used in the exemplification of the present
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Gaps

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1442 TACATGGAAGATGGGT 1457

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TACATGGATGATTTGT

ABZ34121 standard; DNA; 16 BP.

RESULT 252

ABZ34121

(first entry)

92US-00968436. 93US-00173489

Wang C;

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Disclosure; Col 23-24; 168pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PROF-) PROFILE DIAGNOSTIC SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABI60621 standard; DNA; 12
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hes 11; Conservative
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                                                                                                                                                                                                                      Chlamydophila caviae.
                                                                                                                                        oncogene; virus; ss.
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                                                                                                                                                                                                                                                                                                                                                                                        22-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-1992;
24-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepburn AG,
                                                                                                                                                                                                                                                                                   US5861244-A
                                                                                                                                                                                                                                                                                                                                       19-JAN-1999
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                                                                                                                                                                                               Synthetic
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(first entry)

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This invention describes novel oligonuclectide primers or peptide nucleic
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                                                                                                                                                                                                                                                        set or oligonucleotides, useful for diagnosis and cell typing, i
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
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100.0%; Pred. No. 2.4e+02;
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nes 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a polynucleotide that is able to form a triple helix with a double stranded sequence. Cytosine bases in the present can be replaced with 5-methyloytosine for increased triplex cabality. The present sequence is used in the assay of the invention, where it can be part of the anchor DNA or reporter DNA sequence. The assay comprises adding a sample containing double-stranded DNA test sequences to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple-strand structure with part of the test sequence. Triplex formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. Triplex formation results in sequences, particularly for identification of bacteria (by detecting genes for ribosomal RNA) in clinical samples, but also detection of oncogenes and Hepatitis B virus
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                                                                     friplex formation; DNA detection; triple helix; identification; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide primer SEQ ID NO 360594 for detecting SNP TSC0052150.
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                                   Triple helix third strand of 23S rRNA gene nucleotides 203-213.
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100.0%; Pred. No. 2.2e+02;
ive 0; Mismatches 0; Indels
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Best Local Similarity 100.0
Matches 11, Conservative
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Oligonucleotide primer SEQ ID NO 268599 for detecting SNP TSC0001245. BP. ABH68622 standard; DNA; 12 (first entry) 22-FEB-2002 ABH68622; RESULT 256 **ABH68622**

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Homo sapiens,

WO200177384-A2

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 268599; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,

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8.5%; Score 11; DB 1; Length 12;
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Matches 11; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.4e+02;
iive 0; Mismatches 0;
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es 11; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                   Oligonucleotide primer SEQ ID NO 335063 for detecting SNP TSC0038581.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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              Oligonucleotide primer SEQ ID NO 279373 for detecting SNP TSC0007280.
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100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 11; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 282131; 29pp + Sequence Listing; German.
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100.0%; Pred. No. 2.4e+02;
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ftp.wipo.int/pub/published_pct_sequences
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06-APR-2001; 2001WO-IB000713
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nes 11; Conservative
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                                                                    (EPIG-) EPIGENOMICS AG
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Matches
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABF09989, ABF00010-ABF9989 and ABI00010-ABF9073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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                                                                                                          acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE9989, ABE00010-ABE9989, ABE00010-ABE998, ABE00010-ABE998,
                                                                                   This invention describes novel oligonucleotide primers or peptide nucleic
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                          Claim 1; SEQ ID NO 285252; 29pp + Sequence Listing; German.
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11; Conservative 0; Mismatches 0; Indels
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ABI78224 standard; DNA; 12 BP.
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nes 11; Conservative
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                             8.5%; Score 11; DB 1; Length 12; 100.0%; Pred. No. 2.4e+02; tive 0; Mismatches 0; Indels
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was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prereated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fitp.wipo.int/pub/published_pct_sequences
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                                                             Set of oligonucleotides, useful for diagnosis and cell typing, i
designed to detect single-nucleotide polymorphisms and cytosine
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100.0%; Pred. No. 2.4e+02;
ive 0; Mismatches 0; Indels
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                Piepenbrock
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methylation
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 central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fitte wipo.int/pub/published_pct_sequences
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF0010-ABF9989, ABF0010-ABF99999, ABF0010-ABF99999 and ABI0010-ABF82073 tapeseent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but they wipo int/pub/published_pct_sequences
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8.5%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
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ABI34761 standard; DNA; 12 BP.
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XXX AB18.
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XXX SNP;
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XXX HOMO COLIGORY
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schultz911-3.rng

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                      Oligonucleotide primer SEQ ID NO 357907 for detecting SNP TSC0004855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 357907; 29pp + Sequence Listing; German.
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100.0%; Pred. No. 2.4e+02;
Live 0; Mismatches 0; Indels
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                                   (first entry)
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Best Local Similarity 100.0
Matches 11, Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin

Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG

WPI; 2001-657177/75.

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

18-OCT-2001.

Claim 1; SEQ ID NO 315231; 29pp + Sequence Listing; German.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide primer SEQ ID NO 353427 for detecting SNP TSC0048513.
                                                                                                                                                                                                                                                                                                                            Gaps
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0
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                                                                                                                                                                                                                                                                                        Sequence 12 BP; 4 A; 0 C; 2 G; 6 T; 0 U; 0 Other;
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ABI53454/c
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

WO200177384-A2

Homo sapiens

Oligonucleotide primer SEQ ID NO 315231 for detecting SNP TSC0026789.

ABI15258 standard; DNA; 12 BP.

RESULT 271 ABI15258/c

AB115258

22-FEB-2002 (first entry)

BXSXEXEXEXEX

schultz911-3.rng

Page 127

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABP9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic forma part of the printed specification, but the continuation of the printed specification, but
                         designed to detect single-nucleotide polymorphisms and cytosine methylation status.
oligonucleotides, useful for diagnosis and cell typing,
                                                                                           Claim 1; SEQ ID NO 353427; 29pp + Sequence Listing; German.
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  Set of
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Sequence 12 BP; 3 A; 0 C; 2 G; 7 T; 0 U; 0 Other;

٠. 8.5%; Score 11; DB 1; Length 12; 100.0%; Pred. No. 2.4e+02; ative 0; Mismatches 0; Indels Conservative Query Match Best Local Similarity Matches 11; Conserv

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ABH88491 standard; DNA; 12 ABH88491; RESULT 273

BP.

(first entry) 22-FEB-2002

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 288484 for detecting SNP TSC0013537.

Homo sapiens.

WO200177384-A2

18-OCT-2001

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

Berlin K; Piepenbrock C, Olek A,

WPI; 2001-657177/75.

set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 288484; 29pp + Sequence Listing; German.

acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclocides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 invention describes novel oligonucleotide primers or peptide nucleic

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-ABC99989, ABF00010-ABF99989, ABH00010-ABH99889 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                             Sequence 12 BP; 2 A; 1 C; 0 G; 9 T; 0 U; 0 Other;
                                                                                                        ftp.wipo.int/pub/published_pct_sequences
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Score 11; DB 1; Length 12; Pred. No. 2.4e+02; 8.5%; 8 Query Match
Best Local Similarity 100.0
....hes 11; Conservative

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Gaps

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0; Indels

0; Mismatches

RESULT 27 ABI45142

ABI45142 standard; DNA; 12

BP.

ABI45142;

(first entry) 22-FEB-2002

Gaps

Oligonucleotide primer SEQ ID NO 345115 for detecting SNP TSC0043880.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Piepenbrock C, olek A,

ξ.

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 345115; 29pp + Sequence Listing; German.

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastrointestinal, respiratory, oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABF9989, ABH00010-ABF9989, ABH00010-ABF99989, ABH00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99999, ABF00010-ABF999999, ABF00010-ABF999999, ABF00010-ABF999999, ABF00010-ABF99999, ABF00010-ABF999999, ABF00010-ABF999999,

Sequence 12 BP; 9 A; 0 C; 1 G; 2 T; 0 U; 0 Other;

.. Query Match 8.5%; Score 11; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 2.46+02; Matches 11; Conservative 0; Mismatches 0; Indels

1352 AAGAAAAATAT 1362

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Gaps

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABF00010-ABF99999, and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at fire printed specification, but fire wipo.int/pub/published_pct_sequences
                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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84.6%; Pred. No. 2.7e+02;
tive 1; Mismatches 1; Indel8
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                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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100.0%; Pred. No. 2.4e+02;
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                                                                                                                           ABI47820 standard; DNA; 12 BP.
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                  1 AAGAAAATAT
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                                                                                                                                                                       ABI47820;
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Matches
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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine
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                                                                                                              Claim 1; SEQ ID NO 16456; 29pp + Sequence Listing; German.
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07-APR-2000; 2000DE-01019173.
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                                     Piepenbrock C,
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                  (EPIG-) EPIGENOMICS AG
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Claim 1; SEQ ID NO 143211; 29pp + Sequence Listing; German.

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and merabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
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                                                                                                                                                                                                                                                                                                                                         This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO 151881 for detecting SNP TSC0038376.

ABF51884 standard; DNA; 13 BP.

ABF51884

21-FEB-2002

ABF51884;

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                                                    DB 1; Length 13; 2.7e+02;
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                                                  Query Match 8.5%; Score 11; DB Best Local Similarity 100.0%; Pred. No. 2.7 Matches 11; Conservative 0; Mismatches
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set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

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Piepenbrock C,

olek A,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

WO200177384-A2. Homo sapiens.

18-OCT-2001

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. Abcrosses, Abrotolo-Abresses, Abrotolo-Abresses, Abrotolo-Abresses, and cential including invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomorbides are used for diagnosis and/or prognosis of cancer and a crange of diseases including immune system, gastrointestinal, respiratory, entrang of diseases including immune system, gastrointestinal, respiratory, oligomers are also used for detecting call type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99889, ABH00010-ABH999889 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine
Oligonucleotide SEQ ID NO 121397 for detecting SNP TSC0030317.
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WO200177384-A2

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RESULT 288

ABC88578;

Query Match

Matches

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABF09989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine
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                                                                                                    Sequence 13 BP; 8 A; 0 C; 1 G; 3 T; 0 U; 1 Other;
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100.0%; Pred. No. 2.7e+02;
ative 0; Mismatches 0;
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                                                                                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99889 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                  Claim 1; SEQ ID NO 121397; 29pp + Sequence Listing; German.
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Best Local Similarity 100.0%; Pred. No. 2.7e+02;
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                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                       Oligonucleotide SEQ ID NO 221991 for detecting SNP TSC0054021.
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ABH22014 standard; DNA; 13 BP.
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peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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44.6%; Pred. No. 2.7e+02;
ve 1; Mismatches 1; Indels
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nes 11, Conservative
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RESULT 296
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                                                                                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989, and pattod. ABIS2073 data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                      uer or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                          Claim 1; SEQ ID NO 248477; 29pp + Sequence Listing; German.
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14.6%; Pred. No. 2.7e+02;
ve 1; Mismatches 1; Indels
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(EPIG-) EPIGENOMICS AG
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABC0010-ABC99899 ABH0010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but thousupo.int/pub/published_pct_sequence
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tive 0; Mismatches 0;
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABH59860 standard; DNA; 13 BP.

RESULT 298 ABH59860 ID ABH5980

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WFPO at the printed specification, but the wipo.int/pub/published_pct_sequences
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                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                               Oligonucleotide SEQ ID NO 259837 for detecting SNP TSC0063098.
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100.0%; Pred. No. 4...
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers a also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but typ.wipo.int/pub/published_pct_sequences
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     occorrections of the control of the diagnosis and cell typing, indesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                           German.
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Pred. No. 2.7e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 11446; 29pp + Sequence Listing; German.
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100.0%; Pred. No. 2.7e+02;
ive 0; Mismatches 0; Indels
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oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99889, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                         8.5%; Score 11; DB 1; Length 13; 100.0%; Pred. No. 2.7e+02; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide SEQ ID NO 11445 for detecting SNP TSC0002795.
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acid (DNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABC9989, ABF00010-ABC9989, ABF00010-ABC9989, ABF00010-ABC9080, ABC90010-ABC9080, ABC900010-ABC9080, ABC90010-ABC9080, ABC900010-ABC9080, ABC900000-ABC9080, ABC9000010-ABC90000, ABC90000000, ABC9000000000000000000000000000000000
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABC00100-ABE9989, ABC00100-ABE9989, ABC00100-ABE9989, and ABI0010-ABE9989 and ABI0010-ABE90001 represent the oligomers described in the invention. NOTE: The sequence data for this partent did not form part of the printed specification, but typu, wipo.int/pub/published_pct_sequences
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Claim 1; SEQ ID NO 217297; 29pp + Sequence Listing; German.
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Matches 11; Conservative
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84.6%; Pred. No. 2.7e+02;
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84.6%; Pred. No. 2.7e+02;
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ABF59621;

RESULT 309

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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8.5%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
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                                                                                                                                                                                  Oligonucleotide SEQ ID NO 159618 for detecting SNP TSC0040184.
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ABF37536

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                       Claim 1; SEQ ID NO 174981; 29pp + Sequence Listing; German.
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84.6%; Pred. No. 2.7e+02;
ive 1; Mismatches 1; Indels
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Piepenbrock C,
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                                                                                                         methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cycosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire.wipo.int/pub/published_pct_sequences
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oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; Ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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100.0%; Pred. No. 2.7e+02;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form at from WIPO at
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                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                         Oligonucleotide SEQ ID NO 77 for detecting SNP TSC000021.
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100.0%; Pred. No. 2.7e+02;
iive 0; Mismatches 0; Indels
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    84.6%; Pred. No. 2.7e+02;
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Matches 11; Conserv
      Best Local Similarity
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WO200177384-A2

ABC00086 standard; DNA; 13 BP.

RESULT 315 ABC00086
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AC ABC0

à 8 ABC00086

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                                                                                                                                                                                                                                                                                                              RESULT 318
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                                                                                                                                                                                         This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                   bet or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide SEQ ID NO 150146 for detecting SNP TSC0037898
                                                                                                                                                                       Claim 1; SEQ ID NO 145424; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                        8.5%; Score 11; DB 1; Length 13; 100.0%; Pred. No. 2.7e+02;
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                                                                                    Berlin K;
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                      06-APR-2001; 2001WO-IB000713
                                          07-APR-2000; 2000DE-01019173
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                                                                                                                                                                                                                                                                                                                                                                                                                      2 AAAATATTCCA 12
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                                                                                    Piepenbrock C,
                                                                (EPIG-) EPIGENOMICS AG
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Best Local Similarity
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                                                                                     olek A,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytoshis meethylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, axidovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
                                                                                                                                                                                                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire printed specification, but ftp.wipo.int/pub/published_pct_sequences
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designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                               Claim 1; SEQ ID NO 150146; 29pp + Sequence Listing;
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8.5%; Score 11; DB 1; I

Best Local Similarity 84.6%; Pred. No. 2.7e+02;

Matches 11; Conservative 1; Mismatches 1;
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(first entry)

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                          Oligonucleotide SEQ ID NO 30756 for detecting SNP TSC0009454
                                                                         ABC30739 standard; DNA; 13
                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                   20-FEB-2002
                                                                                                      ABC30739;
                                                 RESULT 320
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ID ABF1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989 and ABI00010-ABF2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide SEQ ID NO 27546 for detecting SNP TSC0007666.
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8.5%; Score 11; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                      8.5%; Score 11; DB 1; Length 13; 84.6%; Pred. No. 2.7e+02; ative 1; Mismatches 1; Indels
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                                                                              Sequence 13 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 1 Other;
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                                                                                                        Query Match
Best Local Similarity 84.6'
Matches 11, Conservative
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ABC27529
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a cange of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 +ABC99989, ABF0010-ABF99989, ABF0010-ABF99989 and ABI00010-ABIS2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel oligonucleotide primers or peptide nucleic
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                                                                                                                                                                                                                                                                                                                                                                                  typing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 30756; 29pp + Sequence Listing; German.
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100.0%; Pred. No. 2.7e+02;
ive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 11; Conservative
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WO200177384-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 2.7e+02;
1; Mismatches 1; Indels
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Best Local Similarity 84.6%;
Matches 11; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABP99989, ABH00010-ABH99999 and ABI00010-ABH99913
-ABC9989, ABF000110-ABP99989, ABH00010-ABH99999 and ABI00010-ABP82073
-ABC9989, ABF000110-ABP99989, ABH00010-ABH999999 and ABI00010-ABP98073
-ABC9980, ABP00010-ABP99989, ABH00010-ABH999999 and ABI00010-ABP998073
-ABC9989, ABP000110-ABP99989, ABH00010-ABH99989 and ABI00010-ABP998073
-ABC9980, ABP000110-ABP99989, ABH00010-ABH999899 and ABI00010-ABP998073
-ABC9980, ABP000110-ABP99989, ABP00010-ABH99989999 and ABI00010-ABP998073
-ABC9980, ABP00010-ABP99989, ABP00010-ABH999899 and ABP00010-ABP998073
-ABC9980, ABP00010-ABP99980, ABP00010-ABH999899 and ABP00010-ABP998074
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                                                                                                                                                                                               Claim 1; SEQ ID NO 134328; 29pp + Sequence Listing; German.
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                                                   Piepenbrock C,
             (EPIG-) EPIGENOMICS AG.
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Query Match Best Local Similarity 100. Matches 11; Conservative

1357 AAATATTCCAC 1367

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13 AAATATTCCAC 3

Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC00989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABC99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

WO200177384-A2. Homo sapiens.

18-OCT-2001.

Piepenbrock C,

Olek A,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS AG

Oligonucleotide SEQ ID NO 82280 for detecting SNP TSC0020783

BP.

ABC82263 standard; DNA; 13

RESULT 325

ABC82263;

21-FEB-2002 (first entry)

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100.0%; Pred. No. 2.7e+02;
ive 0; Mismatches 0; Indels
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RESULT 326 ABF34022/c

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                            Oligonucleotide SEQ ID NO 134019 for detecting SNP TSC0033419.
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100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0; Indels
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  ABF34022 standard; DNA; 13
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                                                       (first entry)
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nes 11; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory. Central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABP00010-ABH99989, ABH00010-ABH99989 and ABL00010-ABH99989, and ABL00010-ABH9989 and control of the printed specification, but was obtained in electronic forma part of the printed specification, but was obtained in electronic format from WIPO at
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84.6%; Pred. No. 2.7e+02;
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                                                                                                                                                                    Piepenbrock C,
                                                                                                                         (EPIG-) EPIGENOMICS
                                                                                                                                                                                                              WPI; 2001-657177/75
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18-OCT-2001
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ABH20328
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WPI; 2001-657177/75

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis adjor prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,
                                                                                                                                            This invention describes novel oligonuclectide primers or peptide nucleic acid (FNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABH00010-ABH99989 and ABI00010-ABI22073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
                           Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                            Claim 1; SEQ ID NO 220305; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.5%; Score 11; DB 1; Length 13; 34.6%; Pred. No. 2.7e+02; Ve 1; Mismatches 1; Indels
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Matches 11; Conservative
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Best Local Similarity
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ABF50148
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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, and ABI00010-ABF98182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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100.0%; Pred. No. 2.7e+02;
ive 0; Mismatches 0;
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84.6%; Pred. No. 2.7e+02;
iive 1; Mismatches 1;
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                11; Conservative
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Oligonucleotide SEQ ID NO 144840 for detecting SNP TSC0036426.
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                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                          Oligonuclectide SEQ ID NO 236360 for detecting SNP TSC0057697.
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Best Local Similarity 84.6%;
Marches 11; Conservative
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                       1356 AAAATATTCCA 1366
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                                        AAAATATTCCA 13
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RESULT 332 ABF44843

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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RESULT 335
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                                                                                                                                                                                                           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99899 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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06-APR-2001; 2001WO-IB000713
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                                                                             Piepenbrock C,
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                                                    (EPIG-) EPIGENOMICS AG
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                                                                                                       WPI; 2001-657177/75.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989, ABH00010-ABF99989, ABH00010-ABF99989, ABH00010-ABF99980 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
                                                                      This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequence
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Claim 1; SEQ ID NO 184485; 29pp + Sequence Listing; German.
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8.5%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 11; Conservative 0; Mismatches 0; Indels
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SNP; single nucleotide polymorphism; human; diagnosis; pNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

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olek A,

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cortral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99989, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                  Olek A,
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nervous system; gastrointestinal; respiratory; immune; metabolic.
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100.0%; Pred. No. 2.7e+02;
ive 0; Mismatches 0; Indels
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Query Match

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
               oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
cytosine methylation status in chemically pretreated genomic DNA. The
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designed to detect single-nucleotide polymorphisms and cytosine
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8.5%; Score 11; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 11; Conservative 0; Mismatches 0; Indels
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χ. Berlin

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This invention describes novel oligomucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABP00010-ABF99989, and not all one of the sequence the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                          Oligonucleotide SEQ ID NO 236359 for detecting SNP TSC0057697.
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34.6%; Pred. No. 2.7e+02;
ve 1; Mismatches 1; Indels
8.5%; Score 11; DB 1; Length 13;
100.0%; Pred. No. 2.7e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                          ABH36382 standard; DNA; 13 BP
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Matches 11; Conservative
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 Query Match
Best Local Similarity 100.
Matches 11, Conservative
                                                                        1398 GAGGTAAATT 1408
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                                                                                                       12 GAGGTAAAATT
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schultz911-3.rng

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABE9989, ABF00010-ABE9989, ABF00010-ABE99989, and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                     Oligonucleotide SEQ ID NO 96950 for detecting SNP TSC0024053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 96950; 29pp + Sequence Listing; German.
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Matches 11, Conservative
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Matches 11, Conservative
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                                                                                                                                          Dlek A, Piepenbrock C,
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8.5%; Score 11; DB 1; Length 13; 84.6%; Pred. No. 2.7e+02; tive 1; Mismatches 1; Indels

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Homo sapiens

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                                                                                                                                                     (first entry)
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                                                                                               11; Conservative
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                                                                                                               CCACGCATCAC 13
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The contral nervous system, cardiovascular and metabolic disorders. Abcounceding oligomers are also used for detecting cell type differentiation. Abcounce represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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84.6%; Pred. No. 2.7e+02;
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Matches 11; Conservative
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                                                                                                                                                              This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABP0010-ABF99989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                           Claim 1; SEQ ID NO 53384; 29pp + Sequence Listing; German
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Pred. No. 2.7e+02;
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100.0%; Pred. No. 4...
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                   Oligonucleotide SEQ ID NO 16455 for detecting SNP TSC0003586.
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                                  ABC16448 standard; DNA; 13 BP
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Best Local Similarity 100.
Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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100.0%; Pred. No. 2.7e+02;
ive 0; Mismatches 0; Indels
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les 11; Conserv
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                                                                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but typ.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                  Claim 1; SEQ ID NO 219254; 29pp + Sequence Listing; German.
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                                            Piepenbrock C,
                        (EPIG-) EPIGENOMICS AG
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                                                                WPI; 2001-657177/75
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Best Local Similarity
                                                                                                   designed to detect methylation status.
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                                            Olek A,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, asriovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cycosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascullar and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two obtained in electronic format from WIPO at
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Local Similarity 84.6%;
les 11; Conservative
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ABF21401 standard; DNA; 13 BP.

21-FEB-2002 (first entry)

ABF21401;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                               8.5%; Score 11; DB 1; Length 13; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels
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BP; 5 A; 0 C; 3 G; 5 T; 0 U; 0 Other;
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                                                                      11; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in Chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
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                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 85; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                             Oligonucleotide SEQ ID NO 121398 for detecting SNP TSC0030317.
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Similarity 100.0%; Pred. No. 2.7e+02;
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                                                                                                                                                                        This invention describes novel oligonucleotide primers or peptide nucleic
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                                                                                                                                 Claim 1; SEQ ID NO 174149; 29pp + Sequence Listing; German.
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84.6%; Pred. No. 2.7e+02;
ive 1; Mismatches 1; Indels
                                    designed to detect single-nucleotide polymorphisms and methylation status.
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Pred. No. 2.7e+02;
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8.5%; Score 11; DB
Best Local Similarity 100.0%; Pred. No. 2.7
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                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide SEQ ID NO 27545 for detecting SNP TSC0007666.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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84.6%; Pred. No. 2.7e+02;
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                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                            Oligonucleotide SEQ ID NO 85203 for detecting SNP TSC0021429.
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine

WPI; 2001-657177/75.

WO200177384-A2

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Homo sapiens

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for disenses and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE039989, ABE00010-ABE99989 and ABI00010-ABE99989, represent the oligomers described in the invention. NOTE: The sequence
                                                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                         Claim 1; SEQ ID NO 64315; 29pp + Sequence Listing; German.
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Matches 11; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                        Oligonucleotide SEQ ID NO 139295 for detecting SNP TSC0034884.
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peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                        set or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                Piepenbrock C,
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(EPIG-) EPIGENOMICS AG.
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                                  olek A,
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABC0010-ABC99989, ABC0010-ABC99989, ABC0010-ABC99989, ABC0010-ABC99989, and ABC0010-ABC99989, and ABC0010-ABC99989, as obtained in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                      8.5%; Score 11; DB 1; Length 13;
100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0; Indels
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Sequence 13 BP; 6 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABC0010-ABC99989, ABC0010-ABC9989, ABC0010-ABC9989, ABC0010-ABC9989, and ABI00010-ABCG010 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic
                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                    Oligonucleotide SEQ ID NO 248478 for detecting SNP ISC0060726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 248478; 29pp + Sequence Listing; German.
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nes 11; Conservative
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Matches
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                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
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             8.5%; Score 11; DB 1; Length 13; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels
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             Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                      1357 AAATATTCCAC 1367
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RAAAAAATTCCA 1
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Matches
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                                Length 13;
                             8.5%; Score 11; DB 1; Length 13; 34.6%; Pred. No. 2.7e+02; ve 1; Mismatches 1; Indels
Sequence 13 BP; 0 A; 4 C; 0 G; 8 T; 0 U; 1 Other;
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ABH48501 standard; DNA; 13 BP.

RESULT 371 ABH48501/c ID ABH485

ò P German.

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diseases and/or prognosis of cancer and a range of diseases including immune system, gastroninestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABF09989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF9973. represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but twipo.int/pub/published_pot_sequences
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                                                                                                                                                                             This invention describes novel oligonucleotide primers or peptide nucleic
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                     Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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84.6%; Pred. No. 2.7e+02;
ive 1; Mismatches 1; Indels
                                                                                                                        Claim 1; SEQ ID NO 119735; 29pp + Sequence Listing;
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ABF37537/c
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100.0%; Pred. No. 2.7e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                   07-APR-2000; 2000DE-01019173.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.5
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                 Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 GTAAAATTGTT 3
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WO200177384-A2

18-OCT-2001

Homo sapiens

ABF19738;

RESULT 373 ABF19738

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Gaps

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1357 AAATATTCCAC 1367

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oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF0010-ABF99889, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             set or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide SEQ ID NO 178652 for detecting SNP TSC0044255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 178652; 29pp + Sequence Listing; German.
                                                                                                                                                                         8.5%; Score 11; DB 1; Length 13; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
                                                                                                                                          Sequence 13 BP; 4 A; 1 C; 0 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was obtained in electronic format from W1
ftp.wipo.int/pub/published_pct_sequences
                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                    ABF78655 standard; DNA; 13 BP.
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                                                                                                                                                                                                                                                                                                 13 AGAAAAATATT 3
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Matches 11; Conserve
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                                                                                                                                                                               Query Match
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The invention describes a method of detecting whether a compound alters transcription of a transcription unit comprising providing a reaction mixture comprising a RNA polymerase and a first polymucleotide that contains a first promoter operably linked or a transcription unit, adding the compound to the reaction mixture and detecting amount of transcription product. The method is useful for determining whether the compound alters the transcription unit. The compound can be used to inhibit expression of transcription unit. The compound can be used to finhibit expression of transcription units and inhibit growth of bacteria. This sequence represents a promoter element associated with the method of detecting altered transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting whether compound alters transcription of transcription unit by providing reaction mixture of first polynucleotide, adding test compound to reaction mixture and detecting amount of transcription product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E. coli ompA gene fragment, comprising ribosome binding site and 5'UTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                          Transcription inhibition detection related promoter element seqid 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                        antibacterial; transcription; transcription unit; gene expression inhibition; transcription unit inhibitionn; bacterial growth inhibitionn; promoter element; ds.
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100.0%; Pred. No. 3e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; SEQ ID NO 6; 38pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROSS WE,
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                                                                                             ADE15253 standard; DNA; 14
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                                                                                                                                                           (first entry)
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nes 11; Conservative
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1 AAATATTCCAC 11
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                                                                                                                                                                                                                                                                                                                                                                                                                        17-AUG-1999;
                                                                                                                                                                                                                                                                                                                       US6605431-B1
                                                                                                                                                           29-JAN-2004
                                                                                                                                                                                                                                                                                          Unidentified
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                                                                                                                           ADE15253;
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                                                              RESULT 376
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Gaps

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8.5%; Score 11; DB 1; Length 13; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels

Query Match Best Local Similarity 100.(Matches 11; Conservative

schultz911-3.rng

Nandabalan K,

Denton RR,

Anastasio AE, Chew A, WPI; 2001-522460/57.

(GENA-) GENAISSANCE PHARM INC

08-FEB-2001; 2001WO-US004130. 08-FEB-2000; 2000US-0181059P.

16-AUG-2001

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A new method for developing vaccines has been identified, in which a non-
naturally occurring molecular scaffold, having a core particle and a
covalently attached organiser, is attached to an antispen or antispenic
determinant. The scaffold and antigen or antispenic determinant interact
to form an ordered and repetitive antigen array. The composition is
cueful as a vaccine against infectious diseases, to induce immune
responses in farm animals and also in the treatment of cancer and
allergies. The human Growth Hormone, hGH, protein was used as the
caffold in the present invention, and was fused to B. coli outer
membrane protein, OmpA signal sequence which is a FOS leucine zipper
protein domain. The FOS domain formed the antigen attachment site. The
present sequence is B. coli ompA gene fragment, comprising the ribosome
binding site and 5'OTR. This sequence was used in the construction of the
proteins in B. coli
proteins in B. coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human interleukin 15 (IL-15) gene polymorphism detecting ASO probe #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Composition for use as vaccine against infectious diseases and in treatment of cancer and allergies comprises non-naturally occurring molecular scaffold and antigen or antigenic determinant.
Antigen presentation; vaccine; infectious disease; allergy; cancer; molecular scaffold; immune response; farm animal; organiser; hGH; immunostimulatory; cytostatic; antiallergy; human growth hormone; FOS leucine zipper; OmpA; outer membrane protein; ss.
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                                                                                                                                                                                                                                                                                                                                 Bachmann M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                 Nieba L,
                                                                                                                                                                                                                                                                                             (CYTO-) CYTOS BIOTECHNOLOGY AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD15741 standard; DNA; 15 BP.
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99US-0142788P.
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                                                                                                                                                                                                                                                                                                                                 Hennecke F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AGGAGGTAAAA 11
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                                                                                        Escherichia coli
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                                                                                                                                                                                                   30-NOV-1999;
                                                                                                                                                                                                                                       30-NOV-1998;
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                                                                                                                                                                08-JUN-2000
                                                                                                                                                                                                                                                                                                                                 Renner WA,
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The present sequence is allele-specific oligonuclectide (ASO) probe useful for detecting human interleukin-15 (IL-15) gene polymorphism [Cocated on chromosome 4031. The polymorphic variants of IL-15 genes are useful for studying the expression and function of IL-15 genes are useful for studying the expression and function of IL-15 genes are individual at the novel IL-15 polymorphic sites are useful for studying or hardwidth at the novel IL-15 polymorphic sites are useful for studying or individual at the novel IL-15 polymorphic sites are useful for studying of versity anthropological lineage, the significance of diversity and lineage of the phenotypic level, paternity testing, corresponding and a trait such as level of drug response or susceptibility to disease. Identifying associations between IL-15 genetic variation and a trait, is useful for developing diagnostic tests and therapeutic treatments for infections, human immunodeficiency virus and T-10-11 leukaemia. The identification of an association between a clinical response and a genotype or haplotype (or haplotype pair) for the IL-15 gene may be the basis for designing a diagnostic method to determine those individuals who will or will not respond to the treatment, or alternatively, will respond at a lower level and thus may require more treatment, i.e. a greater dose of a drug. The genotyping or haplotyping curders affected by expression of function of novel IL-15 isogene and genotyping and haplotyping methods are also useful in designing clinical trials. IL-15 DNA is useful for therapeutic purposes for treating clinical subscribed organ, tissue or cell population of an experience of an incention of an entrangle of an experience of also in gene therapy. Expression of function of also may be turned off by expression of function of also may be the expression of function of an entrangle of an experience of an experience of also in gene therapy. Expression of function of when the and a supple of the expression of function of which are also as a supple of the
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                                                                                                                                                                                                                                                                                                                              Novel polynucleotides comprising one of 11, PS1-PS11, single nucleotide polymorphisms in human interleukin-15 gene, and useful for treating disorders affected by expression of function of interleukin-15 isogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression vector that expresses high levels of untranslatable mRNA for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; Page 16; 78pp; English.
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AAF52311/
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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antiboderide, (for Insulin-11ke Growth Factor [168]-1 receptor, 1GF binding protein [1688]-2 or 1GFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, or inflammation and/or other disorders. The present sequence is an inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the effects of psoriasis, oligonucleotides of the present invention (see AAF45151 and AAF45151-75161). The method is useful for ameliorating the effects of psoriasis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, the present factor mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense therapy; antiproliferative; antinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityrisais; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neophasia; scleroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasia; kidney disease; neobacular condition; thereis; kidney disease;
growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
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                                                                                                                                                                                                                                                                                                                                                             Edmondson SR;
                                                                                                                                                                                                                                                                                                                  (MURD-) MURDOCH CHILDRENS RES INST.
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                                                                                                                                                                                                                                 21-JUN-2000; 2000WO-AU000693.
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                           WO200078341-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation.
                                                                                                                                                                                                                                                                          21-JUN-1999;
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                                                                                                                                                                                       28-DEC-2000.
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                                                                                                        Homo
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                                                                                                                                                                                                                                                                                                                        Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer;
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                                                                                                                                                                                                                                                Edmondson SR;
                                                                                                                                                                                                          (MURD-) MURDOCH CHILDRENS RES INST.
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                                                    WO200078341-A1.
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                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                    inflammation.
                                                                                                                                                                    21-JUN-1999;
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comprising a core particle of natural original and an organisary as comprising a core particle of natural origin and an organisar comprising at least one first attachment site, where the organisar is connected to the core particle by at least one covalent bond. Also disclosed is an antigen or antigenic determinant with at least one second attachment is settingen or antigenic determinant with at least one second attachment is selected from an attachment site naturally occurring with the antigen or antigenic determinant is and an attachment site is selected from an attachment site naturally occurring with the antigen or antigenic determinant, where the second attachment site is selected from an attachment site naturally occurring with the antigen or antigenic determinant, where the second attachment site is capable of association through at least one non-peptide bond to the first attachment site and where the antigen or antigenic determinant and the scafeold interact through the association to form an ordered and repetitive antigen array. The invention also comprises a coat protein capable of forming a capsid which comprises mutant tober a coat protein and an antion acid sequences expected from five anning and anning an aming an aspectification. The compounds of the invention may the antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular antigen array used in the production of vaccines for infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a novel ordered and repetitive antigen array used in the production of vaccines for infectious diseases. The invention also discloses a composition comprising a non-natural molecular scaffold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiviral, antidiabetic, or hypoglycaemic activities and may be used in immunisation and as a vaccine. The present sequence represents a DNA sequence used to create the compositions of the invention
                                  cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array; vaccine; infectious disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          have antimicrobial, antiallergic, immunomodulatory, cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bachmann M, Tissot A, Maurer P, Lechner F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.5%; Score 11; DB 1; Length 15; 100.0%; Pred. No. 3.2e+02; ive 0; Mismatches 0; Indels
Molecular antigen array associated DNA sequence #13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 311; 441pp; English.
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                                                                                                                                                                                                                                                                                                                                                              21-JAN-2002; 2002WO-IB000166.
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04-MAY-2001; 2001US-0288549P.
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hes 11; Conservative
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                                                                                                                                                                                                                                      WO200256905-A2.
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                                                                                                                                                                                Unidentified.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a composition comprising: (a) a non-natural molecular scaffold (molecular scaffold) which comprises a core particle such as a bacterial pilus or pilin protein, a recombinant form of the protein, as a bacterial pilus or pilin protein, a recombinant form of the protein, a virus-like particle or a hepatitis B virus capsid protein (HBCAG), and an organiser; and (b) an antigen or antigenic determinant, conclude the molecular scaffold and antigen or antigenic determinant interact to form an ordered and repetitive antigen array. Suitable antigenic determinants in conclude JUN, FOS, HIV gp140, measles virus N protein, bee venom to an ordered and repetitive antigen array. Suitable antigenic determinants or protective influence an immune response, such as humoral, cellular or protective immune response, preferably a Th type 2 T-helper (Th2) response that is specific for the antigenic determinant. The administration induces specific for the antigenic determinant. The administration induces corresponding to the Th2 subtype in the subject. The subject of generate a Th2 subtype that is specific for pilus or pilus or pilu polypeptide or antigenic determinant. The composition is useful for the production of corresponding to the Th2 subtype in the subject. The subject or substance or prevention of infectious diseases such as human corrections is syphilis, malaxia, and for treating allergy, cancer, and chronic diseases induced or accelerated by a Th1 type immune response, composition is useful to generate defined self-specific antibodies and specific immune responses of the Th2 type and and allows the creating correction of specific immune responses of the Th2 type and and for treating allergy, cancer, and chronic diseases induced or accelerated by a Th1 type immune responses of the Th2 type and and allows the creating correction of the responses of the Th2 type and and for treating the remain is an entire immune response the protection in the implication is allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New composition, useful for vaccine production, comprises antigen or antigenic determinant and non-natural molecular scaffold comprising organizer and core particle such as bacterial pilus or pilin protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Bachmann M, Tissot A,
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                                                                                                                                                                                                         CYTOS BIOTECHNOLOGY AG.
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                                                                                                                                             05-MAY-2000; 2000US-0202341P.
                                                                                     02-MAY-2001; 2001WO-IB000741.
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                                                                                                                                                                                                                                                               (DUNA/) DUNANT N.
(BACH/) BACHWANN M.
(TISS/) TISSOT A.
(LECH/) LECHENER F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-055561/07.
                                                                                                                                                                                                                                                                                               BACHMANN M.
TISSOT A.
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Matches 11; Conserv
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DUNANT N.
                      15-NOV-2001.
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Gaps

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ABS70925;

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RESULT 382 ABS70925

Query Match

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Isolated polynucleotide, comprising a polymorphic variant of the acetyl-Coenzyme A acyltransferase 1 (peroxiscmal 3-oxoacyl-Coenzyme A thiolase) gene useful for providing haplotype information and in therapy for treating related disorders.
                                                                                                              Human; acetyl-Coenzyme A acyltransferase; ACAA1; chromosome 3p23-p22; peroxisomal 3-oxoacyme A thiolase; SNP; genotype; haplotype; single nucleotide polymorphism; polymorphic variant; enzyme; probe; primer; allele specific oligonucleotide; ss.
                                                          Human ACAAl gene polymorphism detection ASO probe SEQ ID NO:19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 15; Page 13; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAY-2001; 2001WO-US014330.
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22-APR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a new polymucleotide which comprises flavin containing monooxygenase-2 (FWO2) isogenes. The invention is useful in screening for drugs that are useful for treating drug toxicity. The methods of the invention are useful for improving the efficiency and containints of several steps in the discovery and development of drugs of the invention are useful for improving the efficiency and creating diseases associated with FWO2 activity. The methods are also used by the pharmaceutical research scientist to validate FWO2 as a candidate target for treating a specific condition or disease predicted to be associated with FWO2 activity. e.g. drug toxicity, and in the design of clinical trials for treating a specific condition of disease associated with FWO2 activity. The methods are also useful for screening compounds targeting FWO2. The nucleic acid of the invention is useful in studying the expression and innexpressing FWO2 protein for use in screening for candidate drugs to treat diseases compounds targeting FWO2 activity of FWO2 as well as on the binding affinity of candidate drugs targeting FWO2 for the treatment of drug affinity of candidate drugs targeting FWO2 sevening and testing of drugs targeted against FWO2 protein, and for testing the expression of FWO2 isogenes in vivo, for in vivo screening and testing of the against FWO2 protein, and for testing the efficacy of thereseed against FWO2 protein, and for testing the efficacy of thereseed and compounds for treating drug toxicity in a biological system. The present nucleic acid sequence represents an allele-specific consensed on the number of the formal processing the human FWO2 gene located on the human from the hu
                                                                                                              Human; flavin containing monooxygenase-2; FMO2; isogene; drugs targeting; drug toxicity; bone disorder; gene therapy; polymorphism; chromosome lq; allele-specific oligonucleotide; ASO; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel genetic variants of Flavin Containing Monooxygenase 2 isogenes, useful for improving efficiency and reliability in drug development ftreating developmental bone disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parks KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.5%; Score 11; DB 1; Length 15; 100.0%; Pred. No. 3.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Messer C,
                                                          Human FMO2 gene polymorphism detection ASO primer #27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 15 BP; 1 A; 4 C; 3 G; 6 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee HH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kazemi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; Page 16; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-DEC-2000; 2000US-0259062P.
                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2001; 2001WO-US049059.
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duda A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-590627/63.
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                                                                                                                                                                                                                                                                                          WO200253579-A2
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Best Local Simil
Matches 11; (
                                                                                                                                                                                                                                  Homo sapiens
05-NOV-2002
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EXEXENTAL SALES COURSE CONTRACTOR SALES CONTRACTOR SALES

Koshy B; Ξ.

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The present invention describes a polypeptide (I) which is a polymorphic variant (PV) of the acetyl-Coenzyme A acyltransferase (peroxisomal 3-coxoacyl-Coenzyme A thiolase) ACAA1 protein (ABB05516). ACAA1 is located on circomosome 3p23-p22. (I) can be encoded by ABA92286 (or ABA93288) where the sequence comprises one of the haplotypes shown in Table 4 or one of the haplotype shown in Table 3, where tables 3 and 4 are given in the specification. The polymucleotide encoding ACAA1 can be used for providing haplotype and genotype information of an individual. Furthermore, the polymucleotide is useful for the treatment of disorders related to its abnormal expression or function. ABA93289 to ABA93383 represent allele specific oligonucleotides (ASOS) which are used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human GRM8 allele-specific oligonucleotide (ASO) primer, SEQ ID NO:62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; glutamate receptor metabotropic 8; GRM8; receptor; chromosome 7q31.3-32.1; neurotransmission; glutamate-mediated; Smith-Lemli-Opitz syndrome; retinitis pigmentosa; neuropathological disorder; neuroprotective; ophthalmological; gene therapy; haplotyping; genotyping; haplotype; genetic variant; single nucleotide polymorphism; SNP; drug screening; drug discovery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.5%; Score 11; DB 1; Length 15;
84.6%; Pred. No. 3.2e+02;
tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                               represent allele specific oligonucleotides (ASUS) (
detection of polymorphisms in the human ACAAl gene
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15 BP; 4 A; 5 C; 4 G; 1 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1414 TGATGACCAGTCG 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ72858 standard; DNA; 15
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Matches 11; Conservative
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Gaps

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BP.

ABA93304 standard; DNA; 15

RESULT 384

ABA93304;

ABA93304/c ID ABA93 XX AC ABA93 XX

1424 TCGTTCTATGC 1434

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Conservative

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The invention relates to a method for haplotyping the glutamate receptor, and also describes 21 novel polymorphic sites within the human GRAMB gene. The also describes 21 novel polymorphic sites within the human GRAMB gene. The GRAMB gene is located on chromosome 7431.3-32.1 and contains 10 exons which encode a 908 amino acid protein (ABB09564). GRAMB is involved in glutamate-mediated neurotransmission, being a member of a subfamily of metabotropic glutamate receptors that inhibit the activity of adenylate cyclase in response to glutamate stimulation. The chromosomal location of the GRAMB gene encompasses regions linked to Smith-Lenli-Optizs syndrome and a form of retinitis pigmentosa. GRAMB nucleic acid sequences are useful in studying the expression and function of GRAMB, and in expressing GRAMB protein for use in screening drugs for the treatment of GRAMB. Syndrome and retinitis pigmentosa). GRAMB nucleic acids and proteins are also useful in studying the effect of polymorphisms on the biological activity of GRAMB. Polymorphisms in the target region may be determined by the use of allele-specific oligonucleotides (ASOS; ABG72800-ABG72862) as probes and primers, and by primer extension using oilsonucleotide primers comprising sequences ABG72883-ABG72803-ABG72801-ABG72862) as probes and primers, and by primer extension using oilsonucleotide primers comparising sequences ABG72883-ABG72804. The method of the invention is enabling decisions to be made as to whether GRAMB is a likely therapeutic target for a disease of interest, and in the design of clinical trials of candidate drugs for treating GRAMB associated disorders. In addition, transgenic animals comprising a human GRAMB associated disorders. In addition, the expression of GRAMB isogenes in vivo, for in vivo screening and contrar a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetic variants of Glutamate Receptor, Metabotropic 8 isogenes, useful for improving efficiency and reliability in drug development for treating neuropathological conditions and retinitis pigmentosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oligonucleotide (ASO) primers used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapeutic agents and compounds for treating GRMB associated
in a biological system. Sequences ABO72821-ABQ72862 represent
specifically claimed allele-specific oligonucleotide (ASO) pri
                                                                                                                                                                                                                                                                                                                                                                             Koshy B, Parks KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 BP; 3 A; 1 C; 5 G; 5 T; 0 U; 1 Other;
allele-specific oligonucleotide; ASO; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or detecting polymorphisms in the GRM8 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 15; Page 15; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                           Choi JY,
                                                                                                                                                                                                                                                                                                                       (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                               09-NOV-2001; 2001WO-US047325.
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                                                                                                        WO200238587-A2.
                                                                                                                                                                                                                                                                                                                                                                             Bieglecki KM,
                                                     Homo sapiens.
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.. 0 8.5%; Score 11; DB 1; Length 15; 34.6%; Pred. No. 3.2e+02; Ive 1; Mismatches 1; Indels 84.6%; Local Similarity 84.6 les 11; Conservative Query Match Matches

GRM8-associated conditions

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Gaps

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ABS66351 standard; DNA; 15 BP. (first entry) 29-NOV-2002 ABS66351; RESULT 386 ü NX X

allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma; Grave's disease; systemic lupus erythematosus; osteoporosis; inflammatory immune disease; myasthenia gravis; multiple sclerosis; immunoproliferative disease lymphadenopathy; Alzheimer's disease; angloimmunoproliferative lymphadenopathy; immunoblastive lymphadenopathy; rimmunoblastive lymphadenopathy; rheumatoid arthritis; diabetes; infectious disease. molecular scaffold, amyloid beta, Abeta 1-42; influenza; graft versus host disease; IgE-mediated allergic reaction; anaphylaxis; adult respiratory distress syndrome; ARDS; Crohn's disease; Molecular antigen array related modified ribosome binding site. Molecular antigen array; vaccine; ss; primer; antimicrobial; CYTOS BIOTECHNOLOGY AG. 04-MAY-2001; 2001US-0288549P. 05-OCT-2001; 2001US-0326998P. 07-NOV-2001; 2001US-0331045P. 21-JAN-2002; 2002WO-IB000168 .9-JAN-2001; 2001US-0262379P. NOVARTIS PHARMA AG. MAURER P. STAUFENBIEL M. LECHNER F. ORTMANN R. LUEOEND R. WO200256907-A2. Unidentified. 25-JUL-2002. (LECH/) (ORTM/) (LUEO/) (STAU/) (FREY/) (FREY/) (CYTO-) (NOVS)

Frey P; Staufenbiel M, Piossek C; Luecend R, Sebbel P, Ortmann R, 1 , Tissot A, Bachmann M, Ŀ Lechner Maurer P, Renner WA,

WPI; 2002-636514/68.

FREY P.

Molecular antigen array used in the production of vaccines for infectious

Disclosure; Page 289; 418pp; English.

diseases.

The invention relates to a composition comprising: (a) a non-natural molecular scaffold comprising: (i) a core particle selected from: (1) a core particle of a non-natural origin, and (2) a core particle of natural origin; and (ii) an organiser comprising at least one first attachment site, where the organiser is connected to the core particle by at least one econd attachment site one excord attachment site where the antigen or antigenic determinant with at least one second attachment site is selected from: (i) an attachment site not naturally occurring with the antigen or antigenic determinant; and where the second attachment site naturally occurring with the antigen or antigenic determinant; where the second attachment site naturally occurring with the antigen or antigenic determinant; where the second attachment site attachment site, and where the antigen or antigenic determinant site naturally occurring with the antigen or antigenic determinant and the scaffold interact through the association to form an ordered and repetitive antigen array. The composition is used in condered and repetitive antigen array. The composition is used in fimunisation and as a vaccine for diseases such as influence, gath the versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma, gravis, immunoproliferative disease lymphadenopathy, and immunoproliferative lymphadenopathy, and immunoproliferative lymphadenopathy, immunoblastive lymphadenopathy, and immunoproliferative lymphadenopathy, immunoblastive lymphadenopathy, and infermatis, diabetes, multiple sclerosis, Alzheimer's disease, osteoporosis and infectious diseases. The present sequence is a Molecular antigen array related DNA sequence which is included in the sequence acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease, systemic lupus erythematosus, inflammatory immune diseases, myasthenia

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The invention relates to an isolated polypeptide comprising a sequence which is a polymorphic variant of a reference sequence for the amyloid beta precursor protein binding protein 1, 59kD (APPBPI) protein or its fragment. The polymorphic variants are useful in studying the expression and function of APPBPI, in expressing APPBPI protein for use in screening for candidate drugs to treat diseases related to APPBPI activity, in studying the effect of the variation on the biological activity, in the reatment of disorders such as Alzheimer's disease. The haplotyping methods are useful in validating APPBPI as a candidate target for treatment of disorders such as Alzheimer's disease. The haplotyping methods are useful in validating APPBPI as a candidate drugs to treating a specific condition or disease associated with APPBPI condition or disease associated with APPBPI activity, or in the design of clinical trials of candidate drugs for treating a specific condition or disease associated with APPBPI isogenes in vivo, for in vivo screening and testing of drugs carivity. The transgenic animals are useful for studying expression of the APPBPI isogenes in vivo, for in vivo screening and testing of drugs charapeutic agents and compounds for disorders related to platelet agents and compounds for disorders related to platelet in a biological system. ABK32771-ABK32377 represent human in a such a second of the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amyloid beta precursor protein binding protein 159 kD (APPBP1) gene polymorphic variants, useful e.g. in studying the expression and function of APPBP1 and screening candidate drugs for treating Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, amyloid beta precursor protein binding protein 1; APPBP1; probe; Alzheimer's disease; transgenic animal; platelet aggregation; single nucleotide polymorphism; SNP; allele-specific oligonucleotide; ss.
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sausker EA;
listing but is not mentioned anywhere else in the specification
                                                                                                                         ..
                                                                             8.5%; Score 11; DB 1; Length 15;
.larity 100.0%; Pred. No. 3.2e+02;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human APPBP1 gene, allele-specific oligonucleotide #33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Koshy B,
                                       BP; 8 A; 1 C; 5 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kazemi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; Page 13; 104pp; English.
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                                                                                                                                                                                                                                                                                                                  BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000; 2000US-0215511P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-2001; 2001WO-US020951.
                                                                                                                                                                                                                                                                                                                ABK32803 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                   1396 AGGAGGTAAAA 1406
                                                                                                                                                                                                          1 AGGAGGTAAAA 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-164539/21.
                                                                                                Local Similarity
es 11, Conserv
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Stephens CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                   23-APR-2002
                                       Sequence 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                         ABK32803;
                                                                               Query Match
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                                                                                                                         Matches
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C; 1 G; 8 T; 0 U; 1 Other;

Sequence 15 BP; 3 A; 2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition for treating immunoglobulin (Ig) E-mediated disorder such as anaphylactic shock, allergic rhinitis and conjunctivitis, comprises a polypeptide that includes CH1 and/or CH4 domains of IgE molecule coupled
                                                                                                                                                                                                                                                                                                                         Ribosome binding site, RBS; ompA gene; IgE; immunoglobulin B; allergy; asthma; eczema; urticaria; anaphylactic shock; allergic rhinitis; conjunctivitis; antianaphylactic; immunosuppressive; antiallergic; antiaflammatory; dermatological; vasotropic; ophthalmological; vaccine; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                               Gaps
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Score 11; DB 1; Length 15, Pred. No. 3.2e+02;
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100.0%; Pred. No. 3.2e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                            Escherichia coli ompA gene ribosome binding site
 8.5%; Scc. No. 5...
84.6%; Pred. No. 5...
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Page 38; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CYTO-) CYTOS BIOTECHNOLOGY AG.
                                                                                                                                                                                              ABA91820 standard; DNA; 15 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JUL-2001; 2001WO-IB001353.
                                                                              1396 AGGAGGTAAAATT 1408
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                                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Renner WA;
                                                                                                             ASAAGGTAAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BACH/) BACHMANN M F. (RENN/) RENNER W A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-227076/28.
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Best Local Similarity
                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200209751-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to a carrier.
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                                                                                                                                                                                                                              ABA91820;
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             Query Match
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Matches
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                                               Matches
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The probe (N-2) was used to screen a gene bank prepd. from mRNA isolated from ATL-2 cells from a patient with adult T leukaemia virus. Vectors cong. the DNA can be used to transform host cells for prodn. of hADF polypeptide. The polypeptide causes differentiation and induces growth of lymphocytes and fibroblasts. See also AANA4500-N94509. (Updated on 03-OCT -2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR
                                                                                                                                                     T cell leukaemia derived factor; hADF; cancer; probe; ss;
                                                                                                                              Probe for N-terminal of human adult T cell leukaemia derived factor.
                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant human adult T cell leukaemia derived factor polypeptide used for treating cancer, immuno-deficiency disease etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rb gene; antisense oligonucleotide; modulate; gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 8.3%; Score 10.8; DB 1; Length 14; Similarity 75.0%; Pred. No. 3.2e+02; 9; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                       Kondo N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14 BP; 6 A; 1 C; 2 G; 2 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene antisense oligonucleotide rb-N-96.
                                                                                                                                                                                                                                                                                                                                                                      Matsui H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 8; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                      Tagaya Y, Maeda M,
                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         踞.
                                                                                                                                                                                                                                                                                                    87JP-00146348.88JP-00134218.
                                                                                                                                                                                                                                                                           88EP-00109311
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                        AAN94501 standard; DNA; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1461 TCAAGCAAATAG 1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                      (first entry)
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TYAARCARATAG 13
                                                                                                                                                       Human adult T cell leuka
immunodeficiency disease
                                                                            (revised)
                                                                                       revised)
                                                                                                                                                                                                                                                                                                                                           (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1989-016762/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                          10-JUN-1988;
                                                                                                                                                                                                                                                                                                      12-JUN-1987;
                                                                                                                                                                                                                                                                                                                  31-MAY-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-0CT-1998
                                                                            25-MAR-2003
                                                                                        03-OCT-2002
                                                                                                   25-JUN-1990
                                                                                                                                                                                                                                                 18-JAN-1989
                                                                                                                                                                                                                        EP299206-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                 AAN94501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV49148;
                                                                                                                                                                                                                                                                                                                                                                      Yodoi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        field.)
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Matches
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RESULT 389
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Hamuro J;

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AAV49008-236 represent antisense oligonucleotides directed against the rb

Gene. Of these, only oligonucleotides AAV49008-52 resulted in effective

Gwarregulation of negative growth control by rb, while oligonucleotides

AAV49052-236 had little effect. The oligonucleotides exemplify the

invention. The specification describes oligonucleotides that contain 8-30

mucleotides, which contain at most 8 nucleotides that contain 8-30

mucleotides, which contain at most 8 nucleotides that contain 8-30

mucleotides, which contain at most 8 nucleotides that contain 8-30

mucleotides, which contain at most 8 nucleotides that contain 8-30

contain two sequences of three consecutive cytosines; do not

three H-bonds to three consecutive cytosines, and the ratio between

cresidues able to form two H-bonds each (2R) or three such bonds (3R) is

given by 2R/3R = 0.33-0.72. The oligonucleotides are used to modulate

expression of genes, particularly the genes for p53, ErB-2, junB, junD,

TGF-beta 1 or beta 2 to control proliferation of primary cell cultures

(e.g. bone marrow stem, liver or kidney cells, osteoclasts, osteoblasts

and/or keratinocytes). The oligonucleotides can also be used to analyse

function of proteins (by altering their expression or activity) and

thereapeutically, e.g. in cases of cancer or (targeting TGF) for

stimulating the immune system
                                                                                                                                                                                                                                                                                                                             Preparation of antisense oligo:nucleotide(s) which lack long runs of consecutive guanossine or inosine - and have specific ratio of residues able to form two or three hydrogen bonds, have greater activity and reduced toxicity, used therapeutically or to modulate growth of cells in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.3%; Score 10.8; DB 1;
85.7%; Pred, No. 3.2e+02;
                                                                                                                                                                                               (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Fig 9b; 286pp; English.
                                                                                                                                                     97EP-00101531.
                                                                                                                                                                                                                                           Brysch W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1402 TAAAATTGTTAATG 1415
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nes 12, Conservative
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                                                                                                                                                                                                                                           Schlingensiepen K,
                                                                                                           31-JAN-1997;
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                                                              05-AUG-1998.
                  EP856579-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Gaps

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Substrate for hairpin ribozyme which cleaves HCV at nt. 7593. 뮴. AAZ64860 standard; RNA; 14 1 TAAAATTTTGAATG 14 (first entry) 28-MAR-2000 AAZ64860; RESULT 391 AAZ64860

Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage; cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer; autoimmune disease; ss.

Hepatitis C virus.

W09955847-A2.

04-NOV-1999

Macejak

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Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia; multiple scleroals; osteoprosis; osteomydlitis; asthma; inflammation; systemic lupus erythematosus; graft -versus-host disease; septic shock; acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain; coronary condition; mycoardial infarction; cancer; diabetes; psoriasis; endometriosis; fever; glomerulonephritis; inflammatory bowel disease; ischaemia; Parkinson's disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                              enzymatic nucleic acid, especially a hairpin ribozyme, which cleaves the Hepatitis C virus (HCV) RNA sequence at the base position given in the descriptor line. The HCV sequence was screened for optimal ribozyme target sites using a computer folding algorithm and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme cleavage sites were identified. Ribozymes were synthesised to target these sites and their activities optimised by either varying the length of the binding arms or by modification to prevent degradation by nucleases. The ribozymes of the invention inhibit gene expression and/or viral replication, and are used to treat diseases associated with Hepatics C virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular carcinoma. The ribozymes may be used in combination with interferon to treat HCV infection, other infectious diseases, autoimmune
                                                                                                                                                                                                                                                        Novel ribozymes for the treatment of diseases and conditions related to hepatitis C infection.
                                                                                                                                                                                                                                                                                                                                                 The present sequence represents the preferred target sequence of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.3%; Score 10.8; DB 1; Length 14; 57.1%; Pred. No. 3.2e+02; tive 4; Mismatches 2; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14 BP; 2 A; 5 C; 3 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                  Pavco PA,
                                                                                                                                                                                  Mcswiggen JA, Roberts E,
                                                                                                                                                                                                                                                                                                           Claim 2; Page 100; 123pp; English.
                                                   98US-0083217P.
98US-0100842P.
99US-00257608.
99US-00274553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUL-2000; 2000WO-US018667.
                  99WO-US009027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1382 CGTCTTCTGATCAA 1395
                                                                                                                                              (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF57803 standard; DNA; 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human OPG PCR primer #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                    WPI; 2000-062023/05
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Les 8; Conserv
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                  26-APR-1999;
                                                                                                           23-MAR-1999;
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                                                                       18-SEP-1998
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                                                                                         25-FEB-1999
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99US-00350670

09-JUL-1999;

Gaps

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to bone loss. The method comprises administering a purified and isolated osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976) in conjunction with other substances such as tumour necrosis factor-alpha inhibitors, interleukin (ID-6, -8 and -18 inhibitors, ICE modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet activating factor (PAF) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid authritis, multiple sclerosis, osteoporosis, osteomyelitis and asthma. The method is also graft-versus-host disease (GvHD). Other diseases that can be treated include acute pancreatitis, Alzheimer's disease, anorexia,
                                                                                                                                         Treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis and asthma, comprises administering an osteoprotegerin protein in conjunction with e.g. inhibitors of interleukin and tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atherosclerosis, coronary conditions (e.g. myocardial infarction), cancer, diabetee, endometriosis, fever, glomerulonephritis, hyperalgesia, inflammatory bowel disease, ischaemia, pain, Parkinson's disease, psoriasis and septic shock. The present sequence is a PCR primer used in
                                                                                                                                                                                                                                                                       The present invention relates to a method for treating conditions leading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enzymatic nucleic acid, RNA cleavage, Hepatitis C virus infection, HCV ribozyme, HCV expression, HCV replication, cirrhosis, virucide, liver failure, hepatcocellular carcinoma, HCV infection, drug therapy, type I interferon, interferon alpha; interferon beta, cytostatic, interferon gamma; consensus interferon, hepatchropic, antiinflammatory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus substrate #182 for HCV hairpin ribozyme #182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 10.8; DB 1; Length 14; Pred. No. 3.2e+02; 0; Mismatches 2; Indels
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                                                                         Senaldi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 14 BP; 5 A; 4 C; 1 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interferon gamma; consensus interferon; hepat
substrate; hairpin ribozyme; HP ribozyme; ss.
                                                                       Chang M,
                                                                                                                                                                                                                                     Example 8; Page 127; 316pp; English.
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                                                                         Calzone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.3%;
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99US-00457647
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Best Local Similarity 85.00
Best Local 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 TGTTAATGAGGATC 1
                                                                                                                                                                                                  necrosis factor alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BLAT/) BLATT L.
(MCSW/) MCSWIGGEN J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the present invention
                                                                       Lacey DL,
                                                                                                         WPI; 2001-103031/11.
                                   (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus
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09-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABX01697;
                                                                       Boyle WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 393
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RESULT 395
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                                                                                                                                                           The present invention relates to enzymatic nucleic acids which specifically cleave RNA derived from Hepatitis C virus (HCV). The cary matter nucleic acid or ribozyme is in a hammerhead (HH) or hairpin (HP) motif where the binding arms comprise sequences complementary to one of the substrate sequences defined in the specification. The HCV it bozymes are useful for modulating the expression and/or replication of HCV. They can be used to treat cirrhosis, liver failure and/or replication of hepatocellular carcinoma. The HCV infection in conjunction with one or more conter fug therapies, particularly type I interferon, especially interferon abpha, beta or gamma or consensus interferon. The present sequence represents a substrate for a HCV hairpin (HP) ribozyme. Note: Some of the sequence data for this patent did not form part of the printed specification. The complete sequence data for this patent was obtained in electronic format directly from the USPTO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting whether compound alters transcription of transcription unit by
                                                                                         New ribozymes targeting RNA derived from hepatitis C virus inhibit viral replication and are useful to treat hepatitis C virus infections and cirrhosis, liver failure or hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription inhibition detection related promoter element seqid 27.
                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                       8.3%; Score 10.8; DB 1; Length 14; 57.1%; Pred. No. 3.2e+02; ative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibacterial; transcription; transcription unit; gene expression inhibition; transcription unit inhibition; bacterial growth inhibitionn; promoter element; ds.
                                               Macejack D;
                                                                                                                                                                                                                                                                                                                                                                  Sequence 14 BP; 2 A; 5 C; 3 G; 0 T; 4 U; 0 Other;
                                                 Pavco PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaal T;
                                                 Roberts B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROSS WE,
                                                                                                                                         Claim 2; Page 63; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE15274 standard; DNA; 14 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
                                               Mcswiggen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Estrem ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-851203/79.
                                                                     WPI; 2002-617759/66
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
(ROBE/) ROBERTS B. (PAVC/) PAVCO P A. (MACE/) MACEJACK D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE15274;
                                             Blatt L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 394
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                           The invention describes a method of detecting whether a compound alters transcription of a transcription unit comprising providing a reaction mixture comprising a RNA polymerase and a first polymeralectide that contains a first promoter operably linked to a transcription unit, adding the compound to the reaction mixture and detecting amount of transcription product. The method is useful for determining whether the compound alters the transcription unit. The compound can be used to inhibit expression of transcription units and inhibit growth of bacteria. This sequence represents a promoter element associated with the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnostic method for atopy - comprises detecting presence of mutation or polymorphism in gene encoding beta-sub:unit of high affinity IgE receptor.
providing reaction mixture of first polynucleotide, adding test compound to reaction mixture and detecting amount of transcription product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14 BP; 4 A; 0 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                               8.3%; Score 10.8; DB 1;
85.7%; Pred. No. 3.2e+02;
ative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High affinity IgE receptor beta-subunit variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shirakawa T;
                                                                        Example 3; SEQ ID NO 27; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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"T in wt"
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"A in wt"
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"G in wt"
                                                                                                                                                                                                                                                                                                                                       detecting altered transcription.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ80598 standard; DNA; 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IgE receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-AUG-1994;
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27-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
                                                                                                                                                                                                                                                                                                                             Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atheroselerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                 Human IL-5 hammerhead ribozyme target sequence (nt. position 579)
                                             ô
3; DB 1; Leus-
3.5e+02; Indels
              Length 15;
              Score 10.8; DE
Pred. No. 3.5e+
0; Mismatches
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94US-00218934.
94US-00224935.
94US-00227958.
94US-00271280.
94US-00271280.
94US-00291433.
94US-00291632.
94US-00291632.
94US-00303039.
94US-00303039.
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94US-00319492.
94US-00321993.
                                                                                                                                                                                     AAT54299 standard; RNA; 15 BP.
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94US-00337608,
94US-00345516,
94US-00357577,
             8.3%;
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95US-00380734
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                                                                            1405 AATTGTTAATGATG 1418
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                                                                                                          AATTGGTAGTGATG 15
                                                                                                                                                                                                                                                                     (first entry)
                                               Conservative
                                                                                                                                                                                                                                                   25-MAR-2003 (revised)
24-MAR-1997 (first er
              Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-AUG-1994;
16-AUG-1994;
17-AUG-1994;
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07-OCT-1994;
11-OCT-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1994;
30-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAY-1994;
06-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-1994;
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                             The sequence corresponds to exon 6 of a variant gene encoding the high affinity IgE receptor on chromosome-11q, starting at position 5640. The specified mutations in this region result in a substitution of Leu for Ile-181 and Leu for Val-183. The mutations can be detected in a method for the diagnosis of atopy or predisposition to atopy. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnostic method for atopy - comprises detecting presence of mutation or polymorphism in gene encoding beta-sub:unit of high affinity IgE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence corresponds to exon 6 of a variant gene encoding the high affinity IgE receptor on chromosome-11q, starting at position 5640. The specified mutations in this region result in a substitution of Leu for Ile-181. The mutations can be detected in a method for the diagnosis of atopy or predisposition to atopy. (Updated on 25-MAR-2003 to correct PM field.)
                                                                                                                                                                                                       Gaps
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                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutation; polymorphism; atopy diagnosis; ds.
                                                                                                                                                                                                      2; Indels
                                                                                                                                                                     8.3%; Score 10.8; DB 1; Length 85.7%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 4 A; 0 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                         Sequence 15 BP; 4 A; 0 C; 5 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           High affinity IgE receptor beta-subunit variant
                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hopkin JM, Shirakawa T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in wt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 33; 48pp; English.
 4; Page 32; 48pp; English
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                                                                                                                                                                      Query Match
Best Local Similarity 85.7
Matches 12; Conservative
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/note= '
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IgE receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
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21-OCT-1995
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Claim
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AAT52182
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                                                                                                            The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-5) mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Rhozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the IL-5 target sequences and thereby inhibit IL-5 expression, making them useful for treating chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes and preventing the recruitment and activation of eosinophils. The ribozymes can also be used to treat eosinophila (related to parasitic infection or with pulmonary infiltration) and L-tryptophan-associated eosinophila "myalgia syndrome. (Updated on 25-MAR-2003 to correct PI
                                                Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; INF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; philadelphia chromosome; inflammation; autoimmune disease; atheroselerosais; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse IL-5 hammerhead ribozyme target sequence (nt. position 557).
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                                                                                                                                                                                                                                                                                                                                                  8.3%; Score 10.8; DB 1; Length 15;
4.3%; Pred. No. 3.5e+02;
ve 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                        Sequence 15 BP; 6 A; 2 C; 2 G; 0 T; 5 U; 0 Other;
 Woolf T;
                                                                                        Claim 2; Page 215; 407pp; English.
Usman N, Wincott FE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-00201109.
94US-00218934.
94US-00222795.
94US-00224483.
94US-00224958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT54593 standard; RNA; 15 BP.
                                                                                                                                                                                                                                                                                                                                                                                                     1357 AAATATTCCACGCA 1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95WO-IB000156
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               2 AAAUAUUUCAGGCA 15
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22-APR-1997 (first entry)
                         WPI; 1995-351090/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-APR-1994;
15-APR-1994;
15-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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 Tracz D,
                                                                                                                                                                                                                                                                                                  field.)
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The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-5) mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the IL-5 target sequences and thereby inhibit IL-5 expression, making them useful for treating chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes and preventing the recruitment and activation of eosinophils. The ribozymes can also be used to treat eosinophila (related to parasitic infection or with pulmonary infiltration) and L-tryptophan-associated eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   b DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Karpelsky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15 BP; 3 A; 2 C; 0 G; 0 T; 10 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 220; 407pp; English.
94US-00245736.
94US-00291280.
94US-00291433.
94US-00292620.
94US-00300000.
94US-003103039.
94US-00311749.
94US-00311749.
94US-0031186.
94US-003118771.
94US-0031937.
94US-0031937.
94US-0031937.
94US-0031937.
94US-0031937.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-00380734
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(first entry)
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01-APR-1997
                                                                               16-AUG-1994;
17-AUG-1994;
19-AUG-1994;
                                                                                                                                                                       02-SEP-1994
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Modak A,
Tracz D,
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The present sequence represents a preferred target sequence for an enzymatic nuclecide acid (i.e. a ribosyme) which cleaves ICAM-1 mRNA at the nuclectide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the ICAM-1 target sequences and thereby inhibit ICAM-1 expression, making them useful for reducing transplant asjection and alleviating symptoms in patients with rheumatoid arthritis, estimate II field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            o DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Usman N, Wincott FE, Woolf T;
Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-ab; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atheroselerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
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94US-00218934.
94US-00227958.
94US-00228041.
94US-002180.
94US-00291632.
94US-00291633.
94US-00291639.
94US-00303039.
94US-00311486.
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94US-00311498.
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94US-00337608.
94US-00345516.
94US-00357577.
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03-OCT-1994;
07-OCT-1994;
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06-JUL-1994;
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16-AUG-1994;
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10-NOV-1994
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Modak A,
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                                                            Gaps
                                                                                                                                                                                                                                                             Human IL-5 hammerhead ribozyme target sequence (nt. position 581).
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                                  Length 15;
                                                           Indels
                                8.3%; Score 10.8; DB 1;
50.0%; Pred. No. 3.5e+02;
tive 5; Mismatches 2;
         BP; 1 A; 4 C; 4 G; 0 T; 6 U; 0 Other;
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94US-00224483
94US-00224483
94US-00227958.
94US-00271280.
94US-00291433.
94US-00291433.
94US-00391520.
94US-00391520.
94US-00391520.
94US-00314397.
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                                                                                     1421 CAGTCGTTCTATGC 1434
                                                                                                                                                                          AATS4303 standard; RNA; 15
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                                                                                                            CAGUGGUUCUCUGC 14
                                                                                                                                                                                                                                      (first entry)
                                                             Conservative
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                                               Local Similarity
nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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15-APR-1994;
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06-JUL-1994;
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24-MAR-1997
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             Sequence 15
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17-AUG-1994
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23-DEC-1994
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                                    Query Match
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                                                             Matches
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K, Matulic-Adamic J, Mcswiggen JA;
, Sullivan SM, Sweedler D, Thompson JD;
Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; philadelphia chromosome; inflammation; autoimmune disease; atheroselerosis; mycoradial infarction; stroke, restenosis; transplant rejection; rheumatoid arthritis; psoriasis; mycoradial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                                                                                                     Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 15 BP; 6 A; 2 C; 2 G; 0 T; 5 U; 0 Other;
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         Karpeisky A, Kisich K,
Pavco P, Beigleman L,
Usman N, Wincott FE, W
                                                                                                                                                                             Claim 2; Page 215; 407pp; English.
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94US-00222795.
94US-00224483.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 57.1%;
nes 8; Conservative
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                                                                                    WPI; 1995-351090/45.
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04-APR-1994;
07-APR-1994;
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09-APR-1997
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           Grimm S,
Modak A,
Tracz D,
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Matches
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The present sequence represents a preferred target sequence for an enzymatic nuclecide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the ICAM-1 target sequences and thereby inhibit ICAM-1 expression, making them useful for reducing transplant rejection and alleviating symptoms in patients with rheumatoid arthritis, asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to correct PI field.)
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Mcswiggen JA;
Aler D, Thompson JD;
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Pred. No. 3.5e+02;
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Local Similarity 50.0%; Pred. No. 3.5e
hes 7; Conservative 5; Mismatches
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9403-00227958.
9403-00228041.
9403-00271280.
9403-00291433.
9403-00291633.
9403-00292620.
9403-00393620.
9403-00314397.
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9403-00314986.
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94US-00363233.
95US-00380734.
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19-AUG-1994;
02-SEP-1994;
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Modak A,
Tracz D,
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AAV60860
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AAX30947-11815 represent tag sequences of transcripts that are differentially expressed in colorectal cancer, in pancreatic cancer, or in both. The tag sequences can be used to identify genes by matching the tag to a gen data base member, or by using the tag sequences as probes to isolate unidentified genes from cDNA libraries. The tag sequences can also be used in a method for diagnosing colon or pancreatic cancer in a sample suspected of being neoplastic. The method comprises comparing the level of at least one transcript in a first sample of a tissue to a being neoplastic and the second sample is a normal human colonic tissue. The transcript is identified by a tag selected from AAX30947-31815. The methods of the invention can be used in the diagnosis, prognosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage; cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
                                                                                                                                                    ose or issuated gene transcripts - useful for developing products for diagnosis, prognosis and treatment of cancers, particularly colon and pancreatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel ribozymes for the treatment of diseases and conditions related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 2513.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.3%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 3.5e+02; ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macejak D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 10 A; 1 C; 3 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pavco PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roberts E,
                                                                                                                                                                                                                                                       Claim 13; Page 63; 120pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0083217P.
98US-0100842P.
99US-00257608.
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  97US-0047352P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ63880 standard; RNA; 15
                                           (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATGGGAAAAAAA 14
                                                                                   3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mcswiggen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cirrhosis; liver failur
autoimmune disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-062023/05
                                                                                                                            WPI; 1999-070161/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
ses 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus.
  21-MAY-1997;
                                                                                   Vogelstein B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09955847-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-SEP-1998;
25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ63880;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method of generating mutations in proteins by synthesising a mixture of oligonuclectides in order to alter the codons for specific amino acids within a defined region of the protein. Using a range of oligonuclectides for the mutations, expression libraries of the mutant protein can be constructed. As an example of the method, the mutant protein can be constructed. As an example of the method, the mutant protein can be constructed. As an example of the method, the binds phosphocholine) is altered to contain the catalytic triad residues for a serine protease. Specifically the amino acids to be altered are selected from the Asp of the complementarity determining region (CDR) 1 region of the variable heavy chain (W) of the antibody, the His of Wh CDR3 and the Ser of the CDR2 from the light chain variable region (VI). The mutagenesis is by a "walk-through" method. The sequence presented of the Mab. The coding sequence for the CDR1 from the Vh region of the Mab. The coding sequence is mutagenised using oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                 Mutagenesis of pre-determined gene sequences - useful for systematic changes of pre-determined amino acids to see their effect on protein activity, and to create gene expression libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tag sequence; colorectal cancer; pancreatic cancer; colon cancer; diagnosis; prognosis; treatment; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tag sequence of a transcript increased in pancreatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.3%; Score 10.8; DB 1; Length 15; 35.7%; Pred. No. 3.5e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 15 BP; 4 A; 3 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 3A; 33pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US010277.
                                                                                                                                                                    92US-00930600.
                                                                                                                                                                                                             90US-00505314.
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                                                                                                                                                                                                                                                                                                                                        WPI; 1998-480376/41.
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tes 12; Conserv
      88
                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAW68512
                                                                                                                                                                                                                                                       (CREA/) CREA R
walk-through;
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                                           Homo sapiens
                                                                                                                                                                    02-NOV-1992;
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                                                                                JS5798208-A
                                                                                                                            25-AUG-1998
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Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or (MURD-) MURDOCH CHILDRENS RES INST. WPI; 2001-041421/05 21-JUN-1999; Wraight CJ, AAF50405; RESULT 405 AAF50405 ð

Edmondson SR

Werther GA,

99US-0140345P

Example 8; Page 69; 201pp; English

inflammation.

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AAF46530
g
                                                                                                                 contributed to be a second to the preferred target sequence of an enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves the Hepatitis C virus (HCV) RNA sequence at the base position given in the descriptor line. The HCV sequence was screened for optimal ribozyme carget sites using a computer folding algorithm and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme cleavage sites were identified. Ribozymes were synthesised to target these sites and their activities optimised by either varying the cleavage sites of the invention inhibit gene expression by nucleases. The ribozymes of the invention inhibit gene expression and/or viral replication, and are used to treat diseases associated with the phatocellular carcinoma. The ribozymes may be used in combination with interferon to treat HCV infection, other infectious diseases, autoimmune contained cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; kaloid; skin discorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBB3; inflammation; psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neophasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neobascular condition; the retina; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.3%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 3.5e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15 BP; 0 A; 5 C; 2 G; 0 T; 8 U; 0 Other;
                                                                  Claim 1; Page 73; 123pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 CAGGAGAAGGAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.7
Matches 12, Conservative
   hepatitis C infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200078341-A1.
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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, collgonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF4151 and AAF45153-CF F45161). The method is useful for ameliorating the effects of psoriasis, chthyosis, pityriasis, ruba, pilaris, serborrhoea, keloida, keratosis, chenchasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; Keloid; skin discorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pityriasis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasia; kidney disease; neovascular condition; hyperplasia; kidney disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

8.3%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 12; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 BP; 7 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wraight CJ, Werther GA, Edmondson SR
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                                                                                                                                                                                                                                                                                                                                                                       vessels or any other hyperplasia
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                                                  inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriaais, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplaeias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
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inhibiting or reducing growth factor mediated cell proliferation,
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Pred. No. 3.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 BP; 6 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vessels or any other hyperplasia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1350 GGAAGAAAATATT 1363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Best Local S
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8 \times 9 
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BP. AAF50409 standard; DNA; 15 GGAAGAGAAATTTT 14 30-MAR-2001 (first entry) AAF50409; RESULT 407 AAF50409 g

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin discorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; necobarcic of the retina; ss. IGF-I oligonucleotide #1369

Homo sapiens.

WO200078341-A1

21-JUN-2000; 2000WO-AU000693.

99US-0140345P. 21-JUN-1999; (MURD-) MURDOCH CHILDRENS RES INST.

Edmondson SR; Werther GA, Wraight CJ,

WPI; 2001-041421/05

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or

Example 8; Page 69; 201pp; English.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, infilammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-

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F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
                                                                                                                                                                                   vessels or any other hyperplasia
              8
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Sequence 15 BP; 8 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Gaps ö Length 15; 2; Indels Score 10.8; DB 1; Pred. No. 3.5e+02; 8.3%; Scor. 85.7%; Pred. No. s.c. 0; Mismatches 12, Conservative Local Similarity Query Match Matches

.; 0

1394 AAAGGAGGTAAAT 1407 1 AAAGCAGGGAAAAT 14 g

RESULT 408

BP. IGFBP3 oligonucleotide #1526. AAF48106 standard; DNA; 15 30-MAR-2001 AAF48106; AAF48106,

Antisense therapy; antiproliferative; antinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin discorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFB-2; IGFBP3; inflammation; psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scaleroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasia; kidney disease; neovascular condition; hyperplasia; kidney disease;

Homo sapiens.

WO200078341-A1.

28-DEC-2000

21-JUN-2000; 2000WO-AU000693.

99US-0140345P 21-JUN-1999; (MURD-) MURDOCH CHILDRENS RES INST.

Werther GA, Edmondson SR;

WPI; 2001-041421/05.

Wraight CJ,

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation

Example 7; Page 54; 201pp; English.

skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP]), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF4151 and AAF45153 oligonucleotides of the present invention (see AAF4151 and AAF45153 ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, present invention relates to a method for ameliorating the effects of

Sequence 15 BP; 3 A; 2 C; 2 G; 8 T; 0 U; 0 Other

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; 0

Gaps

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Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; Keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neophasia; scleroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasia; kidney disease; neobascular condition; hyperplasia; kidney disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia
                                                                                   8.3%; Score 10.8; DB 1; Length 15;
85.7%; Pred. No. 3.5e+02;
tive 0; Mismatches 2; Indels
                                                         Sequence 15 BP; 3 A; 2 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Edmondson SR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 7; Page 54; 201pp; English.
                                                                                                                                                                                                                                                   AAF48104 standard; DNA; 15 BP.
                                                                                                                                                                                                                                                                                                                                        IGFBP3 oligonucleotide #1524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUN-2000; 2000WO-AU000693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0140345P
                                                                                                                                                1432 TGCAGACATATACA 1445
                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                           14 TGAAGACATAAACA 1
                                                                                                     Best Local Similarity 85.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Werther GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-041421/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200078341-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUN-1999;
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                                                                                                                                                                                                                                                                                AAF48104;
                                                                                        Query Match
                                                                                                                                                                                                                       RESULT 409
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                                                                                                                                                                                                                                                                                                                                                                                                                           Detection; probe; diagnosis; oral disease; paradontitis; caries; therapy; polymorphism; virulence factor; antibiotic resistance gene; prognosis; oral infection; detection; pathogen; coronary heart disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide array, useful for diagnosing oral diseases, particularly paradontitis, carries human or microbial reference sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                 Gaps
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    Length 15;
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 BP; 6 A; 2 C; 0 G; 7 T; 0 U; 0 Other;
8.3%; Score 10.8; DB 1;
85.7%; Pred. No. 3.5e+02;
ative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 19; 58pp; German.
                                                                                                                                                                                                                                                                                                                                                                                   C. sputigena 16S rRNA fragment.
                                                                                                                                                                                                                                                  BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-2001; 2001DE-01012348.
13-MAR-2001; 2001DE-02010013.
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                                                                                           1433 GCAGACATATACAT 1446
                                                                                                                                                                                                                                                     ABX03919 standard; DNA; 15
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Best Local Similarity 85.73
Matches 12; Conservative
                                                                                                                       GAAGACATAAACAT 2
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Capnocytophaga sputigena.
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diabetic symptom; ss.
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                       Local Similarity
Les 12, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ROET/) ROETGER A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention
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                                                                                                                                                                                                                                                                                                                                           09-JAN-2003
                                                                                                                                                                                                                                                                                               ABX03919;
       Query Match
                                                                                                                                                                                                        RESULT 410
                                                                                                                                                                                                                                ABX03919/c
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The present invention relates to a method for ameliorating the effects of

ABL95788 RESULT

23-JAN-2001; 2001FR-00000899.

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Tumour; cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; tumour suppression; tumour reversion; apoptosis; viral resistance; human; viral infection; cell degeneration disease; neurodegeneration; ds; Alzheimer's disease; schizophrena; immune disease; inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                          Production of recombinant proteins in prokaryotes or eukaryotes particularly with target proteins obtainable through gene recombination technique, for use as drugs, reagents, raw materials for industries and feeding stuffs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins. The method comprises preparing a recombinant vector for transforming a host cell before culturing the obtained transformant, assaying expression of the reporter gene and confirming high expression of the recombinant proteins are useful as drugs, reagents, raw materials for industries and feeding stuffs. Also, the proteins are obtainable on large-scale production. The present sequence was used to illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention relates to a method for producing recombinant
                                                                                      Myeloid progenitor inhibitory factor-1delta23 oligonucleotide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                   Recombinant protein production; drug; reagent; food stuff; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.3%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 3.5e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour suppression-related oligonucleotide #1763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15 BP; 5 A; 5 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6; Page 42; 137pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABQ96112 standard; DNA; 15 BP
ABL95788 standard; DNA; 15 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1357 AAATATTCCACGCA 1370
                                                                                                                                                                                                                                          25-JUL-2001; 2001WO-JP006392.
                                                                                                                                                                                                                                                                       25-JUL-2000; 2000JP-00229064.
                                                                                                                                                                                                                                                                                                      (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                   Tanaka Y, Kondo M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACAGATTCCACGCA 15
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                                                           (first entry)
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                                                                                                                                                                                WO200208417-A1
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                                                                                                                                                    Unidentified
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                                                           19-JUN-2002
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The present invention relates to novel human nucleic acid sequences (I).

The present sequence is one such nucleic acid sequence. Expression of (I) are implicated in tumour suppression or reversion and apoptosis and viral resistance. (I) are useful as probes or primers for detecting, clentifying, measuring and/or amplifying nucleic acid sequences, as attisense reagents and for recombinant production of polypeptides. (I), polypeptides (II) encoded by (I), vector containing (I), cells containing these vectors and antibodies (Ab) against (II) are all useful for treatment/prevention of viral, tumour and cell degeneration diseases (especially neurodegeneration, such as Alzheimer's disease and schizophrenia). Analysing the expression of (I) is also useful for cliances of such diseases. Transgenic animals carrying (I) are used for grudying the actiology of these diseases (also immune and inflammatory diseases). Note: In the present specification, SEQ ID 1 to 2270 are shown
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                                                                                                                                                                      New nucleic acid implicated e.g. in tumor suppression, useful for diagnosis of tumors, viral infection and cellular degeneration and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
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85.7%; Pred. No. 3.5e+02;
.ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15 BP; 4 A; 2 C; 2 G; 7 T; 0 U; 0 Other;
                                                                                                         Susini L;
                                                                                                         Tuijnder M,
                                                                          SA.
                                                                                                                                                                                                                                       Claim 1; Page 486; 623pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus 1.
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                                                                          (MOLE-) MOLECULAR ENGINES LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JAN-2001; 2001EP-00870005.
20-APR-2001; 2001EP-00870085.
24-APR-2001; 2001US-0286102P.
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                                            23-JAN-2001; 2001FR-00000899
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                                                                                                           Felerman A, Amson R,
                                                                                                                                          WPI; 2002-610803/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200255741-A2.
                                                                                                                                                                                                            drug screening.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABZ34164;
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                                                                                                                                                                                                                                                                                                                            (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                      Kinzler KW,
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                                                                                                                                                                                                                  ABK32556 standard; DNA; 15
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                                                                                                                                                                  Local Similarity 85.7
nes 12; Conservative
    Smet K, Stuyver L;
                                                                                                                                                                                                                                                                                                                                               WPI; 2002-153821/20.
             WPI; 2002-590680/63
                                                                                                                                                                                                                                                                 cancer marker; ss.
                                                                                                                                                                                                                                                                                                                                      Vogelstein B,
                                                                                                                                                                                                                                                                                     US6333152-B1
                                                                                                                                                                                                                                                                                                        20-MAY-1998;
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                                                                                                                                                                                                                                                                                                                  20-MAY-1998;
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                                                                                                                                                                                                                                     23-APR-2002
                                                                                                                                           invention
                                                                                                                                                                                                                            ABK32556;
                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                        Human;
                                                                                                                                                                                                                                                             serial
                                                                                                                                                                                                         RESULT 414
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                                                                                                                                                                                                              ABK32556
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23-DEC-2002 12; ABX00933; Query Match Best Loca Matches RESULT 415 ABX00933/c à 셤 the secontacted with anti-HIV drug resistance in a patient by detecting at least one of the mutations K103N/R, V106A/I/L, Y181C/I, M184V/I, Y18BL, C190A/S/R, Y152Y/FV/D/S/A and/or Q151M/L in the reverse transcriptase (RT) of HIV strains in a biological sample using a specific set of probes optimised to function together in a reverse-hybridisation assay. The method and the nucleic acid sequences used in the method are useful for determining viral mutations and/or polymorphisms in the HIV RT gene associated with resistance. The probes are useful for the genetic cluckally in vitro detection of the mutations K103N/R, T215Y/F/D/S/A in the RT of HIV will a biological sample, where the mutation is associated with anti-HIV drug resistance. The method provides a rativiral drug resistance or mutations associated with drug resistance or mutations associated with drug resistance or mutations associated with drug resistance of viruses containing RT genes. ABZ33759 to ABZ34642 represent HIV RT subjects and probes which are used in the exemplification of the present ö Detecting mutations associated with anti-HIV drug resistance comprises detecting at least one of the mutations in the HIV reverse transcriptase gene by using probes optimized to function together in a reverse-hybridization assay. Gaps present invention describes a method for detecting mutations ; 0 Score 10.8; DB 1; Length 15; Pred. No. 3.5e+02; 0; Mismatches 2; Indels Sequence 15 BP; 3 A; 1 C; 7 G; 4 T; 0 U; 0 Other; Claim 2; Page 26; 117pp; English. 85.7%;

Human pancreatic cancer SAGE tag #108.

colon cancer; colorectal cancer; pancreatic cancer; SAGE tag; analysis of gene expression; diagnostic; prognostic; probe;

Zhou W; Zhang L, New human nucleic acid containing specific SAGE tags, useful as

ó The present invention relates to enzymatic nucleic acids which specifically cleave RNA derived from Hepartits C virus (HVV). The enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin (HP) motif where the binding arms comprise sequences complementary to one of the substrate sequences defined in the specification. The HCV ribozymes are useful for modulating the expression and/or replication of HCV. They can be used to treat cirrhosis, liver failure and/or (serial analysis of gene expression) tag comprising a single stranded probe contraining at least 10 consecutive nucleotides. SAGE tags, are diagnostic and prognostic markers of cancer, especially of the colon and pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer New ribozymes targeting RNA derived from hepatitis C virus inhibit viral replication and are useful to treat hepatitis C virus infections and cirrhosis, liver failure or hepatocellular carcinoma. Enzymatic nucleic acid, RNA cleavage, Hepatitis C virus infection;
HCV ribozyme, HCV expression, HCV replication, cirrhosis, virucide;
liver failure, hepatococallular carcinoma, HCV infection, drug therapy;
type I interferon, interferon alpha, interferon beta, cytostatic;
interferon gamma; consensus interferon, hepatotropic; antiinflammatory; purified human nucleic acid (I) Gaps The invention relates to an isolated, purified human nucleic acid (that has the same sequence as a mRNA found in humans and is a SAGE Hepatitis C virus substrate #715 for HCV hammerhead ribozyme #715. . 0 8.3%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 3.5e+02; ive 0; Mismatches 2; Indels Macejack D; diagnostic markers for cancer, also derived probes Sequence 15 BP; 10 A; 1 C; 3 G; 1 T; 0 U; 0 Other; interferon gamma; consensus interferon; nepatoc: substrate; hammerhead ribozyme; HH ribozyme; ss Pavco PA, Roberts B, Disclosure; Col 75; 161pp; English Claim 1; Page 42; 80pp; English. 0; ABX00933 standard; RNA; 15 BP. 99US-00274553. 99US-00274553 1346 CAGGGAAGAAAA 1359 SAGE tags of the invention CATGGGAAAAAAA 14 (first entry) Conservative Mcswiggen JA, BLATT L. MCSWIGGEN J A. WPI; 2002-617759/66. ROBERTS B. PAVCO P A. MACEJACK D. Local Similarity Hepatitis C virus US2002082225-A1. 23-MAR-1999; 23-MAR-1999; 27-JUN-2002. Blatt L, (MCSW/) N (ROBE/) F (PAVC/) E (MACE/) N (BLAT/)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutagenesis of a protein comprises introducing a predetermined amino acid into each set of selected sequence positions in a predefined region of the protein to produce a protein library comprising mutant proteins.
hepatocellular carcinoma. The HCV ribozymes are also useful for treating a condition associated with HCV infection in conjunction with one or more other drug therapies, particularly type I interferon, especially interferon alpha, beta or gamma or consensus interferon. The present sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note: Some of the sequence data for this patent did not form part of the printed specification. The complete sequence data for this patent was obtained in electronic format directly from the USPTO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of mutagenesis of a protein. The methods are useful for generating libraries of mutant proteins that are of a practical size for screening, for studying the role of amino acids in protein structure and function and for developing new or improved proteins and polypeptides such as enzymes, antibodies their binding fragments or analogues. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                      8.3%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 3.5e+02; ative 0; Mismatches 2; Indels
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                                                                                                                                                                                    Sequence 15 BP; 0 A; 5 C; 2 G; 0 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heavy chain variable region CDR1 DNA #1
                                                                                                                                                  seqdata.uspto.gov/psipsDIDEntry.html
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95US-00453623.
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                                                                                                                                                                                                                                                                                               1346 CAGGGGAAGAAAA 1359
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Best Local Similarity
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30-MAY-1995;
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The present invention describes a method (MI) for designing capture oligonucleotide probes (I) for use on a support to which complementary cligonucleotide probes (II) will hybridise with little mismatch, where cligonucleotide probes (II) will hybridise with little mismatch, where cligonucleotide probes (II) will hybridise with little mismatch, useful conditions and marrow range. The method is useful conditions and policy of virus, and parasition infectious agents confident and properties infectious and policy virus, and parasitic infectious agents confident and procupulations. Epstein-Barr virus and policy virus, and parasitic infectious agents conditions. The method is also useful for detecting genetic diseases such as 21 hydroxylase deficiency, Turner Syndrome and Obesity defects.

Concer is specifically associated with a gene selected from BRCAH gene, concer is specifically associated with a gene selected from RRCAH gene, proving cancer involving comparises scanning (using e.g. a scanning electron microscope and infrared microscope) the support at the correlating comprises scanning (using electron microscope and infrared microscope) the support at the sets occurred and correlating (using a computer) identified to a presence or absence of the target nucleotide sequences. ABI820746 to the present invention
                                                                                                                                                                                                                                               Human, K-ras; PCR primer; probe; capture probe; mutation detection; ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease; infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer; oncogene; tumour suppressor; human papillomavirus; forensic; environmental monitoring; food industry; feed industry; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Designing capture oligonucleotide probes for use on a support complementary oligonucleotides hybridize with little mismatch.
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                                                                                                                                                                                                           Capture oligonucleptide Zip ID#1251 oligo #9.
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                                                                                            BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-APR-2001; 2001WO-US010958.
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                                                                                            ABI94164 standard; DNA; 20
1 GACTTCTACATGGA 14
                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-034366/04.
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                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                  ABI94164;
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ID ABI9
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Gaps

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8.3%; Score 10.8; DB 1; Length 20; 85.7%; Pred. No. 4.8e+02; rative 0; Mismatches 2; Indels

1374 CGAGCGATCGTCTT 1387

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Gaps

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Indels

0; Mismatches

1436 GACATATACATGGA 1449

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12; Conservative

Matches

Query Match 8.3%; Score 10.8; DB 1; Length 15; Best Local Similarity 85.7%; Pred. No. 3.5e+02;

12; Conservative

Local Similarity

Query Match Best Local Matches 1

CGATCGATCGTGTT

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BP.

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                           Oligonucleotide SEQ ID NO 66307 for detecting SNP TSC0017421.
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                             ABC66290 standard; DNA; 13
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                                                                                                (first entry)
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Matches 10; Conserv
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABH00010-ABH99989 and ABI00010-ABIS2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained, in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                      Piepenbrock C,
                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG
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Best Local Similarity
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                                                                        Homo sapiens
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06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

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Piepenbrock C,

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ABC46120 standard; DNA; 13 BP
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ses 10; Conservative
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    (EPIG-) EPIGENOMICS AG.
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                     WPI; 2001-657177/75
                                        methylation status.
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methylation status.

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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABR99899 and ABI00010-ABB19989 represent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at figure int/pub/published_pct_sequences
This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, and holion-ABC9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel oligonuclectide primers or peptide nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                             This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                  Berlin K;
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Wed Apr

ABC79607 standard; DNA; 13 BP.

Oligonucleotide SEQ ID NO 79624 for detecting SNP TSC0020222

(first entry)

21-FEB-2002

ABC79607;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fire wipo.int/pub/published_pct_sequences
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Pred. No. 3.2e+02;
1; Mismatches 0; Indels
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Sequence 13 BP; 6 A; 1 C; 1 G; 4 T; 0 U; 1 Other;
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                                 Query Match
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Matches 10; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, certification of diseases including immune system, gastrointestinal, respiratory, coligomers are also used for detecting call type differentiation. ABC0010-ABC99889, ABR00010-ABF99889, ABH00010-ABF9989, ABH00010-ABF9989, ABH00010-ABF9989, ABH00010-ABF9989, ABH00010-ABF9989, ABH00010-ABF9989, ABH00010-ABF9989, ABH00010-ABF9989, ABH0010-ABF9989, ABH00010-ABF9989, ABF00010-ABF9989, ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF9989, 
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                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 3.2e+02;
1; Mismatches 0; Indel8
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Matches 10; Conservative
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AAS99209 standard; DNA; 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fire wipo.int/pub/published_pct_sequences
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Matches 10; Conservative
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                                                                           18-OCT-2001
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The invention relates to an isolated polynucleotide, which comprises CC polymorphisms in the human interleukin 15 (ILI5) gene. The polynucleotide comprises genes and haplotypes of the ILI5 gene. The polynucleotide comprises polymorphic sites referred to as PSI-13 to designate the order in which they are located in the gene. The polynucleotide comprising comprises suscinciated to ILI5 activity, e.g. infections, human communicated to ILI5 activity, e.g. infections, human reat immunodeficiency virus or T cell leukaemia. The ILI5 isogenes are especially useful for treating these diseases. The methods and haplotypes are useful in improving the efficiency of drug discovery and development correcting the specific condition or disease. The transgenic animals are useful for studying expression of the ILI5 isogenes in vivo, for in vivo screening and testing of drugs targetted against ILI5 protein, and for testing the efficiency of the ILI5 isogenes in vivo, for in vivo screening the efficiency of the therapeutic agents. The present sequence is human ILIS gene polymorphism detecting ASO (allele-specific oligonucleotide) probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, N-acetyltransferase 1; arylamine N-acetyltransferase; NAT1; ss;
haplotyping; cytostatic; haplotype pair; single nucleotide polymorphism;
genotyping; gene therapy; drug screening; lung cancer; sequencing primer;
New genetic variants comprising haplotypes of the human interleukin 15 (ILL5) gene, useful for treating infections, human immunodeficiency virus or T cell leukemia, or for screening drugs for treating these diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15 BP; 10 A; 0 C; 2 G; 2 T; 0 U; 1 Other;
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                                                                                                                                                                                           Claim 16; Page 14; 84pp; English
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human N-acetyltransferase 1 (arylamine N-acetyltransferase), NAT1 gene
         Claim 16; Page 13; 55pp; English
                                                                                                                                                                                Oligonucleotide 5 (451) donor.
                                                                                                                                                         AAX19088 standard; DNA; 12 BP.
                                                                                                                                                                         13-MAY-1999 (first entry)
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                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                 AAX19088;
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                                                                                                                                                   RESULT 428
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The invention relates to single nucleotide polymorphisms in the gene encoding the human N-acetyltransferase I (arylamine N-acetyltransferase) or NATI polymeptide. A method for haplotyping the NATI gene in an individual comprises identifying the nucleotide at one or more individual comprises identifying whether one of the copies of the gene polymorphic sites and determining whether one of the copies of the gene is defined by one of the NATI haplotypes given in the specification or wether both copies are defined by a haplotype pair. This method is useful in genotyphing, whereby all possible haplotype pairs can be assigned to specific genotypes. An association between a trait and a comparing the frequency of the NATI gene can be identified by comparing the frequency of the haplotype or haplotype pair in a reference population, where a higher haplotype or haplotype or the haplotype or haplotype pair. NATI and its corresponding DNA are used for candidate durgs to treat diseases related to NATI activity, such as the nature of the haplotype or the biological activity of NATI as well as on the biological activity of NATI as well as on the biological activity of NATI as well as on the biological activity of NATI as well as on the biological activity of NATI as well as one the binding represent allele-specific oligonucleotide probes, sequencing primers and property or pair was a polymorphisms. ö Gaps .. Score 10.6; DB 1; Length 15; Pred. No. 3.8e+02; 1; Mismatches 0; Indels Sequence 15 BP; 6 A; 3 C; 3 G; 2 T; 0 U; 1 Other; 8.2%; Query Match
Best Local Similarity 90.9
Matches 10; Conservative

Human; peroxisome proliferator activated receptor gamma; PPAR-gamma; regulatory sequence; promoter; obesity; anorexia; lipoma; cachexia; lipodystrophy; liposarcoma; human immunodeficiency virus; HIV; insulin resistance; non-insulin-dependent diabetes mellitus; polycystic ovary syndrome; gastrointestinal tract; Crohn's disease; inflammatory bowel disease; ulcerative colitis; bowel cancer; ss.

98WO-US015411

97US-0053692P

(LIGA-) LIGAND PHARM INC. (INSP) INST PASTEUR.

Fajas L; Auwerx J, Saladin RS,

WPI; 1999-142844/12.

Newly isolated nucleic acid comprising a control region of a human

The present invention describes an isolated, purified or enriched nucleic acid comprising a control region of a human peroxisome proliferator acid comprising a control region of a human peroxisome proliferator.

Compositions that are useful for treating diseases associated with the pparamagene. These agents (modulators) form pharmaceutical compositions that are useful for treating diseases associated with nuclein to high/low levels of human PPAR-gamma gene expression. The diseases include obesity, anorexia, cachexia, lipodystrophy, lipomas, liposarcomas, cobesity, anorexia cachexia, lipodystrophy, lipomas, liposarcomas, cobesity, anorexia easociated with anti-human immunodeficiency vitue (HIV) treatment, insulin resistance, non-insulin-dependent diabetes mellitus (NIDDM), polycystic ovary syndrome, diseases of the gastrointestinal (GI) treat, inflammantory bowel disease, (Tohn's disease, ulcerative colitis and bowel cancer. The nucleic acids are useful for studying the role of the PPAR-gamma enables genetic studies of PPAR-gamma mane, can disease associated with altered adipose tissue function, like and evaluation of its role in disorders in the insulin resistance. Cor obesity and lipodystrophic syndromes. The nucleic acids are also useful cor gene therapy and the production of transgenic animals, which are costil in screening for modulators of the human PPAR-gamma gene. Which are useful in designing drugs for treating diseorders or diseases associated with the level of PPAR-gamma gene expression. The present invention cover the present invention of trepresents an oligonucleotide sequence from the present invention ö for proliferator activated receptor (PPAR) gamma gene - useful i modulators that are useful in treating diseases associated Gaps ö Score 10.4; DB 1; Length 12; Pred. No. 3.18+02; 0; Mismatches 1; Indels with abnormal levels of human PPAR-gamma gene expression Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other; Disclosure; Page 95; 102pp; English. H. 8.0%; AAX14803 standard; DNA; 12 1397 GGAGGTAAAATT 1408 Query Match Best Local Similarity 91.7 Matches 11, Conservative 1 GGAGGTAAGATT 12 dentifying. RESULT 429 AAX14803, à d

AAX14803;

24-MAR-1999 (first entry)

DNA detection; triple helix; identification; bacteria; Triple helix third strand of Hepatitis B virus nucleotides 2258-2269. oncogene; virus; ss. Triplex formation;

Hepatitis B virus. Synthetic

US5861244-A.

19-JAN-1999

93US-00173489. 22-DEC-1993; 92US-00968436. 29-OCT-1992; (PROF-) PROFILE DIAGNOSTIC SCI INC.

Hepburn AG, Wang C;

WPI; 1999-130384/11.

Assay of genetic sequences based on triplex formation from double

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The present sequence represents a polynucleotide that is able to form a triple helix with a double stranded sequence. Cytosine bases in the present can be replaced with 5-methylcytosine for increased triplex ctability. The present sequence is used in the assay of the invention, where it can be part of the anchor DNA or reporter DNA sequence. The assay comprises adding a sample containing double-stranded DNA test compared to a solid support, and reporter DNA, where either a part of the anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA test of the test sequence. Triplex formation results in cisplacement of the reporter DNA is designed to form a triple-strand containing the part of the rest sequence. Triplex formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (by detecting genes for ribosomal RNA) in clinical samples, but also detection of
- and hybrid of anchor and reporter sequences, with if triplex formation occurs, used e.g. to identify
                                                                                                                                                                                                                                       Disclosure; Col 19-20; 168pp; English
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                            analyte
                            stranded
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8.0%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 3.1e+02; ive 0; Mismatches 1; Indels Sequence 12 BP; 0 A; 5 C; 1 G; 6 T; 0 U; 0 Other; 1348 GGGGAAGAAAA 1359 Local Similarity 91.7 nes 11; Conservative GGGCAGAAAA 1 12 Query Match Matches 셤 8

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Gaps

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Human hypocretin receptor 2 (HCRTR2) splice donor site SEQ ID NO:33. Human, narcolepsy; hypocretin receptor 2; orexin receptor 2; HCRTR2; AAH21571 standard; DNA; 12 BP. (first entry) diagnosis; PCR primer; ss WO200130991-A2 Homo sapiens. 03-MAY-2001 10-AUG-2001 AAH21571; 430

22-AUG-2000; 2000WO-US023021 25-OCT-1999;

(DECO-) DECODE GENETICS EHF Olafsdottir BR, Gulcher J;

WPI; 2001-300504/31.

Gene for hypocretin (orexin) receptor 2 (HCRTR2) which is associated with narcolepsy, useful in methods of diagnosis of narcolepsy and pharmaceutical compositions for therapy.

The present invention describes the human hypocretin (orexin) receptor 2 (HCRTR2) gene (given in AAH21613), which is associated with narcolepsy. Identification of the HCRTR2 nucleic acid molecule permits the diagnosis of narcolepsy. A method from the present invention is provided for treating narcolepsy by administering to the individual an isolated HCRTR2 Example 1; Page 26; 85pp; English

ö produce native HCRTR2 receptor. The diagnosis of narcolepsy has been difficult to differentiate from other conditions such as chronic fatigue syndrome or other sleep disorders but detection of HCRTR2 nucleic acid makes it possible to accurately diagnose narcolepsy. AAH21541 to AAH2161 represent primers used in the identification of the narcolepsy gene in an example from the present invention. AAH21613 represents the HCRTR2 gene which encodes the HCRTR2 protein given in AAB98007 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 298531 for detecting SNP TSC0018143. Gaps acid in a therapeutically effective amount so that the cells typing, i cytosine ô Claim 1; SEQ ID NO 298531; 29pp + Sequence Listing; German. 8.0%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 3.1e+02; iive 0; Mismatches 1; Indels Set of oligonucleotides, useful for diagnosis and cell designed to detect single-nucleotide polymorphisms and Sequence 12 BP; 8 A; 0 C; 3 G; 1 T; 0 U; 0 Other; Berlin K; ВÞ 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 ABH98538 standard; DNA; 12 1395 AAGGAGGTAAAA 1406 22-FEB-2002 (first entry) Query Match
Best Local Similarity 91.7
Matches 11; Conservative 1 AAAGAGGTAAAA 12 Piepenbrock C, (EPIG-) EPIGENOMICS AG methylation status. WPI; 2001-657177/75 WO200177384-A2. Homo sapiens 18-OCT-2001 ABH98538; olek A, 888888888 g 8

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, and not account in the invention. NOTE: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at Length 12; Sequence 12 BP; 2 A; 2 C; 0 G; 8 T; 0 U; 0 Other; 8.0%; Score 10.4; DB 1; 91.7%; Pred. No. 3.1e+02; Best Local Similarity Query Match

Wed Apr

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22-FEB-2002 (first entry)
                                                                                          Homo sapiens
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                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 273667 for detecting SNP TSC0003265.
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Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                     ABH73682 standard; DNA; 12
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                     1352 AAGAAAATATT 1363
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11; Conservative
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ABI27243 standard; DNA; 12

RESULT 433

ABI27243

ABI27243;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonuclectide primer SEQ ID NO 327216 for detecting SNP TSC0033502.
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cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell designed to detect single-nucleotide polymorphisms and
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schultz911-3.rng

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06-APR-2001; 2001WO-IB000713.
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                                                                                     Similarity
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                                                                                                                                               Homo sapiens
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12 AB115688; RESULT 436 ABI15688/ ID ABI1 à 셤 ö This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99899, ABF00010-ABF99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire wipo.int/pub/published_pct_sequences Gaps Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status. ö 8.0%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 3.1e+02; Claim 1; SEQ ID NO 308016; 29pp + Sequence Listing; German. 1; Indels Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other; 0; Mismatches Berlin 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 11; Conservative Piepenbrock C, (EPIG-) EPIGENOMICS AG

ABI40085 standard; DNA; 12 BP. (first entry)

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 340058 for detecting SNP TSC0041323.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K;

Set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE09989, ABE00010-ABE99989, ABH00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABE32073 represent the oligomers described in the invention. NOTE: The sequence SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 315661 for detecting SNP TSC0027026. Gaps Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. ö 8.0%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 3.1e+02; tive 0; Mismatches 1; Indels Claim 1; SEQ ID NO 340058; 29pp + Sequence Listing; German. Claim 1; SEQ ID NO 315661; 29pp + Sequence Listing; German. Sequence 12 BP; 2 A; 4 C; 0 G; 6 T; 0 U; 0 Other; Berlin K; ABI15688 standard; DNA; 12 BP. 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 1349 GGGAAGAAAAT 1360 22-FEB-2002 (first entry) Ouery Match
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Best Local 11, Conservative Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG. GGGTAGAAAAT WPI; 2001-657177/75. methylation status. WO200177384-A2. Ното варіеля 18-OCT-2001.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABR00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                            Oligonucleotide primer SEQ ID NO 377842 for detecting SNP TSC0062519.
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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ABI77869 standard; DNA; 12
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This invention describes novel oligonuclectide primers or peptide nucleic
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                                                                                      ligonucleotides, useful for diagnosis and cell typing, i
to detect single-nucleotide polymorphisms and cytosine
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                                  Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                 This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) oligomers for detecting single nucleotide polymorphisms (SNP) oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but was obtained in electronic format from WIFO at
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peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE9989, ABF0010-ABE9989 and ABI0010-ABIS2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
                                                                                                                                                                                                                                                                        was obtained in electronic format from WI ftp.wipo.int/pub/published_pct_sequences
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Sequence 12 BP; 5 A; 0 C; 2 G; 5 T; 0 U; 0 Other;

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Gaps
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8.0%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 3.1e+02; ive 0; Mismatches 1; Indels
                                  Conservative
             Local Similarity
mes 11; Conserv
 Query Match
                                Matches
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1399 AGGTAAAATTGT 1410 à g

ABI04840 standard; DNA; 12 RESULT 442

BP.

ABI04840;

(first entry) 22-FEB-2002

Oligonucleotide primer SEQ ID NO 304813 for detecting SNP TSC0021122.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173,

(EPIG-) EPIGENOMICS

Berlin K; Piepenbrock C, Olek A,

WPI; 2001-657177/75.

oet or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 304813; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for addiovascular and metabolic disorders. The ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences

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Gaps

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Indels

8.0%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 3.1e+02;

0; Mismatches

1395 AAGGAGGTAAAA 1406 11; Conservative

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Local Similarity

Matches

Query Match

12

AAGGTGGTAAAA

Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

ABI13653 standard; DNA; 12 BP.

RESULT 444

ABI13653 ID ABI1

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                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                       Gaps
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     Length 12;
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                                       Indels
   Score 10.4; DB 1;
Pred. No. 3.1e+02;
0; Mismatches 1;
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Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative (
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                                                                      GGTAAAATTGTT 1411
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Berlin K;

Olek A, Piepenbrock C,

(EPIG-) EPIGENOMICS AG.

06-APR-2001; 2001WO-IB000713.

WO200177384-A2

18-OCT-2001

07-APR-2000; 2000DE-01019173.

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This invention describes novel oligonuclectide primers or peptide nucleic acid (DNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABH00010-ABH9989 and ABT00010-ABR3073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                        Oligonucleotide primer SEQ ID NO 313626 for detecting SNP TSC0025873.
                                                                                                                                                                                                                                                                                                                                                                                                                Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Best Local Similarity 91.75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 343889; 29pp + Sequence Listing; German.
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Best Local Similarity 91.74

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Gaps

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

Oligonucleotide primer SEQ ID NO 343889 for detecting SNP TSC0043288.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
             designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                          Claim 1; SEQ ID NO 344833; 29pp + Sequence Listing; German
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ftp.wipo.int/pub/published_pct_sequences
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Sequence 12 BP; 6 A; 1 C; 0 G; 5 T; 0 U; 0 Other;

Gaps ö Query Match
8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels

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ABI52611 standard; DNA; 12 RESULT 447

BP.

(first entry) 22-FEB-2002 ABI52611;

Oligonucleotide primer SEQ ID NO 352584 for detecting SNP TSC0007996

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Berlin Piepenbrock C, Olek A,

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WPI; 2001-657177/75.

set or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 352584; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The

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oligomers are also used for detecting cell type differentiation. ABC00010 -ABC9989, ABF0010-ABF9989, ABH0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at from the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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SNP TSC0008049.

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Oligonucleotide primer SEQ ID NO 280021 for detecting
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                                                                                                                                                                                                 Olek A, Piepenbrock C,
                                                                                                                                                                          (EPIG-) EPIGENOMICS
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                                                                                      WO200177384-A2.
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                                                                 Homo sapiens
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                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                        Oligonucleotide primer SEQ ID NO 293307 for detecting SNP TSC0015566.
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                                                                         ABH93314 standard; DNA; 12 BP.
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 1398 GAGGTAAATTG 1409
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 91.7
Matches 11; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
Claim 1; SEQ ID NO 283401; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                   Sequence 12 BP; 6 A; 0 C; 2 G; 4 T; 0 U; 0 Other;
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ive 0; Mismatches 1; Indels
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                                                                                   Berlin K;
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                 07-APR-2000; 2000DE-01019173.
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                                               (EPIG-) EPIGENOMICS AG
                                                                                                                 WPI; 2001-657177/75.
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8.0%; Score 10.4; DB 1; Length 12; 31.7%; Pred. No. 3.1e+02; ve 0; Mismatches 1; Indels

Local Similarity 91.7%; nes 11; Conservative

ftp.wipo.int/pub/published_pct_sequences

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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1404 AAATTGTTAATG 1415
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

EPIG-) EPIGENOMICS AG

07-APR-2000; 2000DE-01019173. 06-APR-2001; 2001WO-IB000713.

WO200177384-A2 Homo sapiens

18-OCT-2001

Oligonucleotide primer SEQ ID NO 283401 for detecting SNP TSC0011291.

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ABI73097;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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1 Similarity 91.7%; Pred. No. 3.1e+02;
11; Conservative 0; Mismatches 1; Indels
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                                                    Sequence 12 BP; 4 A; 0 C; 2 G; 6 T; 0 U; 0 Other;
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                                                                                                                     Oligonucleotide primer SEQ ID NO 373070 for detecting SNP TSC0059827.
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastrointestinal, respiratory. Central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABC0010-ABB9989, ABR0010-ABB9989 ABR0010-ABB9989 ABR0010-ABB9999 ABI0010-ABB82073 and ABI0010-ABB82073 data for this patent dim not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                         This invention describes novel oligonucleotide primers or peptide nucleic
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                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                         Claim 1; SEQ ID NO 296443; 29pp + Sequence Listing; German.
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Olek A, Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ö This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. oligonuclectides are used for diagnosis and/or prognosis of cancer and a Oligonucleotide primer SEQ ID NO 307971 for detecting SNP TSC0022819. Gaps Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status. ·; Claim 1; SEQ ID NO 307971; 29pp + Sequence Listing; German. Length 12; 1; Indels Sequence 12 BP; 6 A; 0 C; 5 G; 1 T; 0 U; 0 Other; Sequence 12 BP; 5 A; 0 C; 1 G; 6 T; 0 U; 0 Other; Score 10.4; DB 1; Pred. No. 3.1e+02; 0; Mismatches ftp.wipo.int/pub/published_pct_sequences ftp.wipo.int/pub/published_pct_sequences Berlin K; BP 8.0%; 91.7%; 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 ABI07998 standard; DNA; 12 1402 TAAAATTGTTAA 1413 (first entry) 11; Conservative TAAATTTGTTAA 12 Piepenbrock C, (EPIG-) EPIGENOMICS AG. WPI; 2001-657177/75 Best Local Similarity WO200177384-A2. Homo sapiens 22-FEB-2002 18-OCT-2001 Query Match ABI07998; olek A, Matches 8X33333333X8 ò

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 269017 for detecting SNP TSC0001555.
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                                                                                                                                                                                                                                                  Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.0%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 3.1e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 351735; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosite methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABC0010-ABB9989, ABC0010-ABB9989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPD at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                           Oligonucleotide primer SEQ ID NO 339929 for detecting SNP TSC0041267.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 339929; 29pp + Sequence Listing; German.
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ABI51762;

RESULT 462

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABF9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                     Claim 1; SEQ ID NO 269017; 29pp + Sequence Listing; German.
                                                                           methylation status.
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Sequence 12 BP; 6 A; 1 C; 0 G; 5 T; 0 U; 0 Other;

Gaps ; 0 8.0%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 3.1e+02; vative 0; Mismatches 1; Indels 11; Conservative Local Similarity Query Match Matches

AB126667;

BP.

ABI26667 standard; DNA; 12 (first entry) 22-FEB-2002

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 326640 for detecting SNP TSC0033187.

Homo sapiens

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin ပဲ Piepenbrock olek A,

WPI; 2001-657177/75

designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 326640; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 ABC000

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represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 329173 for detecting SNP TSC0034804. (first entry) 22-FEB-2002

ABI29200 standard; DNA; 12 BP.

AB129200/

Homo sapiens.

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

ÅG. (EPIG-) EPIGENOMICS Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 329173; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at tp.wipo.int/pub/published_pct_sequences

Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

Gaps ö 8.0%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 3.1e+02; ive 0; Mismatches 1; Indels 91.7%; Best Local Similarity 91.7 Matches 11; Conservative Query Match

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                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide primer SEQ ID NO 336856 for detecting SNP TSC0039556.
                                                                                                                        Oligonucleotide primer SEQ ID NO 286325 for detecting SNP TSC0012671.
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                                                       ABH86332 standard; DNA; 12
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12 ATGGGTTGATAA
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 91.7%; Pred. No. 3.18+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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                Piepenbrock C,
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     (EPIG-) EPIGENOMICS AG
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                                               methylation status.
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                olek A,
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Claim 1; SEQ ID NO 370403; 29pp + Sequence Listing; German.

methylation status.

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acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                             Sequence 12 BP; 5 A; 0 C; 2 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABR00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 288604; 29pp + Sequence Listing; German.
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Oligonucleotide primer SEQ ID NO 332453 for detecting SNP TSC0036930.

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ABI32480 standard; DNA; 12

22-FEB-2002

ABI32480;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABR00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
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Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                    8.0%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 3.1e+02; ive 0; Mismatches 1; Indels
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Sequence 12 BP; 4 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
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                                                         Local Similarity
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, axidovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but was obtained in clear part of the printed specification, but
                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABI13971 standard; DNA; 12
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06-APR-2001; 2001WO-IB000713
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                                                                                                                                                                                                                                                            Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG
                               (EPIG-) EPIGENOMICS AG
                                       Piepenbrock
                                             WPI; 2001-657177/75
                                                                                                                                   Local Similarity
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,
                                                                                                                                                                         invention describes novel oligonucleotide primers or peptide nucleic
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designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
                                   Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                     Claim 1; SEQ ID NO 339866; 29pp + Sequence Listing; German.
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WPI; 2001-657177/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 -ABC9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00100-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Query Match 8.0%; Score 10.4; DB 1; Length 12; Best Local Similarity 91.7%; Pred. No. 3.1e+02; Matches 11; Conservative 0; Mismatches 1; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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               Oligonucleotide primer SEQ ID NO 328388 for detecting SNP TSC0034264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.0%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 3.1e+02; ive 0; Mismatches 1; Indels
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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06-APR-2001; 2001WO-IB000713.
                               07-APR-2000; 2000DE-01019173
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                                                               (EPIG-) EPIGENOMICS
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABC0010-ABE9989, ABC0010-ABE9989, ABC0010-ABE9989, ABC0010-ABE9989, ABC0010-ABE9989, and ABI0010-ABE99989 and ABI0010-ABE9073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
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                              Claim 1; SEQ ID NO 335461; 29pp + Sequence Listing; German.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 343856 for detecting SNP TSC0005775.

18-OCT-2001

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

× Berlin Olek A, Piepenbrock C,

WPI; 2001-657177/75.

set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 343856; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABF99989, ABH00010-ABF99989, ABF00010-ABF99989, ABH00010-ABF99989, ABF900010-ABF99989, ABF900010-ABF99989, ABF900010-ABF99989, ABF900010-ABF99989, ABF900010-ABF99989, ABF900010-ABF99989,

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC00010-ABC99889, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine
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                                               Seguence 12 BP; 6 A; 1 C; 0 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99899, ABH00010-ABF99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                Berlin K;
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Matches 11; Conservative
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ABI61668
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                                                                                                                                                                                                                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but firm wipo.int/pub/published_pct_sequences
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                                                                                                          of oligonucleotides, useful for diagnosis and cell typing, is igned to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                        Claim 1; SEQ ID NO 354801; 29pp + Sequence Listing; German.
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AGGTAATATTGT 1
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                          Piepenbrock C,
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Best Local Similarity
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                                                                                                                                                               methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but they wish olicybublished_pot_sequences
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and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABR9989. ABF00010-ABH99989 and ABI00010-ABR9989. ABR00010-ABR9989 and control of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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Best Local Similarity 91.,",
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC00010-ABC09989, ABC0010-ABE9989, ABM00010-ABH99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form par to f the printed specification, but the wipo.int/pub/published_pct_sequences
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Score 10.4; DB 1; Length 12;
Pred. No. 3.1e+02;
0; Mismatches 1; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABE9989, ABH00010-ABE99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                               Oligonucleotide primer SEQ ID NO 379867 for detecting SNP TSC0009746
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         methylation status.
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 ABI 79894;
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ABI79894/c ID ABI79894 standard; DNA; 12 BP. XX

RESULT 489

1460 ATCAAGCAAATA 1471

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide primer SEQ ID NO 306649 for detecting SNP TSC0022106.
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Best Local Similarity 91.7
Matches 11, Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                          Claim 1; SEQ ID NO 306649; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                          Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                  06-APR-2001; 2001WO-IB000713
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                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 312521 for detecting SNP TSC0025110.
                                   Gaps
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8.0%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 3.1e+02; ive 0; Mismatches 1; Indel8
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                                                                    1404 AAATTGTTAATG 1415
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                                     11; Conservative
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                   Best Local Similarity
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     Query Match
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                                     Matches
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Berlin K;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide primer SEQ ID NO 338525 for detecting SNP TSC0040532.
                                                                                                                                                                                           Gaps
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                                                                                                                                                8.0%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 3.16+02; tive 0; Mismatches 1; Indels
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                                                                                                                   Sequence 12 BP; 2 A; 0 C; 2 G; 8 T; 0 U; 0 Other;
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Best Local Similarity 91...
Fire 11; Conservative
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cortral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99998 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 3.1e+02;
0; Mismatches 1; Indels
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                                                                                    BP.
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                                                                                      ABI14031 standard; DNA; 12
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Best Local Similarity 91.79
Matches 11; Conservative
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1 GGAGGATGGGTT 12
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Query Match Best Local Similarity

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8.0%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 3.1e+02;

0; Mismatches

37-APR-2000; 2000DE-01019173.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; .Mismatches 1; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99899, ABH00010-ABF99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide primer SEQ ID NO 376709 for detecting SNP TSC0061943.
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                                                                                                                                                                                              claim 1; SEQ ID NO 362270; 29pp + Sequence Listing; German.
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Gaps

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99889, ABH00010-ABH99889 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonuclectide primer SEQ ID NO 273012 for detecting SNP TSC0003013.
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                                                                                                                                                                                                                                    ch 8.0%; Score 10.4; DB 1; Length 12; I Similarity 91.7%; Pred. No. 3.1e+02; 11; Conservative 0; Mismatches 1; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cointral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                   Sequence 12 BP; 7 A; 1 C; 0 G; 4 T; 0 U; 0 Other;
                                                              Query Match 8.0%; Score 10.4; DB 1; Best Local Similarity 91.7%; Pred. No. 3.1e+02; Matches 11; Conservative 0; Mismatches 1;
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              This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                          Oligonuclectide primer SEQ ID NO 313947 for detecting SNP TSC0026044.
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8.0%; Score 10.4; DB 1; Length 12;

Best Local Similarity 91.7%; Pred. No. 3.1e+02;

Matches 11; Conservative 0; Mismatches 1; Indels
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BP.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE9989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine

Berlin K;

Piepenbrock C,

olek A,

WPI; 2001-657177/75.

methylation status.

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

WO200177384-A2

18-OCT-2001

Tomo sapiens

Claim 1; SEQ ID NO 352586; 29pp + Sequence Listing; German.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide primer SEQ ID NO 352586 for detecting SNP TSC0007996.

BP.

ABI52613 standard; DNA; 12

RESULT 501

ABI52613

22-FEB-2002 (first entry)

1352 AAGAAAAATATT 1363

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12 AACAAAAATATT 1

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ID AB1733
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                                                                                                                                                                 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fire wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                    Claim 1; SEQ ID NO 358739; 29pp + Sequence Listing; German.
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                    WPI; 2001-657177/75
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH0010-ABF9989, ABH0010-ABF9989, ABH0010-ABF9989, ABH0010-ABF9989, and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide primer SEQ ID NO 364757 for detecting SNP TSC0054698.
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22-FEB-2002 (first entry)
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                                                                                                                                                                                                                      central nervous system; gastrointestinal; respiratory; immune; metabolic
                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88;
                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 365010 for detecting SNP TSC0054867.
  Gaps
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Best Local Similarity 91.7%;
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ABI18232 standard; DNA; 12

RESULT 506 ABI18232/c ID ABI1823 XX AC ABI1823

ABI18232;

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                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide primer SEQ ID NO 318205 for detecting SNP TSC0028516.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                          ligonucleotides, useful for diagnosis and cell typing, it o detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 318749; 29pp + Sequence Listing; German.
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                 06-APR-2001; 2001WO-IB000713
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                                                                                                (EPIG-) EPIGENOMICS AG
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ö Gaps ö 8.0%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 3.1e+02; 1; Indels 0; Mismatches 11; Conservative Query Match Best Local Similarity à

1405 AATTGTTAATGA 1416 1 AATTGTTTATGA 12 g

ABH69518 standard; DNA; 12 BP. ABH69518; **ABH6951** THE SECOND SECON

(first entry) 22-FEB-2002

Oligonucleotide primer SEQ ID NO 269495 for detecting SNP TSC0001782.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C,

Berlin K;

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                         Claim 1; SEQ ID NO 269495; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1;
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methylation status.
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ABH75620 standard; DNA; 12

RESULT 511

ABH75620,

ABH75620;

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                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide primer SEQ ID NO 273627 for detecting SNP TSC0003251.
                                                                                                                                             Gaps
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                                                                                                          Length 12;
                                                                                                                                         1; Indels
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                                                                     Sequence 12 BP; 8 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
                                                                                                        Score 10.4; DB 1;
Pred. No. 3.1e+02;
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                                                                                                      Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                                                                                                                           1348 GGGGAAGAAAA 1359
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ABH73642/c
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prerreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and merabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 tepseent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                 Oligonucleotide primer SEQ ID NO 275611 for detecting SNP TSC0003943.
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Gaps

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Query Match
8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels

1401 GTAAAATTGTTA 1412

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12 GTAAAATTGGTA 1

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This invention describes novel oligonuclectide primers or peptide nucleic acid (RNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0910 ABC091099, ABF00010-ABH99999 and AH100010-ABH32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fitp.wipo.int/pub/published_pct_sequences
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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    8.0%; Score 10.4; DB 1; Length 12;
1 Similarity 91.7%; Pred. No. 3.1e+02;
11; Conservative 0; Mismatches 1; Indels
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                                                  Homo sapiens,
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acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cycosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                              or peptide nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                       beton oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                          Claim 1; SEQ ID NO 303029; 29pp + Sequence Listing; German
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                                                                                                                                                                                                             invention describes novel oligonucleotide primers
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
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                                  Berlin K;
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Matches 11; Conservative
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                                Piepenbrock C,
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(EPIG-) EPIGENOMICS AG.
                                                                   WPI; 2001-657177/75
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Length 12;

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABF99989, ABF0010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC99899, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                               Score 10.4; DB 1; Length 12;
Pred. No. 3.1e+02;
0; Mismatches 1; Indels
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1 Similarity 91.7%;
11; Conservative
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Best Local Similarity
Matches 11; Conserv
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Sequence 12 BP; 6 A; 2 C; 0 G; 4 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                               Oligonucleotide primer SEQ ID NO 289070 for detecting SNP TSC0013790.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Set of oligonucleotides, useful for diagnosis and cell designed to detect single-nucleotide polymorphisms and methylation status.
 Score 10.4; DB 1;
Pred. No. 3.1e+02;
0; Mismatches 1;
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91.7%; Pred. No. 3.1e+02;
ative 0; Mismatches 1;
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Query Match

Best Local Similarity 91.7%;
Matches 11; Conservative (
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WO200177384-A2.

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                        Oligonucleotide primer SEQ ID NO 347791 for detecting SNP TSC0045257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 347791; 29pp + Sequence Listing; German.
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WO200177384-A2
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                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide primer SEQ ID NO 368493 for detecting SNP TSC0057051.
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                                                                                                                             8.0%; Score 10.4; DB 1; Length 12; 11.7%; Pred. No. 3.1e+02; ve 0; Mismatches 1; Indels
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                                                                                                                                                                                          1397 GGAGGTAAATT 1408
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                                                                                                                                                             11; Conservative
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                                                                                                                                             Local Similarity
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Query Match

Matches

à

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

22-FEB-2002

ABIGES20/C ABIGES20/C ID ABIGE XX ABIGE XX XX SNP, XX SNP, XW SNP, XW Cently XW Cently XX Cently XX Cently XX XX ABIGE XX XX ABIGE XX SNP, XM Cently XX XX Cently

ABI68520,

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a renge of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE9989, ABF00010-ABF9989, ABH00010-ABF9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                               Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                06-APR-2001; 2001WO-IB000713.
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Best Local Similarity 91.7
Marches 11; Conservative
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                             18-OCT-2001
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
                                                                                         methylation status.
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Claim 1; SEQ ID NO 363916; 29pp + Sequence Listing; German.

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in Chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 in the interest the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences

Sequence 12 BP; 0 A; 6 C; 0 G; 6 T; 0 U; 0 Other,

Gaps .; 0 Query Match 8.0%; Score 10.4; DB 1; Length 12; Best Local Similarity 91.7%; Pred. No. 3.18+02; Matches 11; Conservative 0; Mismatches 1; Indels 1347 AGGGGAAGAAA 1358 Н 12 AGGGGGAGAAA à

ABH96522 standard; DNA; 12 RESULT 520 ABH96522

BP.

22-FEB-2002 (first entry)

Oligonucleotide primer SEQ ID NO 296515 for detecting SNP TSC0017118.

SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

sapiens, Ношо WO200177384-A2.

18-OCT-2001.

07-APR-2000; 2000DE-01019173

06-APR-2001; 2001WO-IB000713.

(EPIG-) EPIGENOMICS AG

Olek A, Piepenbrock C,

WPI; 2001-657177/75

Berlin K;

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 296515; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for dangonesis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The

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ftp.wipo.int/pub/published_pct_sequences
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 273275 for detecting SNP TSC0003123.

(first entry)

22-FEB-2002

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ABH73290;

WO200177384-A2. Homo sapiens

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Piepenbrock C, Olek A,

Berlin K;

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. WPI; 2001-657177/75.

Claim 1; SEQ ID NO 273275; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastronitestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 abscribes and ABIO0010-ABE9999, ABF00010-ABE9999, ABF00010-ABE99999, ABF00010-ABE9999, ABF00010-ABE99999, ABF000010-ABE99999, ABF000010-ABE99999, AB was obtained in electronic format from Wiftp.wipo.int/pub/published_pct_sequences

Sequence 12 BP; 6 A; 0 C; 0 G; 6 T; 0 U; 0 Other;

Gaps ö Query Match 8.0%; Score 10.4; DB 1; Length 12; Best Local Similarity 91.7%; Pred. No. 3.1e+02; Matches 11; Conservative 0; Mismatches 1; Indels

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide primer SEQ ID NO 290754 for detecting SNP TSC0014500.

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                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                 Oligonucleotide primer SEQ ID NO 328759 for detecting SNP TSC0034536.
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1402 TAAAATTGTTAA 1413
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 ABC09389, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at

Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Piepenbrock C,

olek A,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

WO200177384-A2

18-OCT-2001

Homo sapiens

Claim 1; SEQ ID NO 290754; 29pp + Sequence Listing; German.

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          8.0%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 3.1e+02; tive 0; Mismatches 1; Indels
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                                                             1355 AAAAATATTCCA 1366
                                                                                                                                                    ABI61920 standard; DNA; 12
Query Match
Best Local Similarity 91.75
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ABH90761 standard; DNA; 12

RESULT 523

(first entry)

22-FEB-2002

ABH90761;

ABH90761 1D ABH9 XX AC ABH9 XX DT 22-F XX

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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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ftp.wipo.int/pub/published_pct_sequences
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       07-APR-2000; 2000DE-01019173
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                                 Olek A, Piepenbrock C,
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                  (EPIG-) EPIGENOMICS AG
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                                              WPI; 2001-657177/75.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABI82073 faresees the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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Claim 1; SEQ ID NO 293279; 29pp + Sequence Listing; German.
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91.7%; Pred. No. 3.1e+02;
iive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleatide nolumnambiana (PNA)
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                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                   Oligonucleotide primer SEQ ID NO 298907 for detecting SNP TSC0018340.
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                                               Query Match 8.0%; Score 10.4; DB 1; Length 12; Best Local Similarity 91.7%; Pred. No. 3.1e+02; Matches 11; Conservative 0; Mismatches 1; Indels
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11.7%; Pred. No. 3.1e+02;
ve 0; Mismatches 1; Indels
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                       Sequence 12 BP; 2 A; 3 C; 0 G; 7 T; 0 U; 0 Other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                               peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABI33944 standard; DNA; 12
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ABI10384/c
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91.78;

Best Local Similarity 91.7 Matches 11; Conservative

1353 AGAAAAATATTC 1364

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12 AAAAAAATATTC 1

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This invention describes novel oligomuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989, and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                             Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                Claim 1; SEQ ID NO 286087; 29pp + Sequence Listing; German.
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Berlin K;
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Piepenbrock C,
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Best Local Similarity
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Olek A,
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                                                                                                                                                                                                                                                                                                                                    oet or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Best Local Similarity 91...
These 11; Conservative
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                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG.
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           Homo sapiens.
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Sequence 12 BP; 4 A; 0 C; 2 G; 6 T; 0 U; 0 Other;
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8.0%; Score 10.4; DB 1; Length 12;

Query Match

oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at ô acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF0010-ABC99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 360773 for detecting SNP TSC0052285. Gaps Set of oligonucleotides, useful for diagnosis and cell typing, designed to detect single-nucleotide polymorphisms and cytosine ·: 0 8.0%; Score 10.4; DB 1; Length 12; 11.7%; Pred. No. 3.1e+02; ve 0; Mismatches 1; Indels Claim 1; SEQ ID NO 360773; 29pp + Sequence Listing; German. 1; Indels Sequence 12 BP; 7 A; 0 C; 2 G; 3 T; 0 U; 0 Other; ftp.wipo.int/pub/published_pct_sequences Berlin K; BP. 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 91.78; ABI60800 standard; DNA; 12 1352 AAGAAAATATT 1363 (first entry) Query Match
Best Local Similarity 91.7
Matches 11; Conservative AAGGAAATATT 12 Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75 methylation status. WO200177384-A2. Homo sapiens 22-FEB-2002 18-OCT-2001. ABI60800; RESULT 532 ABI60800/KXX ABI60800/KXX ABI60800/KXX ABI60800 DE XXX CONTRANCE C 셤 ò

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                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                           Oligonucleotide primer SEQ ID NO 298340 for detecting SNP TSC0018036.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and methololic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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91.7%; Pred. No. 3.1e+02;
ative 0; Mismatches 1;
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06-APR-2001; 2001WO-IB000713.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                  Claim 1; SEQ ID NO 306244; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell designed to detect single-nucleotide polymorphisms and
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 3.1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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                                                                                            Sequence 12 BP; 7 A; 0 C; 0 G; 5 T; 0 U; 0 Other;
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Best Local Similarity
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RESULT 539

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABE99889 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                       Oligonucleotide primer SEQ ID NO 349432 for detecting SNP TSC0046139.
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               ABI49459 standard; DNA; 12
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Set of oligonucleotides, useful for diagnosis and cell typing, : designed to detect single-nucleotide polymorphisms and cytosine

methylation status.

Claim 1; SEQ ID NO 328791; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and evicsine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABP00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABF182073 represent the oligomers described in the invention. NTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Best Local Similarity 91.7%;
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                                                                                                                                                                                                                                                                                                                                       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-OBE9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide primer SEQ ID NO 328791 for detecting SNP TSC0034566.
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ВР.

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Page 242

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                Oligonucleotide primer SEQ ID NO 306904 for detecting SNP TSC0022234.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 306904; 29pp + Sequence Listing; German.
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ABI06931 standard; DNA; 12
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                       Piepenbrock C,
                                                                                                                                         (EPIG-) EPIGENOMICS AG
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ABH85134/c
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,
                                                                                                                                                                                                                                                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytoshie methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABC9989, ABF000010-ABC9989
central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABF00010-ABF99899, ABF00010-ABF9989, ABF000010-ABF9989, ABF000010-ABF9989, ABF000010-ABF9989, ABF000010-ABF9989, ABF000010-ABF9989, ABF000000-ABF9989, ABF99899, ABF99899, ABF9989, ABF99899, ABF998999, ABF99899, ABF99899, ABF99899, ABF99899, ABF99899, ABF99899, ABF99999, ABF99899, ABF99899, ABF99999, ABF99999, ABF99999, ABF99
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABC0010-ABE9989, ABH0010-ABE99989, ABH0010-ABE99989, ABH0010-ABE99989, and ABI00010-ABE9073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                        Oligonucleotide primer SEQ ID NO 292736 for detecting SNP TSC0015327.
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designed to detect single-nucleotide polymorphisms and cytosine
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31.7%; Pred. No. 3.1e+02;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                 Oligonucleotide primer SEQ ID NO 278001 for detecting SNP TSC0005468.
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ABI05936 standard; DNA; 12 22-FEB-2002 ABI05936; RESULT 552

BP.

(first entry)

Oligonucleotide primer SEQ ID NO 305909 for detecting SNP TSC0021696.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and merabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-AB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                    Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-657177/75.
                                                                    (EPIG-) EPIGENOMICS
                                                                                                                                      WPI; 2001-657177/75.
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Best Local Similarity
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                                                                                                    olek A,
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Gaps

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Claim 1; SEQ ID NO 338974; 29pp + Sequence Listing; German.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at Gaps . 0 Score 10.4; DB 1; Length 12; Pred. No. 3.1e+02; 1; Indels Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other; 0; Mismatches 8.0%; 1399 AGGTAAAATTGT 1410 Local Similarity 91.7 1 AGGTATAATTGT 12 Query Match Matches 셤

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Hepatocyte nuclear factor 1 alpha DNA binding site consensus. AAV52629 standard; DNA; 13 BP. (first entry) 21-DEC-1998 AAV52629; RESULT 554

Hepatocyte nuclear factor 1 alpha; HNF-1 alpha; MODY3; human; transcription factor; maturity onset diabetes of the young; diabetes; NIDDM; diagnosis; therapy; ss. Homo sapiens WO9811254-A1

96US-0025719P. 96US-0028056P. 96US-0029679P. 97WO-US016037. 10-SEP-1996; 02-OCT-1996; 30-OCT-1996; 10-SEP-1997; 19-MAR-1998

(ARCH-) ARCH DEV CORP.

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Menzel

Furuta H,

Kaisaki PJ,

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Oda

Yamagata K,

Horikawa Y;

Bell GI,

WPI; 1998-271667/24.

Isolated nucleic acid encoding hepatocyte nuclear factor 1-alpha and beta - useful for detecting susceptibility for non-insulin dependent diabetes, especially maturity-onset diabetes of the young.

Disclosure; Page 18; 363pp; English

This is a consensus sequence for a 13 bp palindromic DNA sequence that is deund in hepatocyte nuclear factor 1-alpha (HNF-1 alpha) binding protein gene promoters and which binds to the DNA binding domain, i.e. a POU-like homeodomain, of HNP-1 alpha (see AAW71559). This consensus sequence can be used in methods of identifying modulators of HNP-1 alpha function. The invention concerns the identification of genes responsible for noninsulin dependent diabetes mellitus (NIDDM) for use in diagnostics and

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therapeutics. It demonstrates that the MODY3 locus is the HNF-1 alpha gene, the MODY4 locus is the HNF-1 beta gene (see AAV52730) and the MODY1 locus is the HNF-4 alpha gene (see AAV52867). Analysis of mutations in these HNF genes can be diagnostic for diabetes. The invention also contemplates methods of screening for modulators of HNF function, the modulators being useful for treating diabetes by modulating HNF function
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                                                                                                                                                                               Length 13;
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                                                                                                                                              Seguence 13 BP; 4 A; 2 C; 1 G; 5 T; 0 U; 1 Other;
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Pred. No. 3.5e+02;
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v 84.6%; Pred. No. >...
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                                                                                                                                                                                                                                                                                      1 GTTATNATTACC 13
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ABC42352/
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status. Berlin K; 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 Piepenbrock C, (EPIG-) EPIGENOMICS AG. WPI; 2001-657177/75. WO200177384-A2 Homo sapiens. 18-OCT-2001. olek A,

Oligonucleotide SEQ ID NO 42369 for detecting SNP TSC0012640.

Claim 1; SEQ ID NO 42369; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABF00010-ABB9989, ABF00010-ABB9989 and ABI00010-ABB82073 data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 13 BP; 5 A; 0 C; 3 G; 5 T; 0 U; 0 Other;

Gaps ö 8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; iive 0; Mismatches 1; Indels 11; Conservative Query Match Best Local Similarity Matches

1385

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonuclectide SEQ ID NO 75287 for detecting SNP TSC0019324

schultz911-3.rng

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                            Oligonucleotide SEQ ID NO 48921 for detecting SNP TSC0013887.
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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CTTCTGATCAAA 1396
                                                                                                                                ABC48904 standard; DNA; 13
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                                     CITCITAICAAA 1
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                                                                                            RESULT 556
                                                                                                                ABC4890
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                  Oligonucleotide SEQ ID NO 52751 for detecting SNP TSC0014606.
                                                                                                            BP.
                                                                                                            ABC52734 standard; DNA; 13
                        1394 AAAGGAGGTAAA 1405
                                                                                                                                                           (first entry)
                                               AAAGGAGATAAA 12
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11;
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Gaps

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ABC75270 standard; DNA; 13

RESULT 557 ABC75270

21-FEB-2002 (first entry)

ABC75270;

BXXXE

1403 AAAATTGTTAAT 1414

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8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; ive 0; Mismatches 1; Indels

Conservative

Matches

Similarity

Query Match Local

Sequence 13 BP; 8 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

ftp.wipo.int/pub/published_pct_sequences

acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmet from WIPO at

This invention describes novel oligonucleotide primers or peptide nucleic

Claim 1; SEQ ID NO 75287; 29pp + Sequence Listing; German.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine

Berlin K;

Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG

WPI; 2001-657177/75.

methylation status.

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

WO200177384-A2

18-OCT-2001

Homo sapiens.

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                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 52751; 29pp + Sequence Listing; German.
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06-APR-2001; 2001WO-IB000713.
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                                   07-APR-2000; 2000DE-01019173
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                                                                   (EPIG-) EPIGENOMICS
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABR00010-ABC99989, ABR00010-ABC99989, ABR00010-ABC99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.whpo.int/pub/published_pct_sequences
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                                                                                                          This invention describes novel oligonuclectide primers or peptide nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.0%; Score 10.4; DB 1; Length 13; Best Local Similarity 91.7%; Pred. No. 3.5e+02; Matches 11; Conservative 0; Mismatches 1; Indels
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Claim 1; SEQ ID NO 79876; 29pp + Sequence Listing; German.
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(first entry)

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                     Oligonucleotide SEQ ID NO 11542 for detecting SNP TSC0002802.
                                                                            ABC11543 standard; DNA; 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                Length 13;
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                                                                            Sequence 13 BP; 2 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
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was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WFPO at
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designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                         Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine
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designed to detect single-nucleotide polymorphisms and cytosine
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PRA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two obtained in electronic format from WIPO at
and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 ABC09989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, and ABF00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                     Oligonucleotide SEQ ID NO 172945 for detecting SNP TSC0043092.
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ABF72948
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RESULT 569 ABF50064

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPD at fit, wipo.int/pub/published_pct_sequence
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 expressent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; pepride nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                         Claim 1; SEQ ID NO 191284; 29pp + Sequence Listing; German.
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whiches 11; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, oligomers are also used for detecting cell type differentiation. ABC0010 ingomers are also used for detecting cell type differentiation. ABC0010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ffp.wipo.int/pub/published_pct_sequence
-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         designed to detect methylation status.
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Best Local Similarity
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide SEQ ID NO 259970 for detecting SNP TSC0063118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 259969; 29pp + Sequence Listing; German.
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ABH59993 standard; DNA; 13
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                                                                                    Homo sapiens
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                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                          ABH52658 standard; DNA; 13
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                                                                                                                                  onucleotides, useful for diagnosis and cell typing, is detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                  Claim 1; SEQ ID NO 259970; 29pp + Sequence Listing; German.
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                                                                     Berlin K;
 07-APR-2000; 2000DE-01019173
                                                                                                                                  oligonucleotides,
                                                                 Olek A, Piepenbrock C,
                                (EPIG-) EPIGENOMICS AG.
                                                                                                  WPI; 2001-657177/75
                                                                                                                                                                    methylation status.
                                                                                                                                                     designed to
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Gaps ; Query Match 8.0%; Score 10.4; DB 1; Length 13; Best Local Similarity 91.7%; Pred. No. 3.5e+02; Matches 11; Conservative 0; Mismatches 1; Indels 1439 ATATACATGGAA 1450 Best Loca Matches ð

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ABC42350 standard; DNA; 13 21-FEB-2002 ABC42350; ABC42350,

BP.

(first entry)

Oligonucleotide SEQ ID NO 42367 for detecting SNP TSC0012640.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Berlin K; ú Piepenbrock olek A,

WPI; 2001-657177/75.

oet or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 42367; 29pp + Sequence Listing; German.

ö This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences Gaps ö Oligonucleotide SEQ ID NO 95980 for detecting SNP TSC0023864. Length 13; 1; Indels Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other; 8.0%; Score 10.4; DB 1; 91.7%; Pred. No. 3.5e+02; live 0; Mismatches 1; BP. ABC95963 standard; DNA; 13 1385 CTTCTGATCAAA 1396 (first entry) 11; Conservative CTTCTCATCAAA 1 Best Local Similarity 21-FEB-2002 12 ABC95963; Query Match Matches ABC95963,

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 95980; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytoslie methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989 and metabolic disorders. The represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO 79875 for detecting SNP TSC0020278.

(first entry)

21-FEB-2002

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Gaps

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ABC79858;

BP.

ABC79858 standard; DNA; 13

ABC79858/c

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PRA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a renge of diseases including immune system, gastrointestinal, respiratory, central nervous system, axidovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989 and ABL00010-ABIB3073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                   Query Match 8.0%; Score 10.4; DB 1; Length 13; Best Local Similarity 91.7%; Pred. No. 3.5e+02; Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 13;

Best Local Similarity 91.7%; Pred. No. 3.5e+02;

Matches 11; Conservative 0; Mismatches 1; Indels
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Sequence 13 BP; 8 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine

Berlin K;

Piepenbrock C,

Olek A,

WPI; 2001-657177/75.

methylation status.

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

WO200177384-A2. Homo sapiens.

18-OCT-2001.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. Abcommers are also used for detecting cell type differentiation. Abcommers are also used for detecting cell type differentiation. Abcommers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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91.7%; Pred. No. 3.5e+02;
iive 0; Mismatches 1;
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Gaps

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Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 +ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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                                                          onucleotides, useful for diagnosis and cell typing, i detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                     Claim 1; SEQ ID NO 110758; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02;
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Matches 11; Conservative
                                                              Set of oligonucleotides,
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                                                                                                    methylation status.
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1 AAGAAGAATATT 12
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Best Local Similarity
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Homo sapiens.
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 91.7%;
Matches 11; Conservative
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8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02;

Query Match Best Local Similarity

Sequence 13 BP; 6 A; 0 C; 7 G; 0 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABH17407 standard; DNA; 13
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                            Oligonucleotide SEQ ID NO 144935 for detecting SNP TSC0036443.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 144935; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell designed to detect single-nucleotide polymorphisms and
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les 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               methylation status.
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Query Match

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABP0010-ABH9989, and MB10010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fitp.wipo.int/published_pct_sequences
                      Claim 1; SEQ ID NO 146344; 29pp + Sequence Listing; German.
                                                                                                                                                                                                 Sequence 13 BP; 4 A; 3 C; 0 G; 6 T; 0 U; 0 Other;
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Score 10.4; DB 1; Length 13; Pred. No. 3.5e+02; 0; Mismatches 1; Indels
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                      Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                      Seguence 13 BP; 6 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
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Pred. No. 3.5e+02;
0; Mismatches 1;
data for this patent did not form part of the pass obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Best Local 8
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                                                                                                                                                                                                                                                                 RESULT 589
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                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                            Oligonucleotide SEQ ID NO 182832 for detecting SNP TSC0045175.
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                                            ABF82835 standard; DNA; 13 BP.
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                                                                                      (first entry)
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Best Local Similarity
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, axidovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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peptide nucleic acid; cytosine methylation; cardiovascular; primer; se; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity
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This invention describes novel oligonucleotide primers or peptide nucleic
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Best Local Similarity 91.75
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99898, and ABI00010-ABE99898 and ABI00010-ABE99898, and ABI00010-ABE99898 and ABI00010-ABE99898 and ABIO0010-ABE9989 and ABIO0010-ABE9989 as each and ABIO0010-ABE9989 as an an account and account account and account account and account acco
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Pred. No. 3.5e+02;
0; Mismatches 1; Indels
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Matches 11; Conservative C
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                                         (EPIG-) EPIGENOMICS AG.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically prereated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory. Central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE9989, ABF00010-ABE998, ABF00010-ABE998, ABF00010-ABE998, ABF00010-ABE998, ABF00010-ABE998, A
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                               Oligonucleotide SEQ ID NO 191756 for detecting SNP TSC0047176.
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            ABF91759;
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            Length 13;
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            Score 10.4; DB 1;
Pred. No. 3.5e+02;
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Best Local Similarity 91.79
Matches 11; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Pred. No. 3.5e+02;
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Matches 11; Conservative
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ABF91759 standard; DNA; 13 BP.

RESULT 596 ABF91759/c ID ABF917

1407 TIGITAATGATG 1418

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1347 AGGGGAAGAAA 1358
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The
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                                                                                                                                                                                                                                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-OBE99989, ABH00010-ABE99989 and ABI00010-ABE99989 and ABI00010-ABE99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99889, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at flowlypublished_pct_sequences
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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ftp.wipo.int/pub/published_pct_sequences
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8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; tive 0; Mismatches 1; Indels

Query Match 8.0 Best Local Similarity 91.7 Matches 11; Conservative

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but firm wipo.int/pub/published_pct_sequences
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                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide SEQ ID NO 81586 for detecting SNP TSC0020645.
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Pred. No. 3.5e+02;
0; Mismatches 1; Indels
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Best Local Similarity 91.7%;
Matches 11; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                              Claim 1; SEQ ID NO 56444; 29pp + Sequence Listing; German.
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                                              (EPIG-) EPIGENOMICS AG
                                                                                                           WPI; 2001-657177/75
                                                                                                                                                                             methylation status.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABF9989 and ABI00010-ABI82073 tapeseent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                               This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Claim 1; SEQ ID NO 36071; 29pp + Sequence Listing; German.
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Best Local Similarity
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABM00010-ABH99989 and ABH00010-ABH9989 and ABH00010-ABH9980 and ABH00010-ABH9989 and ABH00010-ABH9998 and ABH000010-ABH9989 and ABH000010-ABH9998 and ABH00010-ABH9999 and ABH00010-AB
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                                                                                                         Length 13;
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                                                   Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                       Score 10.4; DB 1;
Pred. No. 3.5e+02;
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ftp.wipo.int/pub/published_pct_sequences
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                                                                                                         Query Match 8.0%;
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Matches 11; Conservative
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                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                ABE37830 standard; DNA; 13 BP
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, axidiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABIS2073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at

Sequence 13 BP; 3 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

ftp.wipo.int/pub/published_pct_sequences

oligonucleotides, useful for diagnosis and cell typing, is detect single-nucleotide polymorphisms and cytosine

designed to detect smethylation status.

Set of

Berlin K;

Piepenbrock C,

olek A,

WPI; 2001-657177/75

(EPIG-) EPIGENOMICS

36-APR-2001; 2001WO-IB000713.

WO200177384-A2.

18-OCT-2001

Homo sapiens.

Claim 1; SEQ ID NO 139219; 29pp + Sequence Listing; German.

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SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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    Length 13;
                                                                                                       1; Indels
Score 10.4; DB 1;
Pred. No. 3.5e+02;
0; Mismatches 1;
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         8.0%;
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                                                                                                                                                                                                          1400 GGTAAATTGTT 1411
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                                                                                                            11; Conservative
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                                                 Local Similarity
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                   Query Match
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO 139219 for detecting SNP TSC0034874.

(first entry)

21-FEB-2002

ABF39222;

ABF39222 standard; DNA; 13 BP.

RESULT 608

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AAAATATACCAC 2

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99899, ABF00010-ABF99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but twy but publypublished_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The
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                                                                  Set of oligonucleotides, useful for diagnosis and cell typing, : designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                      Claim 1; SEQ ID NO 220461; 29pp + Sequence Listing; German.
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91.78;
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Best Local Similarity 91.7
Matches 11; Conservative
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 Piepenbrock C,
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                                                                                                   methylation status.
                               WPI; 2001-657177/75
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABF97648 standard; DNA; 13 BP.
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Best Local
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a renge of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                   Oligonucleotide SEQ ID NO 153906 for detecting SNP TSC0038907
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Best Local Similarity
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Pred. No. 3.5e+02;
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Olek A,

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but twipo.int/pub/published_pct_sequences
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  designed to detect single-nucleotide polymorphisms and cytosine
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                                                                      Claim 1; SEQ ID NO 188264; 29pp + Sequence Listing; German.
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Query Match

Matches

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                            Oligonucleotide SEQ ID NO 262884 for detecting SNP TSC0063773.
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tive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                           Query Match
8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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Length 13; 1; Indels Oligonucleotide SEQ ID NO 42370 for detecting SNP TSC0012640.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                        Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Pred. No. 3.5e+02;
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                                                                                                                                                                                   Claim 1; SEQ ID NO 49464; 29pp + Sequence Listing; German.
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Sequence 13 BP; 6 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 3.5e+02;
0; Mismatches 1; Indels
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; tive 0; Mismatches 1; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Claim 1; SEQ ID NO 32992; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytoslie methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, certical nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. Abc0010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF9073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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Pred. No. 3.5e+02;
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ABF20333/
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                                                                                                    Oligonucleotide SEQ ID NO 39576 for detecting SNP TSC0012093
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ABC39559 standard; DNA; 13
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                 designed to detect methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF0010-ABF99899, ABF00010-ABF99899, ABF00010-ABF99899, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF0010-ABF99989, ABF0010-ABF99989, ABF0010-ABF99989, ABF0010-ABF99989, ABF0010-ABF99989, ABF0010-ABF9989, ABF00010-ABF9989, ABF9989, A
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Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1;
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                                                                                                  onucleotides, useful for diagnosis and cell typing, i detect single-nucleotide polymorphisms and cytosine
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8.0%; Score 10.4; DB 1; Length 13; 31.7%; Pred. No. 3.5e+02; ve 0; Mismatches 1; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,

Seguence 13 BP; 5 A; 1 C; 0 G; 7 T; 0 U; 0 Other;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, aradiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                 Oligonucleotide SEQ ID NO 197646 for detecting SNP TSC0005726.
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                                                                                                                    Homo sapiens.
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                                                                                                                                                                              This invention describes novel oligonucleotide primers or peptide nucleic acid (RNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers also used for detecting cell type differentiation. ABC0010-ABC9989, ABR00010-ABR9989, ABR00010-ABR9989, ABR00010-ABR9989 and ABL00010-ABR98001 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
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                                                                                                               Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                            Claim 1; SEQ ID NO 223368; 29pp + Sequence Listing; German.
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06-APR-2001; 2001WO-IB000713.
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                                                                    Olek A, Piepenbrock C,
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                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic
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Claim 1; SEQ ID NO 149825; 29pp + Sequence Listing; German.
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Pred. No. 3.5e+02;
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Local Similarity 91.7%; Pre
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                                                                                 Score 10.4; DB 1; Length 13;
Pred. No. 3.5e+02;
0; Mismatches 1; Indels
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                                               Seguence 13 BP; 3 A; 1 C; 5 G; 4 T; 0 U; 0 Other;
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was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABC00010-ABC99899, ABH00010-ABR99899 and ABI00010-ABR82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABF82706 standard; DNA; 13 BP.
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                             Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                    Claim 1; SEQ ID NO 188598; 29pp + Sequence Listing; German.
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Matches 11; Conservative
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RESULT 637

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(EPIG-) EPIGENOMICS AG.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 -ABC99989, ABC0010-ABF9989, ABR00010-ABF9989 and ABI00010-ABF9989 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                       Oligonucleotide SEQ ID NO 259974 for detecting SNP TSC0063118.
Score 10.4; DB 1; Length 13; Pred. No. 3.5e+02; 0; Mismatches 1; Indels
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   8.0%;
91.7%;
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                                                                    1397 GGAGGTAAATT 1408
Query Match
Best Local Similarity 91.77
Matches 11; Conservative
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                                                                                       GGAGGTAAGATT 1
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                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                      RESULT 640
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ID ABC41
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                         Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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nes 11; Conservative
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                   18-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form par of the printed specification, but fire wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                      Oligonucleotide SEQ ID NO 48808 for detecting SNP TSC0013866.
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                                        (first entry)
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ABC48791;
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RESULT 642 ABC01284

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory. Central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABR059889, ABF00010-ABR99898, ABF00010-ABR99898, ABF00010-ABR99898 and ABI00010-ABR82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                        Claim 1; SEQ ID NO 101129; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                        Gaps
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Pred. No. 3.5e+02;
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Best Local Similarity 91.7°
Matches 11; Conservative
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Best Local Similarity
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acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABCO0010

This invention describes novel oligonucleotide primers or peptide nucleic

Claim 1; SEQ ID NO 3645; 29pp + Sequence Listing; German.

methylation status.

1449 AAGATGGGTTGA 1460

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This invention describes novel oligonucleotide primers or peptide nucleic acid (RNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                              Oligonucleotide SEQ ID NO 91972 for detecting SNP TSC0023002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; iive 0; Mismatches 1; Indels
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                               ABC91955 standard; DNA; 13
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Best Local Similarity 91.7
Matches 11; Conservative
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                                                                  ABC91955;
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RESULT 646
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABR99989, ABR00010-ABR9989, ABR00010-ABR99899, ABR00010-ABR9989, ABR00010-ABR998, ABR00010-
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              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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06-APR-2001; 2001WO-IB000713.

Oligonucleotide SEQ ID NO 119550 for detecting SNP TSC0029841.

WO200177384-A2.

18-OCT-2001.

Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                        Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                        Claim 1; SEQ ID NO 120329; 29pp + Sequence Listing; German.
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                                                              Berlin K;
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07-APR-2000; 2000DE-01019173.
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                                                                                            WPI; 2001-657177/75
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine

methylation status.

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Berlin

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Claim 1; SEQ ID NO 132024; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
        This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO 193277 for detecting SNP TSC0047551.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                        Query Match

8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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                        Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
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ABF38163 standard; DNA; 13 BP.
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ABF3163/C
ARP38163/C
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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91.7%; Pred. No. 3.5e+02;
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ABP93280/c

ID ABF93280 standard; DNA; 13 BP.
AC ABP93280;
AC ABP93280;
XX ABP93280;
XX Coligonucleotide SEQ ID NO 1933;
XX SNP; single nuclectide polymon peptide nucleic acid; cytosing peptide nucleic acid; cytosing wentral nervous system; gastra.
XX SNP; single nucleotide polymon peptide nucleic acid; cytosing www.
XX Gentral nervous system; gastra.
XX WO200177384-A2.
XX WO200177384-A2.
XX GFPG-2001; 2001WO-IB000713.
XX GFPG-2001; 2001WO-IB000713.
XX GFPG-1 EPIGENOMICS AG.
XX GFPG-2 EPIGENOMICS AG.
XX GFPG-1 EPIGENOMICS AG.
XX GFPG-1 EPIGENOMICS AG.
XX GFPG-2 EPIGENOMICS AG.
XX GFPG-1 EPIGENOMICS AG.
XX Claim 1; SEQ ID NO 193277; 29, XX Graim 1; SEQ ID NO 193277; 29, XX Claim 1; SEQ ID NO 193277; 29, XX Claim 1; SEQ ID NO 193277; 29, XX Crange of diseases including in central nervous system, carding contraral nervous system, carding contraral nervous system, carding contraral nervous system, carding nervous showed for cange of diseases including in central nervous system, carding nervous system, cardin not contrarance are also used for cange of diseases including in central nervous system, cardin not contrarance are also used for cange of the system, cardin not contrarance are also used for cange of the system, cardin not contrare are also used for cange of the system, cardin not contrare are also used for cange of the system, cardin not contrare are also used for cange of the system, cardin not contrare are also used for cange of the system, cardin not contrare are also used for cange of the system, cardin not c
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Query Match 8.0%; Score 10.4; DB 1; Length 13; Best Local Similarity 91.7%; Pred. No. 3.5e+02; Matches 11; Conservative 0; Mismatches 1; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 144936; 29pp + Sequence Listing; German.
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ftp.wipo.int/pub/published_pct_sequences
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Homo sapiens.
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Berlin K;

WO200177384-A2 Homo sapiens. 21-FEB-2002 18-OCT-2001 ABF46467; olek A, ö SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps ; 0 Oligonucleotide SEQ ID NO 196025 for detecting SNP TSC0048226. 8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; ive 0; Mismatches 1; Indels ABF96028 standard; DNA; 13 BP 06-APR-2001; 2001WO-IB000713 1447 GGAAGATGGGTT 1458 (first entry) 11; Conservative GGAAGATTGGTT 2 WO200177384-A2. Homo sapiens 18-OCT-2001

Berlin K;

Olek A, Piepenbrock C,

(EPIG-) EPIGENOMICS AG

07-APR-2000; 2000DE-01019173.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cycosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Pred, No. 3.5e+02;
                                                                                                                     Claim 1; SEQ ID NO 196025; 29pp + Sequence Listing; German
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABH00010-ABE99989 and ABH00010-ABE99899 are represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at Itp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02;

Query Match Best Local Similarity

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Pred. No. 3.5e+02;
0; Mismatches 1; Indels
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91.7%;
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                                    1434 CAGACATATACA 1445
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                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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21-FEB-2002 (first entry)

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06-APR-2001; 2001WO-IB000713
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                                                                                                                                                                                                                            1397 GGAGGTAAATT 1408
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                                                                                         Piepenbrock C,
                                                                                 (EPIG-) EPIGENOMICS AG
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Matches
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                          Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.0%; Score 10.4; DB 1; Length 13; 31.7%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 241817; 29pp + Sequence Listing; German
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                   06-APR-2001; 2001WO-IB000713.
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Best Local Similarity 91.7%;
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                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                           Oligonucleotide SEQ ID NO 149884 for detecting SNP TSC0037822.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
Oligonucleotide SEQ ID NO 216850 for detecting SNP TSC0052703.
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methylation status

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE09989, ABE0010-ABE9989, ABE00010-ABE9989, ABE00010-ABE9989, ABE00010-ABE9989, and ABI00010-ABE9989, represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 8.0%; Score 10.4; DB 1; Length 13; Local Similarity 91.7%; Pred. No. 3.5e+02; les 11; Conservative 0; Mismatches 1; Indels
                                       Claim 1; SEQ ID NO 216850; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABF00010-ABF99899, ABR00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status. Oligonucleotide SEQ ID NO 258853 for detecting SNP TSC0062910. Claim 1; SEQ ID NO 258853; 29pp + Sequence Listing; German. Berlin ВР. 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 ABH58876 standard; DNA; 13 (first entry) rrarraargarg 1 Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75. WO200177384-A2 Homo sapiens. 22-FEB-2002 18-OCT-2001 12 ABH58876; Olek A,

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABR0010-ABF99989, ABR0010-ABF99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences ö ö data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps Gaps Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine ô .. 0 Oligonucleotide SEQ ID NO 263360 for detecting SNP TSC0063865. 8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; Claim 1; SEQ ID NO 263360; 29pp + Sequence Listing; German. Score 10.4; DB 1; Length 13; Pred. No. 3.5e+02; 1; Indels 1; Indels Sequence 13 BP; 8 A; 2 C; 0 G; 3 T; 0 U; 0 Other; Sequence 13 BP; 4 A; 0 C; 1 G; 8 T; 0 U; 0 Other; 0; Mismatches 0; Mismatches Berlin BP. 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173. Query Match

Best Local Similarity 91.7%;

Matches 11; Conservative 0 1460 ATCAAGCAAATA 1471 1355 AAAAATATTCCA 1366 ABH63383 standard; DNA; 13 22-FEB-2002 (first entry) 11; Conservative 1 ATCAAACAAATA 12 Piepenbrock C, 12 AAAAATATTCTA 1 (EPIG-) EPIGENOMICS AG Query Match Best Local Similarity Matches 11; Conservat WPI; 2001-657177/75. methylation status. WO200177384-A2 Homo sapiens. 18-OCT-2001. ABH63383; olek A, RESULT 662 ABH63383 8 g ឧដ្ឋឧ d ò

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WPI; 2001-657177/75.
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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peptide nucleic acid, cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Piepenbrock C,

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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
(EPIG-) EPIGENOMICS AG.
                       WPI; 2001-657177/75.
                                                 methylation status.
            olek A,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but firm wipo.int/pub/published_pct_sequences Gaps . 0 Query Match

8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels Claim 1; SEQ ID NO 77736; 29pp + Sequence Listing; German. Sequence 13 BP; 6 A; 2 C; 0 G; 5 T; 0 U; 0 Other; 1406 ATTGTTAATGAT 1417 8

12 ATTATTAATGAT 1 g

ABC03657 standard; DNA; 13 20-FEB-2002 (first entry) ABC03657; RESULT 666 CXSX TYPE PARTY SYNTHE STANFORM SONTHE STANFORM SONTH SONTHE STANFORM SONTHE STANFORM SONTHE STANFORM SONTH SONTHE STANFORM SO

BP.

Oligonucleotide SEQ ID NO 3648 for detecting SNP TSC0001395.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K; Piepenbrock C, olek A,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 3648; 29pp + Sequence Listing; German

This invention describes novel oligonucleotide primers or peptide nucleic

acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomicalectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrolintestinal, respiratory, central nervous system, cardiovascular and metabolic diseorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABC0010-ABC99989, ABC0010-ABC09989, ABC0010-AB Sequence 13 BP; 4 A; 1 C; 0 G; 8 T; 0 U; 0 Other;

8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; ive 0; Mismatches 1; Indels 1352 AAGAAAATATT 1363 11; Conservative Query Match Best Local Similarity Matches 11; Conserv

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide SEQ ID NO 58981 for detecting SNP TSC0015803. BP. ABC58964 standard; DNA; 13 (first entry) 21-FEB-2002 ABC58964; 667 ABC58964 RESULT

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06-APR-2001; 2001WO-IB000713. WO200177384-A2. Homo sapiens 18-OCT-2001.

Berlin K; Piepenbrock C, (EPIG-) EPIGENOMICS AG olek A,

07-APR-2000; 2000DE-01019173.

WPI; 2001-657177/75

18 Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 58981; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABC0010-ABE9989, ABE00010-ABE9989, and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Sequence 13 BP; 8 A; 0 C; 3 G; 1 T; 0 U; 1 Other;

schultz911-3.rng

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Berlin K;

(EPIG-) EPIGENOMICS AG.

WPI; 2001-657177/75.

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

WO200177384-A2.

18-OCT-2001

Oligonucleotide SEQ ID NO 91971 for detecting SNP TSC0023002

(first entry)

21-FEB-2002

ABC91954;

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             Score 10.4; DB 1;
pred, No. 3.5e+02;
0; Mismatches 1;
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               8.0%;
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                                        11; Conservative
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                                                                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (RNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABH00010-ABH99989 and ABL00010-AB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                              Claim 1; SEQ ID NO 91971; 29pp + Sequence Listing; German.
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ABC91954 standard; DNA; 13 BP

ABC91954/c ID ABC9199

1439 ATATACATGGAA 1450

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ATATAGATGGAA 12

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequence
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               Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                   Claim 1; SEQ ID NO 146463; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
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                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 170192; 29pp + Sequence Listing; German.
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                                                                                               06-APR-2001; 2001WO-IB000713.
                                                                                                                                             07-APR-2000; 2000DE-01019173.
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Best Local Similarity
Matches 11; Conserv
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ABF46466
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
                                                                                                                                         Gaps
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                                                                                                              Query Match 8.0%; Score 10.4; DB 1; Length 13; Best Local Similarity 91.7%; Pred. No. 3.5e+02; Matches 11; Conservative 0; Mismatches 1; Indels
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                                                                                        Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                         Oligonucleotide SEQ ID NO 198423 for detecting SNP TSC0008139.
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Best Local Similarity 91.7
Matches 11, Conservative
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ABF50065/c
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22-FEB-2002
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                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide SEQ ID NO 150062 for detecting SNP TSC0037873.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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07-APR-2000; 2000DE-01019173
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                                                                                                                                        Piepenbrock C,
                                                                    (EPIG-) EPIGENOMICS AG
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Best Local Similarity
Matches 11; Conserv
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99999, ABF00010-ABE99999, and ABI00010-ABE182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                               This invention describes novel oligomucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, and in the invention. ABC0010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                         8.0%; Score 10.4; DB 1; Length 13; 11.7%; Pred. No. 3.5e+02; ve 0; Mismatches 1; Indels
Claim 1; SEQ ID NO 228567; 29pp + Sequence Listing; German.
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Best Local Similarity 91.79
Matches 11; Conservative
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ABF53908/c
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                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                             Length 13;
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31.7%; Pred. No. 3.5e+02;
ive 0; Mismatches 1;
                               Sequence 13 BP; 3 A; 0 C; 1 G; 9 T; 0 U; 0 Other;
                                                             Score 10.4; DB 1;
Pred. No. 3.5e+02;
0; Mismatches 1;
ftp.wipo.int/pub/published_pct_sequences
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                                                                Query Match 8.0%;
Best Local Similarity 91.7%;
Matches 11; Conservative (
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                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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                                                                ABF58580 standard; DNA; 13 BP.
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RESULT 68
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ABF5880
ABF5
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Set of oligonuclectides, useful for diagnosis and cell typing, idesigned to detect single-nuclectide polymorphisms and cytosine

Berlin K;

Olek A, Piepenbrock C, WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

WO200177384-A2

18-OCT-2001

Homo sapiens.

Claim 1; SEQ ID NO 214400; 29pp + Sequence Listing; German.

methylation status.

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                                                                                                                                                                                                                                                                                                                      cacid (PNA) oligomers for detecting single nucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC099889, ABC00010-ABF99899, ABH00010-ABF99999 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic form part of the printed specification, but who, int/pub/published_pct_sequences
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO 214400 for detecting SNP TSC0052153.

(first entry)

22-FEB-2002

ABH14423;

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Gaps

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Score 10.4; DB 1; Length 13; Pred. No. 3.5e+02; 0; Mismatches 1; Indels

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The
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oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory. Central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99889, ABH00010-ABH99989 and ABI0010-ABI82073. represent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fig.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide SEQ ID NO 62607 for detecting SNP TSC0016595.
                                                                                                                                                                                                          Sequence 13 BP; 7 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                     Query Match 8.0%;
Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                                                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABR00010-ABH99999 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                             Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                 Claim 1; SEQ ID NO 260034; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
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                         Berlin
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                         Piepenbrock C,
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Best Local Similarity
                                                                WPI; 2001-657177/75
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                           Olek A,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-0-ABH99989 and ABI00010-ABF182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
Set of oligonucleotides, useful for diagnosis and cell typing, : designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 13;
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                                                                                                                        methylation status.
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Berlin K;

schultz911-3.rng

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                 Set of oligonucleotides, useful for diagnosis and cell typing, i
designed to detect single-nucleotide polymorphisms and cytosine
                                            Oligonucleotide SEQ ID NO 41014 for detecting SNP TSC0012376.
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               21-FEB-2002 (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                          Oligonucleotide SEQ ID NO 40810 for detecting SNP TSC0012339.
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               Indels
Pred. No. 3.5e+02;
0; Mismatches 1;
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91.78;
                                          1447 GGAAGATGGGTT 1458
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               11; Conservative
                                                                     1 GGAAGGTGGGTT 12
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 Best Local Similarity
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99889, ABH00010-ABH99899 and ABI00010-ABIS2073 the preparent the oligomers described in the invention. NOTE: The sequence data for this patent din obt form part of the printed specification, but was obtained in ejectronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                    8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; ive 0; Mismatches 1; Indels
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)997/c ABC40997 standard; DNA; 13 BP.

RESULT 686

ABC40997, EX X

ABC40997

1347 AGGGGAAGAAAA 1358

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AGGGGAAAAAA 1

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                                                                                                                                                                                 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABP00010-ABH99999, ABH00010-ABH99999 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; Ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                         typing, is cytosine
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                                                                                                                                                                  Claim 1; SEQ ID NO 117057; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                         designed to detect single-nucleotide polymorphisms and methylation status.
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                                                                                     Berlin K;
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Matches 11; Conservative
                        06-APR-2001; 2001WO-IB000713
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                                                                                     Piepenbrock C,
                                                                  (EPIG-) EPIGENOMICS AG.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073
                                                                                                                                                                        This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABL00010-AB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine
designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                       SEQ ID NO 126929; 29pp + Sequence Listing; German.
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Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                          Query Match

8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                    Oligonucleotide SEQ ID NO 172946 for detecting SNP TSC0043092.
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91.7%; Pred. No. 3.5e+02;
iive 0; Mismatches 1;
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Query Match 8.0%; Score 10.4; DB 1; Length 13; Best Local Similarity 91.7%; Pred. No. 3.5e+02; Matches 11; Conservative 0; Mismatches 1; Indels

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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07-APR-2000; 2000DE-01019173

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Pred. No. 3.5e+02;
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                                                                                                                                                                      Claim 1; SEQ ID NO 153537; 29pp + Sequence Listing;
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Sequence 13 BP; 7 A; 0 C; 1 G; 5 T; 0 U; 0 Other;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC00010 ABC99989, ABF00010-ABE99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                   Gaps
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 Length 13;
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                                   1; Indels
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Score 10.4; DB 1;
Pred. No. 3.5e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was obtained in electronic format from WI frp.wipo.int/pub/published_pct_sequences
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8.0%;
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                                                                                                                                                                                       ABF89805 standard; DNA; 13
                                                                   1352 AAGAAAAATATT 1363
                                                                                                                                                                                                                                                        (first entry)
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Best Local Similarity 91.77
Matches 11, Conservative
                                   11; Conservative
                                                                                                   1 AAGAATAATATT 12
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Query Match
Best Local Similarity
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ABF89805
ID ABF8981
                                   Matches
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RESULT 697 ABH57680/c

schultz911-3.rng

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                           ver or oligonucleotides, useful for diagnosis and cell typing, i
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 258854; 29pp + Sequence Listing;
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                                                                                  06-APR-2001; 2001WO-IB000713
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                                                                                                                                                                                        Piepenbrock C,
                                                                                                                                                      (EPIG-) EPIGENOMICS
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                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                  Oligozucleotide SEQ ID NO 257657 for detecting SNP TSC0062680.
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ABH57680 standard; DNA; 13
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                                                                (first entry)
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Best Local Similarity
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ABH58877
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                         Gaps
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Length 13;
                         1; Indels
Score 10.4; DB 1;
Pred. No. 3.5e+02;
0; Mismatches 1;
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 B.0%;
91.7%;
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                                               1355 AAAAATATTCCA 1366
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            Best Local Similarity 91.7
Matches 11; Conservative
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

Oligonucleotide SEQ ID NO 258854 for detecting SNP TSC0062910.

(first entry)

22-FEB-2002

ABH58877;

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Claim 1; SEQ ID NO 20185; 29pp + Sequence Listing; German.
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                                                                                                                                Conservative
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          of oligonucleotides,
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                                                                                                                                                                                                                                                                                                                                         methylation status.
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                     nethylation status.
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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fig. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 89; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                      8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; ive 0; Mismatches 1; Indels
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les 11; Conserv
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Matches
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                                                                                                                                                                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99889, ABF00010-ABF99889 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                             ligonucleotides, useful for diagnosis and cell typing, it o detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                        Claim 1; SEQ ID NO 42368; 29pp + Sequence Listing; German.
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                                                        This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Claim 1; SEQ ID NO 32553; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for dispanosis adors prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPD at ftp.wipo.int/pub/published_pct_sequences
                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                  Oligonucleotide SEQ ID NO 132023 for detecting SNP TSC0032951.
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nes 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Matches 11; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABM00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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Pred, No. 3.5e+02;
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                                                                                                                     acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                             invention describes novel oligonucleotide primers or peptide nucleic
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designed to detect single-nucleotide polymorphisms and cytosine
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                           Claim 1; SEQ ID NO 220057; 29pp + Sequence Listing; German.
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1;
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SNP; single nucleotide polymorphism, human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                              Oligonucleotide SEQ ID NO 149826 for detecting SNP TSC0037804.
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                                            ABF49829 standard; DNA; 13
                                                                                                    21-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Set of oligonucleotides,
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                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                    8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; tive 0; Mismatches 1; Indels
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                                         Sequence 13 BP; 2 A; 1 C; 3 G; 7 T; 0 U; 0 Other;
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 was obtained in electronic format from WIPO at
             ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                              1460 ATCAAGCAAATA 1471
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                                                                  Query Match
Best Local Similarity 91.7
Matches 11; Conservative
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) eligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The Oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligoners are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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ligonucleotides, useful for diagnosis and cell typing, it o detect single-nucleotide polymorphisms and cytosine
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                                                                                                                    Claim 1; SEQ ID NO 149826; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPD at fitted specification, but fit wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 206952; 29pp + Sequence Listing; German.
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                                                                                                                            Set of oligonuclectides, useful for diagnosis and cell designed to detect single-nucleotide polymorphisms and
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91.7%; Pred. No. 3.5e+02;
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                        Olek A,
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central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but they was obtained in electronic format from WIPO at
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Best Local Similarity 91.7<sup>5</sup>
Matches 11, Conservative
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Sequence 13 BP; 2 A; 0 C; 2 G; 9 T; 0 U; 0 Other;

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 Score 10.4; DB 1; Length 13; Pred. No. 3.5e+02; 0; Mismatches 1; Indels
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Query Match 8.0%;
Best Local Similarity 91.7%;
Matches 11; Conservative 0
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cancer also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                       Oligonucleotide SEQ ID NO 259005 for detecting SNP TSC0062939.
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                                    (first entry)
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ABH59028;
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Query Match 8.0%; Score 10.4; DB 1; Length 13; Best Local Similarity 91.7%; Pred. No. 3.5e+02; Matches 11; Conservative 0; Mismatches 1; Indels
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                             Oligonucleotide SEQ ID NO 260033 for detecting SNP TSC0007828.
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1347 AGGGGAAGAAAA 1358
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Berlin K;

Piepenbrock C,

olek A,

WPI; 2001-657177/75

WO200177384-A2

(EPIG-) EPIGENOMICS AG

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
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-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                               Claim 1; SEQ ID NO 260273; 29pp + Sequence Listing; German.
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Best Local Similarity 91.7
Matches 11; Conservative
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              represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at from Lip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                  Score 10.4; DB 1; Length 13; Pred. No. 3.5e+02;
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91.7%; Pred. No. 3.5e+02;
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Best Local Similarity 91.7%
Matches 11, Conservative
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Best Local Similarity
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010

Claim 1; SEQ ID NO 44422; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABC0010-ABE09989, ABC0010-ABE9989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from MIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                   SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
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                                                                                                                                      Oligonucleotide SEQ ID NO 58982 for detecting SNP TSC0015803.
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                                 ABC58965 standard; DNA; 13
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RESULT 718
ABC58965/0
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             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 3.5e+02;
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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91.7%;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at fitte wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide SEQ ID NO 116366 for detecting SNP TSC0029134.
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07-APR-2000; 2000DE-01019173.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIDO at
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

06-APR-2001; 2001WO-IB000713.

MO200177384-A2. Homo sapiens

18-OCT-2001.

Oligonucleotide SEQ ID NO 125127 for detecting SNP TSC0031262.

ВР

ABF25130 standard; DNA; 13

ABF25130;

21-FEB-2002 (first entry)

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                             Score 10.4; DB 1; Length 13; Pred. No. 3.5e+02; 0; Mismatches 1; Indels
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            Sequence 13 BP; 6 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
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ABF17059 standard; DNA; 13 BP.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABR00010-ABF9989, ABH00010-ABH99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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13 AAAGGATGTAAA 2

RESULT 725

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for disquosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF9073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                              This invention describes novel oligonucleotide primers or peptide nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                      set or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                      Claim 1; SEQ ID NO 170635; 29pp + Sequence Listing; German
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Pred. No. 3.5e+02;
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Best Local Similarity 91.7%;
Matches 11; Conservative
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                                    WO200177384-A2
Homo sapiens
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABC0010-ABE99889, ABH00010-ABH99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 91.7%;
Matches 11; Conservative
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8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02;

Best Local Similarity

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                                                                                                                                                                                                                                            SNP, single nucleotide polymorphism, human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 3.5e+02;
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1355 AAAAATATTCCA 1366
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Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                 Oligonucleotide SEQ ID NO 150203 for detecting SNP TSC0037911.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 203099; 29pp + Sequence Listing; German
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Best Local Similarity
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                                                 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                          Claim 1; SEQ ID NO 153538; 29pp + Sequence Listing; German.
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the printed specification, but
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91.7%; Pred. No. 3.5e+02;
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Pred. No. 3.5e+02;
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data for this patent did not form part of the pass obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 3.5e+02;
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                                                                                                                Claim 1; SEQ ID NO 77735; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                          Sequence 13 BP; 5 A; 0 C; 2 G; 6 T; 0 U; 0 Other;
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                      Berlin K;
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                     Piepenbrock C,
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 (EPIG-) EPIGENOMICS AG.
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                                             WPI; 2001-657177/75.
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                      olek A,
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO 33447 for detecting SNP TSC0010636.

(first entry)

20-FEB-2002

ABC33430;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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              Length 13;
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                                                                                 1; Indels
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       Score 10.4; DB 1;
Pred. No. 3.5e+02;
0; Mismatches 1;
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       8.0%;
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Ouery Match
Best Local Similarity 91.74
Marches 11, Conservative
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set or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS

WPI; 2001-657177/75.

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

WO200177384-A2.

18-OCT-2001

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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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ABC33430 standard; DNA; 13 BP.

RESULT 742

ABC33430 ID ABC3

1351 GAAGAAAATAT 1362

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Local Similarity

Matches

GAAGAAAAGTAT

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WO200177384-A2

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                         set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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13 GAGGTAAGATTG 2
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 ABC9989, ABF0010-ABF9989, ABH0010-ABH99989 and ABI00110-ABI82073 represent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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                                                                                                 Claim 1; SEQ ID NO 10540; 29pp + Sequence Listing; German.
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oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                      Seguence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;
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Best Local Similarity
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                               peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                               single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
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                                                                                                                ABF70194 standard; DNA; 13
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1406 ATTGTTAATGAT 1417
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                               13 ATTGATAATGAT
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Best Local Similarity
Matches 11; Conserv
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Query Match
8.0%; Score 10.4; DE
Best Local Similarity 91.7%; Pred. No. 3.564
Matches 11; Conservative 0; Mismatches

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                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide SEQ ID NO 170636 for detecting SNP TSC0042571.
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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|12 ATAAATGGAAGA 1
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                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG
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                                                                                                            Homo sapiens
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 the represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABR00010-ABF9989, ABR00010-ABF9989 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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   Claim 1; SEQ ID NO 228216; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic formmat from WIPO at fire printed specification, but fire wipo.int/pub/published_pct_sequence
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                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                     Oligonucleotide SEQ ID NO 241818 for detecting SNP TSC0058966.
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                                                                                               Claim 1; SEQ ID NO 263359; 29pp + Sequence Listing; German.
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Piepenbrock C,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                  Oligonucleotide SEQ ID NO 15937 for detecting SNP TSC0003511.
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
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ABC15930 standard; DNA; 13 BP.

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designed to detect single-nucleotide polymorphisms and cytosine
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastrointestinal, respiratory. central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABC0010-ABF9989, ABH0010-ABF9989 and ABI0010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                         invention describes novel oligonucleotide primers or peptide nucleic
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represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                 Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) oligomers for detecting single nucleotide polymorphisms (SNP) oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF0010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic form part of the printed specification, but
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, coingomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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Sequence 13 BP; 7 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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RESULT 770 ABH05683/c

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 ABC9989, ABF0010-ABF9989, ABH0010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                 Oligonucleotide SEQ ID NO 205660 for detecting SNP TSC0050412
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91.7%; Pred. No. 3.5e+02;
ive 0; Mismatches 1; Indels
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                             Oligonucleotide SEQ ID NO 210185 for detecting SNP TSC0051322.
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ABH10208 standard; DNA; 13
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                                                                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                      Claim 1; SEQ ID NO 210185; 29pp + Sequence Listing; German.
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WPI; 2001-657177/75
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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989 and ABI00010-ABE182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                   Oligonucleotide SEQ ID NO 245489 for detecting SNP TSC0059938
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                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                   1446 TGGAAGATGGGT 1457
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                                                              2 TGAAAGATGGGT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200177384-A2
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(first entry)

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ABH45512;

RESULT 77
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                                                                                                            ligonucleotides, useful for diagnosis and cell typing, it detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide SEQ ID NO 75919 for detecting SNP TSC0019454.
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                                                                                                                                                        Claim 1; SEQ ID NO 260274; 29pp + Sequence Listing; German.
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                                                                 Piepenbrock C,
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABP9989, ABH00010-ABP9989, ABH00010-ABP32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form at from WIPO at
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                                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic
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Claim 1; SEQ ID NO 75919; 29pp + Sequence Listing; German.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                          ABC40792 standard; DNA; 13 BP.
                                                                                                   21-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                     Score 10.4; DB 1; Length 13; Pred. No. 3.5e+02;
                                                                                                 1; Indels
                                          Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 U; 0 Other;
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was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG.
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Best Local Similarity
                                                                                    Local Similarity
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                                                                        Query Match
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                                                                                                                                                                                                RESULT 780
                                                                                                   Matches
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, aBH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 10.4; DB 1; Length 13; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 40809; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                         Berlin K;
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91.7%;
                                                                                                              07-APR-2000; 2000DE-01019173
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Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                                                               (EPIG-) EPIGENOMICS AG.
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18-OCT-2001
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Gaps

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8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; tive 0; Mismatches 1; Indels

1401 GTAAAATTGTTA 1412

GTAAAATGGTTA

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Matches

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, is
                                                                                                                      to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                   Claim 1; SEQ ID NO 220462; 29pp + Sequence Listing; German.
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                   Berlin K;
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Matches 11, Conservative
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                   Piepenbrock C,
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                   olek A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 91.7%;
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                                         Homo sapiens.
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ABH20485/

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
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8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; tive 0; Mismatches 1; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF0010-ABF9989, ABH0010-ABH99989 and ABI0010-ABH32073 teperesent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABR0010-ABC99989 and ABI0010-ABC99980 and ABI0010-ABC99980 are the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ses 11; Conservative
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ABF58576
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Sequence 13 BP; 7 A; 0 C; 2 G; 4 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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 Score 10.4; DB 1; Length 13;
Pred. No. 3.5e+02;
0; Mismatches 1; Indels
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Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative C
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Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                                                          TAAAATGGTTAA 12
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073. represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                           Oligonucleotide SEQ ID NO 191755 for detecting SNP TSC0047176,
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                                      22-FEB-2002 (first entry)
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  8.0%; Score 10.4; DB 1; Length 13; 11.7%; Pred. No. 3.5e+02; ve 0; Mismatches 1; Indels
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ABH45029 standard; DNA; 13 BP. (first entry) 22-FEB-2002 ABH45029; RESULT 788 ABH45029,

Oligonucleotide SEQ ID NO 245006 for detecting SNP TSC0059825.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, astdowascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 245006; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABH00010-ABH99989 and ABI00010-AB19073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Pred. No. 3.5e+02;
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-ABC39989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Pred. No. 3.5e+02;
0; Mismatches 1; Indels
                                                                                                  8.0%; Score 10.4; DB 1; Length 13; 31.7%; Pred. No. 3.5e+02;
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                                                                           Sequence 13 BP; 2 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                           Oligonucleotide SEQ ID NO 58211 for detecting SNP TSC0015625.
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               ABC58194 standard; DNA; 13
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This invention describes novel oligomucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and extosin methylation status in chemically pretraeted genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABP0010-ABC99989, and nthe invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABC36055 standard; DNA; 13 BP.
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Claim 1; SEQ ID NO 36072; 29pp + Sequence Listing; German

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at fire.wipo.int/pub/published_pct_sequences
      This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABR00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                Oligonuclectide SEQ ID NO 64543 for detecting SNP TSC0017022
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           ABC64526 standard; DNA; 13 BP
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                                         8.0%; Score 10.4; DB 1; Length 13; ilarity 91.7%; Pred. No. 3.5e+02; Conservative 0; Mismatches 1; Indels
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            Sequence 13 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
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Best Local Similarity 91.7%;
Matches 11; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                               Set of oligonucleotides, useful for diagnosis and cell typing, i
designed to detect single-nucleotide polymorphisms and cytosine
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31.7%; Pred. No. 3.5e+02;
Ive 0; Mismatches 1; Indels
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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18-OCT-2001

Olek A,

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acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99889, ABH00010-ABH99889 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel oligonuclectide primers or peptide nucleic
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                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 223880; 29pp + Sequence Listing; German
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                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                 Oligonucleotide SEQ ID NO 173474 for detecting SNP TSC0043213.
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22-FEB-2002 (first entry)
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ABH23903;

RESULT 805

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Score 10.4; DB 1; Pred. No. 3.5e+02; 0; Mismatches 1;

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Query Match 8.0° Best Local Similarity 91.7° Matches 11, Conservative

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13 AAATTGTTATT 2

Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 U; 0 Other;

data for this patent did not form part of the g was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

888888

Length 13;

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO 228568 for detecting SNP TSC0055748.

22-FEB-2002 (first entry)

ABH28591;

ABH28591 standard; DNA; 13 BP.

RESULT 808

ABH28591

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastronintestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABEC99899, ABF00010-ABE9989, ABH0010-ABE99989 and ABI0010-ABE82071 represent the oligomers described in the invention. NOTE: The sequence
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                                                                         This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Claim 1; SEQ ID NO 176214; 29pp + Sequence Listing; German.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide SEQ ID NO 203100 for detecting SNP TSC0049882.

Berlin K;

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 203100; 29pp + Sequence Listing; German.

; 0 Length 13; Indels Sequence 13 BP; 4 A; 3 C; 0 G; 6 T; 0 U; 0 Other; Score 10.4; DB 1; Pred. No. 3.5e+02; 0; Mismatches 1; ftp.wipo.int/pub/published_pct_sequences 8.0%; 1396 AGGAGGTAAAT 1407 11; Conservative 12 AGTAGGTAAAT 1 Query Match Best Local Similarity Matches g ઠે

ö This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at Gaps Claim 1; SEQ ID NO 228568; 29pp + Sequence Listing; German. methylation status.

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine

Berlin K;

Piepenbrock C,

olek A,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

WO200177384-A2. Homo sapiens

18-OCT-2001.

schultz911-3.rng

peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                     ABH10209 standard; DNA; 13
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                                                                                                        (first entry)
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Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                          22-FEB-2002
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                                                                      ABH10209;
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RESULT 809
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at

Sequence 13 BP; 3 A; 0 C; 5 G; 5 T; 0 U; 0 Other;

Query Match

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG.

WPI; 2001-657177/75.

06-APR-2001; 2001WO-IB000713.

WO200177384-A2

18-OCT-2001

Homo sapiens.

07-APR-2000; 2000DE-01019173.

Claim 1; SEQ ID NO 191357; 29pp + Sequence Listing; German

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps ; 0 Oligonucleotide SEQ ID NO 242610 for detecting SNP TSC0059184. 8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; tive 0; Mismatches 1; Indels ABH42633 standard; DNA; 13 BP. 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 1359 ATATTCCACGCA 1370 22-FEB-2002 (first entry) 11; Conservative N ATATTCCACCCA Local Similarity WO200177384-A2 Homo sapiens ABH42633; RESULT 811 Matches ABH42633, 셤 ò ö SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

Oligonucleotide SEQ ID NO 191357 for detecting SNP TSC0047086

(first entry)

22-FEB-2002

ABF91360,

ABF91360 standard; DNA; 13 BP

GAGGTATAATTG 1

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RESULT 813
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                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not from part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                    useful for diagnosis and cell typing, is
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                                                                          designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                Claim 1; SEQ ID NO 242610; 29pp + Sequence Listing; German.
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                       Berlin K;
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Best Local Similarity 91.7
Matches 11, Conservative
                                                                    Set of oligonucleotides,
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                       Olek A, Piepenbrock C,
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(EPIG-) EPIGENOMICS AG
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrom, respiratory. central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABC0010-ABE9989, ABH0010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo int/pub/published_pct_sequences
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schultz911-3.rng

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO 20130 for detecting SNP TSC0004129.

(first entry)

20-FEB-2002

ABC20113;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                   Gaps
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                Length 13;
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                                               1; Indels
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            Score 10.4; DB 1;
Pred. No. 3.5e+02;
0; Mismatches 1;
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                                                                                    1439 ATATACATGGAA 1450
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Query Match
Best Local Similarity 91...
Best Local 11, Conservative
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG

WPI; 2001-657177/75.

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

WO200177384-A2. Homo sapiens,

18-OCT-2001

Claim 1; SEQ ID NO 20130; 29pp + Sequence Listing; German.

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ABC75271 standard; DNA; 13
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Best Local Similarity 91.7<sup>3</sup>
Matches 11, Conservative
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Gaps

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ABC20113 standard; DNA; 13 BP.

RESULT 815 ABC20113/c ID ABC201

1403 AAAATTGTTAAT 1414

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11; Conservative

Matches

Local Similarity

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Berlin K;
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Best Local Similarity 91./7,
These 11; Conservative
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designed to detect single-nucleotide polymorphisms and cytosine
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 tapeseen the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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oligomers are also used for detecting cell type differentiation. ABC00010 -ABC39989, ABF00010-ABF99889, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ftp.wipo.int/pub/published_pct_sequences
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ID ABC03271 standard; DNA; 13 BP.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                     Oligonucleotide SEQ ID NO 3646 for detecting SNP TSC0001395.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory. Central nervous system, artiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 algomers are also used for detecting cell type differentiation. ABC0010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide SEQ ID NO 6923 for detecting SNP TSC0002071.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABE99899, ABH00010-ABE99899 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but two obtained in electronic format from WIPD at

Sequence 13 BP; 4 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine

methylation status.

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Berlin

Piepenbrock C,

Olek A,

WPI; 2001-657177/75

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Claim 1; SEQ ID NO 58212; 29pp + Sequence Listing; German.

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Oligonucleotide SEQ ID NO 10320 for detecting SNP TSC0002624.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-657177/75.
                                                                                                                                                                                                                   WO200177384-A2.
                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                          18-OCT-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide SEQ ID NO 58212 for detecting SNP TSC0015625.

(first entry)

21-FEB-2002

ABC58195;

06-APR-2001; 2001WO-IB000713.

WO200177384-A2

18-OCT-2001

Homo sapiens

BP.

ABC58195 standard; DNA; 13

RESULT 822

ABC58195

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; ive 0; Mismatches 1; Indels
                                                                                                                      BP.
                                                                                                                   ABC10329 standard; DNA; 13
                                          1360 TATTCCACGCAT 1371
                                                                                                                                                              (first entry)
           Local Similarity 91.7
                                                             1 racrecaeder 12
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                                                                                                                                         ABC10329;
 Query Match
                                                                                             RESULT 823
                    Matches
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Gaps

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1; Indels

0; Mismatches

ch 1 Similarity 91.7%; 11; Conservative

Local Similarity

Matches

Query Match

1403 AAAATTGTTAAT 1414

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AAAATTGTTATT 13

Score 10.4; DB 1; Length 13; Pred. No. 3.5e+02;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PRA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a renge of diseases including immune system, gastrointestinal, respiratory, central nervous system, axidovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989 and ABL00010-ABIG2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
Claim 1; SEQ ID NO 10320; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 U; 0 Other;
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91.7%; Pred. No. 3.5e+02;
Live 0; Mismatches 1;
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1402 TAAAATTGTTAA 1413
                  12 TAATATTGTTAA 1
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Gaps

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1; Indels

Length 13;

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ABC13615 standard; DNA; 13
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                                                                                                                                                                                                                                                            20-FEB-2002
                                                                                                                                                                        ABC13615;
RESULT 824
                              ABCIJSTS

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ACX

ABCIJSTS

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ABCIJSTS

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ABCIJSTS

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ABCIJSTS

ABCIDS

CCC A
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BP.

Oligonucleotide SEQ ID NO 13622 for detecting SNP TSC0003139.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K; Piepenbrock C, Olek A,

WPI; 2001-657177/75

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine designed to detect amethylation status.

Claim 1; SEQ ID NO 13622; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleicacid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABH99989, ABF00010-ABH99989, ABF00010-ABH99989, ABF00010-ABH99989, ABF00010-ABH99989 and ABF00010-ABHBR2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

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1352 AAGAAAATATT 1363

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2 AAGAAATATATT 13

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 and PABC99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide SEQ ID NO 137595 for detecting SNP TSC0034394.
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                                                                         / Match
B.0%; Score 10.4; DB 1; Length 13;
Local Similarity 91.7%; Pred. No. 3.5e+02;
les 11; Conservative 0; Mismatches 1; Indels
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                                      Sequence 13 BP; 7 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
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ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-APR-2001; 2001WO-IB000713.
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                                                                                                                                                                                                                                                                            ABF37598 standard; DNA; 13
                                                                                                                                                  1356 AAAATATTCCAC 1367
                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                     2 AAAATATTCAAC 13
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                  ABF37598;
                                                                             Query Match
                                                                                                                                                                                                                                           RESULT 825
                                                                                                            Matches
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                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                             Oligonucleotide SEQ ID NO 220170 for detecting SNP TSC0053577.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Berlin K;
              ABH20193 standard; DNA; 13 BP.
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                                                                               (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                  Homo sapiens
                                                                               22-FEB-2002
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                                               ABH20193;
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ABH20193
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and merabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent din ot form part of the printed specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                           ligonucleotides, useful for diagnosis and cell typing, it detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide SEQ ID NO 150204 for detecting SNP TSC0037911.
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                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 223367; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                 Berlin
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                                                                                                        06-APR-2001; 2001WO-IB000713,
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                                                                                                                                    07-APR-2000; 2000DE-01019173
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                                                                                                                                                                                                                                                             Set of oligonucleotides,
                                                                                                                                                                                                 Piepenbrock C,
                                                                                                                                                                   (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                          methylation status.
                                            WO200177384-A2
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                 Homo sapiens
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Berlin

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastrointestinal, respiratory. central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 appresent the oligomers described in the invention. NOTE: The sequence the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at
                                                                                                                              Set of oligonucleotides, useful for diagnosis and cell typing, : designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 150204; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13 BP; 9 A; 1 C; 0 G; 3 T; 0 U; 0 Other;
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   Piepenbrock C,
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                                                                WPI; 2001-657177/75
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Olek A,
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XX AC ABF51
XX AC ABF51
XX DD COLIG
XX CW SNP;
XW SNP;
XW Cent
XX COLIG
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ch 8.0%; Score 10.4; DB 1; Length 13; 1 Similarity 91.7%; Pred. No. 3.5e+02; 11; Conservative 0; Mismatches 1; Indels 1; Indels 1355 AAAATATTCCA 1366

1 AAAAATATTACA 12

21-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 150693 for detecting SNP TSC0038026.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

봈 Berlin Piepenbrock C,

Set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single-nuclectide polymorphisms and cytosine

Claim 1; SEQ ID NO 150693; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The

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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 ABC09989, ABF00010-ABF09989, aBF00010-ABF9989, aBF00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
oligonuclectides are used for diagnosis and/or prognosis of cancer and
8888888888888888
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Sequence 13 BP; 2 A; 0 C; 5 G; 6 T; 0 U; 0 Other

Gaps ö Query Match 8.0%; Score 10.4; DB 1; Length 13; Best Local Similarity 91.7%; Pred. No. 3.5e+02; Matches 11; Conservative 0; Mismatches 1; Indels

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1434 CAGACATATACA 1445 CACACATATACA 2 13 à

ABH28238 standard; DNA; 13 BP.

ABH28238;

22-FEB-2002 (first entry)

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Oligonucleotide SEQ ID NO 228215 for detecting SNP TSC0004626.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

sapiens. Ношо WO200177384-A2

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75

typing, i cytosine Set of oligonucleotides, useful for diagnosis and cell designed to detect single-nucleotide polymorphisms and methylation status.

Claim 1; SEQ ID NO 228215; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, pastrointestinal, respiratory, calgomers are also used for detecting cell type differentiation. ABC00010 oligomers are also used for detecting cell type differentiation. ABC0001 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 13 BP; 3 A; 1 C; 1 G; 8 T; 0 U; 0 Other;

Query Match

8.0%; Score 10.4; DB 1; Length 13;

RESULT 831

8 g

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, azdiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but they wise obtained in electronic format from WIPO at
                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                    Oligonucleotide SEQ ID NO 180954 for detecting SNP TSC0044779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 180954; 29pp + Sequence Listing; German.
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                             22-FEB-2002 (first entry)
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 3.5e+02;
); Mismatches 1; Indels
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Best Local Similarity 91.7%;
Matches 11; Conservative
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AC ABF8099
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Gaps

06-APR-2001; 2001WO-IB000713.

18-OCT-2001

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for disagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABC0010-ABF9989, ABH0010-ABF9989 and ABI00100-ABI82073 data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fire wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                        This invention describes novel oligonuclectide primers or peptide nucleic
                                                                                                                                                                                                                                       Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 234847; 29pp + Sequence Listing; German.
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                                                                                                                                                            Berlin K;
                                                                             07-APR-2000; 2000DE-01019173
                                                                                                                                                          Piepenbrock C,
                                                                                                                  (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                             WPI; 2001-657177/75.
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.; 0 Score 10.4; DB 1; Length 13; Pred. No. 3.5e+02; 0; Mismatches 1; Indels 8.08; 91.78; 11; Conservative Query Match Best Local Similarity Matches

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Gaps

1401 GTAAAATTGTTA 1412 2 Gradadarctra 13 ð g

ABF60680 standard; DNA; 13 BP. ABF60680;

(first entry) 22-FEB-2002

Oligonucleotide SEQ ID NO 160677 for detecting SNP TSC0040462.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K; Piepenbrock C, olek A,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                               Claim 1; SEQ ID NO 160677; 29pp + Sequence Listing; German.
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1405 AATTGTTAATGA 1416

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2 AATTGTTAAAGA 13

RESULT 835

Oligonucleotide SEQ ID NO 190889 for detecting SNP TSC0046952. ABF90892 standard; DNA; 13 BP 22-FEB-2002 (first entry) ABF90892; ABF90892

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75

ligonucleotides, useful for diagnosis and cell typing, it o detect single-nucleotide polymorphisms and cytosine Set of oligonucleotides, designed to detect amethylation status.

Claim 1; SEQ ID NO 190889; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC0010 ABC0010-ABC0010

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                              cch 8.0%; Score 10.4; DB 1; Length 13; al Similarity 91.7%; Pred. No. 3.5e+02; 11; Conservative 0; Mismatches 1; Indels
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                                                                                         Sequence 13 BP; 2 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
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TTGTTGATGATG 12
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Best Local Similarity
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ABH53511
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, coligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                     Oligonucleotide SEQ ID NO 20129 for detecting SNP TSC0004129.
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Best Local Similarity 91.7%;
Matches 11; Conservative
                                                              ABC20112 standard; DNA; 13
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8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; iive 0; Mismatches 1; Indels

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Matches

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                            Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG
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AAGATTGTTAAT 12

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Oligonucleotide SEQ ID NO 3642 for detecting SNP TSC0001395.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75

set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 3642; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF0010-ABF99989, ABH0010-ABH99989 and ABI00010-ABI82073 targenesm the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Berlin K;

ftp.wipo.int/pub/published_pct_sequences

Sequence 13 BP; 10 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

Gaps . 0 Score 10.4; DB 1; Length 13; Pred. No. 3.5e+02; 0; Mismatches 1; Indels 8.0%; Query Match
Best Local Similarity 91.7
Matches 11; Conservative

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1352 AAGAAAAATATT 1363

ò g RESULT 840

BP. ABC81568 standard; DNA; 13 ABC81568;

21-FEB-2002 (first entry)

Oligonucleotide SEQ ID NO 81585 for detecting SNP TSC0020645.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 81585; 29pp + Sequence Listing; German

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                         Length 13;
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Sequence 13 BP; 4 A; 0 C; 3 G; 6 T; 0 U; 0 Other
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ilarity 91.7%; Pred. No. 3.5e+02;
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Les 11; Conserv
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99899, ABH00010-ABF99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Gaps

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RESULT 843 ABF15353/c

(first entry)

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABC0010-ABF89989, ABC0010-ABF89989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                       Oligonucleotide SEQ ID NO 115350 for detecting SNP TSC0028921.
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 ABF15353 standard; DNA; 13
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Berlin K;

Piepenbrock C,

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Matches 11; Conservative
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8.0%; Score 10.4; DB 1; Length 13; 31.7%; Pred. No. 3.5e+02; ive 0; Mismatches 1; Indels

91.7%;

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was obtained in electronic format from WI ftp.wipo.int/pub/published_pct_sequences
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WPI; 2001-657177/75
                           methylation status.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. designed to detect single-nucleotide polymorphisms and cytosine methylation status. Oligonucleotide SEQ ID NO 119549 for detecting SNP TSC0029841. Berlin ВЪ. 07-APR-2000; 2000DE-01019173. 06-APR-2001; 2001WO-IB000713. ABF19552 standard; DNA; 13 (first entry) Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75 WO200177384-A2.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE9989, ABF00010-ABE998, ABF000 Gaps Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine ö Score 10.4; DB 1; Length 13; Pred. No. 3.5e+02; Claim 1; SEQ ID NO 139220; 29pp + Sequence Listing; German. Indels Sequence 13 BP; 6 A; 4 C; 0 G; 3 T; 0 U; 0 Other; 0; Mismatches ftp.wipo.int/pub/published_pct_sequences ĸ Berlin 8.0%; Matches 11; Conservative Piepenbrock C, (EPIG-) EPIGENOMICS AG. WPI; 2001-657177/75. Query Match Best Local Similarity methylation status. olek A,

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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF89989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Local Similarity 91.7%;
les 11; Conservative
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                                                                                                                                                                                 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99889, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                      oligonucleotides, useful for diagnosis and cell typing, is to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                            Claim 1; SEQ ID NO 117055; 29pp + Sequence Listing; German.
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schultz911-3.rng

SNP, single nucleotide polymorphism, human; diagnosis; PNA, cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO 222533 for detecting SNP TSC0054144.

GGTAAATTGTT 1411

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                            ABF97454 standard; DNA; 13
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GGTAGAATTGTT 2
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Best Local Similarity
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                                                         RESULT 848
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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG

WPI; 2001-657177/75

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

WO200177384-A2

18-OCT-2001.

Homo sapiens

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABF00010-ABF99999, ABF00010-ABF99999, ABF00010-ABF99999, and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
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11; Conservative

Matches

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1 TTTTAATGATGA 12

ABH22556 standard; DNA; 13 BP.

ABH22556

22-FEB-2002 (first entry)

ABH22556;

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Claim 1; SEQ ID NO 176213; 29pp + Sequence Listing; German.
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Matches
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                                                                                                                                                                                                                                                                 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010 +ABC99989, ABF0010-ABF99899, ABF0010-ABF99899, ABF0010-ABF99899, ABF0010-ABF99999 and ABI0010-ABF82073 represent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 173473; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      was obtained in electronic format from WI ftp.wipo.int/pub/published_pct_sequences
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06-APR-2001; 2001WO-IBGG0713
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                                                                                                   Piepenbrock C,
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                                                                    (EPIG-) EPIGENOMICS AG
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-AB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WFPO at they point/pub/published_pct_sequences
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                          Oligonucleotide SEQ ID NO 152249 for detecting SNP TSC0038467.
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                                                                               ABF52252 standard; DNA; 13
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                                                                                                                                 ABF52252;
                             RESULT 854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                              8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; tive 0; Mismatches 1; Indels
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                                                                                 Sequence 13 BP; 8 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity
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XXX SNP;
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomerseare used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                    This invention describes novel oligonucleotide primers or peptide nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single mucleotide polymorphism; human; diagnosis; pNA; cancer; CS; snP; single mucleic acid; cytosine methylation; cardiovascular; primer; ss; peptide nucleic acid; cytosine methylation;
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Claim 1; SEQ ID NO 152249; 29pp + Sequence Listing; German.
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Matches 11; Conservative
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Matches

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                            nnucleotides, useful for diagnosis and cell typing, is detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                      Claim 1; SEQ ID NO 232255; 29pp + Sequence Listing; German.
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Matches 11; Conservative
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                                                                                                          Set of oligonucleotides,
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                  Olek A, Piepenbrock C,
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                                                                                                                                                   methylation status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NUTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.0%; Score 10.4; DB 1; Length 13; 31.7%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 152250; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                     Berlin K;
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nes 11; Conservative
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                                                                                                                                                                                                                                                                                                                       Piepenbrock C,
                                                                                                                                                                                                                                                                              (EPIG-) EPIGENOMICS AG.
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                                                            Homo sapiens.
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Query Match

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8.0%; Score 10.4; DB 1; Length 13; 11.7%; Pred. No. 3.5e+02; ve 0; Mismatches 1; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABC0010-ABE9989, ABC0010-ABE9989, ABC0010-ABE9989, ABC0010-ABE9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Pred. No. 3.5e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABF88600;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABH00010-ABH9989 and ABI00010-ABS182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                   set or oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid (PNA) oligomers for detecting single nucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                      Oligonucleotide SEQ ID NO 188597 for detecting SNP TSC0046437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 188597; 29pp + Sequence Listing; German.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
Oligonucleotide SEQ ID NO 242609 for detecting SNP TSC0059184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EPIG-) EPIGENOMICS AG
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-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
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                                                                                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABC0010-ABC99989, and in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic forms from WIPO at
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  Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; tive 0; Mismatches 1; Indels
                                                                                             Claim 1; SEQ ID NO 242609; 29pp + Sequence Listing; German.
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Best Local Similarity
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represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Pred. No. 3.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                            8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; ive 0; Mismatches 1; Indels
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                                                                                                                                                    Sequence 13 BP; 6 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
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Best Local Similarity 91.7
Matches 11; Conservative
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Best Local Similarity
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABI2073 represent the oligomers described in the invention. NOTE: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                        Oligonucleotide SEQ ID NO 27572 for detecting SNP TSC0007678.
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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                              ABC27555 standard; DNA; 13 BP
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              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 8s; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                         peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
      single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; ide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
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Best Local Similarity
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06-APR-2001; 2001WO-IB000713

WO200177384-A2.

18-OCT-2001.

Homo sapiens.

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Claim 1; SEQ ID NO 116833; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABC0010-ABC99899, ABC0010-ABC99899, ABC0010-ABC99899, ABC0010-ABH99989 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.0%; Score 10.4; DB 1; Length 13; Best Local Similarity 91.7%; Pred. No. 3.5e+02; Matches 11; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.0%; Score 10.4; DB 1; Length 13; 11.7%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 115143; 29pp + Sequence Listing; German.
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                                                                                                         Piepenbrock C,
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ABF98427 standard; DNA; 13 BP
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                                                                                                                                             Oligonucleotide SEQ ID NO 198424 for detecting SNP TSC0008139.
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Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                               (EPIG-) EPIGENOMICS AG
                                            WPI; 2001-657177/75.
                                                         methylation status.
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Homo sapiens.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a
                                                                                                                                                                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989, ABG00010-ABH99989 and ABI00010-ABH82073 arepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                  Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                               Claim 1; SEQ ID NO 152797; 29pp + Sequence Listing; German.
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Pred. No. 3.5e+02;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prosposis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE09989, ABE00010-ABE99999 and ABE00010-ABE182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
central nervous system, cardiovascular and metabolic disorders. The central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABR00010-ABF99989 and ABT00010-ABF99983 are represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; Ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                          8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ve 0; Mismatches 1;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABP0010-ABC99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                              Oligonucleotide SEQ ID NO 165708 for detecting SNP TSC0041557.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     claim 1; SEQ ID NO 165708; 29pp + Sequence Listing; German.
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22-FEB-2002 (first entry)
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. HECO010 oligomers are also used for detecting cell type differentiation. ABC0010 ABC99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173. Claim 1; SEQ ID NO 191283; 29pp + Sequence Listing; German.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide SEQ ID NO 250615 for detecting SNP TSC0061196.
                                                                                                                                                                                                                                                                                                Query Match

8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 3.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                               Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                          ABH50638 standard; DNA; 13 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2001; 2001WO-IB000713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-APR-2000; 2000DE-01019173
                                                                                                                                                                                                                                                                                                                                         1447 GGAAGATGGGTT 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-657177/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-OCT-2001.
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Gaps

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

WO200177384-A2

18-OCT-2001

Homo sapiens

Oligonucleotide SEQ ID NO 191283 for detecting SNP TSC0047056

(first entry)

22-FEB-2002

ABF91286;

BP.

ABF91286 standard; DNA; 13

RESULT 878

ABF91286

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Gaps

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WPI; 2001-657177/75.
                                             Local Similarity
nes 11; Conserva
                                                                                                     WO200177384-A2
                                                                                                Homo sapiens.
                                                                              22-FEB-2002
                                                                                                         18-OCT-2001
                                                                         ABH64589;
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                                           Query Match
                                                                RESULT 880
                                               Matches
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Betaine aldehyde dehydrogenase; BADH; primer; ss; plant gene conversion; salt tolerance; low temperature resistance; drought tolerance; sea-blite;
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data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suaeda liaotungensis kitag betaine aldehyde dehydrogenase gene and its
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                                                                                                                Score 10.4; DB 1; Length 13; Pred. No. 3.5e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Betaine aldehyde dehydrogenase (BADH) cDNA PCR primer #1.
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                                                                           Sequence 13 BP; 1 A; 6 C; 0 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 6 (Disclosure); 15pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV92767 standard; RNA; 14 BP.
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                                                                                                                      Query Match 8.0%;
Best Local Similarity 91.7%;
Matches 11; Conservative
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24-JUL-2003 (first en
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                                                                                                                                                                                                                                                                                                                                                                                 ABX95960;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosid our prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC00010-ABC09989, ABF00010-ABR99989, ABR00010-ABR99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide SEQ ID NO 264566 for detecting SNP TSC0064134.
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                                                                                                                                                                                                                                                                                                                                                                                 8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 3.5e+02; ive 0; Mismatches 1; Indels
                                                     Claim 1; SEQ ID NO 250615; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                   Sequence 13 BP; 4 A; 0 C; 2 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1356 AAAATATTCCAC 1367
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                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                    methylation status.
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Gaps

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18-FEB-1999 (first entry)
AAV92767;
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Human, c-raf, A-raf, B-raf, hammerhead ribozyme; hairpin ribozyme; target, substrate; catalyst; modulation; expression; Raf gene; delivery; screening; identification; synthesis; deprotection; purification; cancer; inflammation; psoriasis; non-hepatic ascites; infection; genetic drift; restenosis; rheumatoid arthritis; ss.
Human A-raf target sequence nucleotide position 167.
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Homo sapiens.

WO9850530-A2

12-NOV-1998.

98WO-US009249 05-MAY-1998; 97US-0046059P. 97US-0049002P. 97US-0051718P. 97US-0051321P. 97US-0061321P. 97US-0061324P. 97US-0068212P. 09-MAY-1997; 09-JUN-1997; 03-JUL-1997; 22-AUG-1997; 02-OCT-1997; 05-NOV-1997;

(RIBO-) RIBOZYME PHARM INC. 19-DEC-1997

Bellon L; Burgin A; Jarvis T., Matulic-Adamic J., Reynolds M., Kisich K., Parry T., Beigelman L., Mcswiggen JA, Karpeisky A. Thompson J., Workman CT., Beaudry A., Sweedler D:

WPI; 1999-009494/01.

Identifying new catalytic nucleic acid that modulates selected processes - especially ribozymes that cleave Raf RNA for treating cancer, restenosis, and also new ribozymes and modified nucleoside triphosphates used as antiviral agents and synthons.

Claim 179; Page 163; 259pp; English.

Amethod has been developed for the identification of a nucleic acid
capable of macdulating a process in a biological system. The method
capable of macdulating a process in a biological system. The method
comprises: (a) introducing into the system a random library of nucleic
confaralysts (NAC) having a substrate binding domain (BBD), comprising
a random sequence, and a catalytic domain (CD); and (b) identifying NAC
in systems where modulation has occurred and/or determining the sequence
of at least part of the SBDs in such systems. Nucleic acid molecules with
condonuclease activity and catalytic activity, from the present invention,
are used to modulate gene expression in plant and ammalian cells and to
cleave target nucleic acid, particularly for treating systemic diseases
conserve target nucleic acid, particularly for treating systemic diseases
contactions in diseased calls and to determine c-raf RNA. Specifically NACs
with RNA-cleaving activity that modulate expression of the Raf gene, are
cused to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
cused to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
cused to treat cancer modulate expression of the Raf gene, are
cused to the condition associated with the level of c-raf. Introduction
cof sugar/phosphate modifications increases stability against nuclease and
activity. AAV90922 to AAV91877 represent NACs that can be used in the
conditional part of the condition of a Raf gene

Sequence 14 BP; 2 A; 7 C; 1 G; 0 T; 4 U; 0 Other;

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Gaps
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8.0%; Score 10.4; DB 1; Length 14;
31.7%; Pred. No. 3.8e+02;
ive 0; Mismatches 1; Indels
     Query Match 8.0%;
Best Local Similarity 91.7%;
Matches 11; Conservative
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1449 AAGATGGGTTGA 1460

14 AAGATGGGCTGA 3

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7, 2004, 07:01:28 Search completed: April Job time : 42 secs

Sequence 26, Appl Sequence 26, Appl Sequence 61, Appl Sequence 6, Appl Sequence 6, Appl Sequence 10, Appl Sequence 10, Appl Sequence 106, Appl Sequence 106, Appl Sequence 108, Appl Sequence 423, Appl Sequence 423, Appl	Sequence 388, App Sequence 699, App Sequence 388, App Sequence 657, App Sequence 657, App Sequence 190, App Sequence 190, App Sequence 279, App Sequence 279, App Sequence 279, App	Sequence 13, Applia Sequence 3, Applia Sequence 3, Applia Sequence 3, Applia Sequence 9, Applia Sequence 10, Applia Sequence 11, Applia Sequence 10, Applia Sequence 5, Applia Sequence 5, Applia Sequence 5, Applia Sequence 5, Applia Sequence 3, Applia Sequence 5, Applia Sequence 6, Applia Sequence 6, Applia Sequence 7, Applia Sequence	Sequence 8, Appl. Sequence 78, Appl. Sequence 123, Appl. Sequence 124, Appl. Sequence 14, Appl. Sequence 24, Appl. Sequence 19, Appl. Sequence 19, Appl. Sequence 19, Appl. Sequence 119, Appl. Sequence 117, Appl. Sequence 25, Appl. Sequence 106, Appl. Sequenc
US-07-704-288C-26 US-08-379-259-26 US-09-479-005A-61 US-08-173-489C-296 US-09-375-673B-6 US-09-375-673B-6 US-08-319-492B-104 US-08-319-492B-104 US-08-319-492B-104 US-08-319-492B-104	US-08-292-620A-388 US-08-292-620A-699 US-09-071-845-699 US-09-081-646-657 US-08-453-623-30 US-08-177-489C-190 US-08-177-489C-279 US-08-177-489C-279 US-08-177-489C-279	US-08-173-489C-22 US-08-173-489C-22 US-09-384-327-3 US-08-458-372-3 US-08-458-372-3 US-08-478-489C-333 US-08-477-489C-333 US-09-470-1135-9 US-09-470-1135-9 US-09-470-378-10 US-09-69-388-9 US-08-607-078-3 US-08-607-078-3 US-08-607-471-5 US-09-66-443-5 US-09-360-344-3 US-09-360-360-344-3 US-09-360-360-360-360-360-360-360-360-360-360	1 US-08-393-744-8 1 US-08-36-022A-8 1 US-08-813-62-022A-8 1 US-08-813-83-78 1 US-09-47-048A-8 1 US-09-47-048A-8 1 US-09-47-048-6 1 US-09-47-6 1 US-09-47-6 1 US-09-47-6 1 US-09-47-6 1 US-08-32407-6 1 US-08-32407-6 1 US-08-32407-6 1 US-08-329-856-2 1 US-08-929-86-2 1 US-08-929-86-2 1 US-08-92-928-8 1 US-08-92-928-8 1 US-08-92-928-8 1 US-08-92-185-116 1 US-08-92-165A-117 1 US-08-941-887A-117 1 US-08-941-887A-117 1 US-08-941-887A-117 1 US-08-941-887A-117 1 US-08-9407-549-25 1 PCT-US91-03680-108
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version 5.1.6 - 2004 Compugen Ltd. v model i:51; Search time 0.001 Sec (without alignments) 373.620 Million cell	ttcggttgatcaagcaaatagga 13 0.5 dues sen parameters: 200	into control of the first 101 summaries Listing first 101 summaries rni.seq:* is the number of results predicted by chance after than or equal to the score of the result rived by analysis of the total score distribute \$\frac{\partial \text{SUMMARIES}}{\text{SUMMARIES}}\$\$	11.7 20 US-09-527-115-21 Sequence 2-15-21 US-09-527-032-3 Sequence 3-15-21 US-09-109-452A-3773 Sequence 3-15-21 US-09-270-956-31 Sequence 3-15-21 US-09-270-956-31 Sequence 3-15-21 US-09-270-959-13 Sequence 3-15-21 US-09-344-520-37 Sequence 3-15-21 US-09-344-520-37 Sequence 3-15-21 US-08-998-099-113 Sequence 6-15-21 US-08-998-099-113 Sequence 6-15-21 US-08-998-099-113 Sequence 6-15-21 US-08-998-099-113 Sequence 1-15-21 US-08-97-12-17-17-17-17-17-17-17-17-17-17-17-17-17-

Gaps

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RESULT 4

(US-09-189452A-3773/C

(US-09-18040EC 3773, Application US/09198452A); Sequence 3773, Application US/09198452A; September 3773, Application US/09198452A; GENERAL INFORMATION:

(CENERAL INFORMATION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmen applicable: Refrete and uses thereof, in particular for the diagnosis, preprint OF INVENTION: and treatment of infection information of INFORMATION: and treatment of infection information and treatment of infection information and treatment of infection information informat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 54, Application US/09232346

| Sequence 54, Application US/09232346
| Sequence 54, Application US/09232346
| Patent No. 6352830
| GENERAL INFORMATION:
| APPLICANT: No. 6552830throp, Jeffrey P. APPLICANT: No. 6552830throp, Jeffrey P. APPLICANT: No. 6552830throp, Jeffrey P. TITLE OF INVENTION: N. MILIAM M. APPLICANT: PLANGAM, WILLIAM M. TITLE OF INVENTION: NFTAPOLYPEPTIDES AND SCREENING ITLLE OF INVENTION: NFTHODS FOR IMMUNOSUPPRESSIVE AGENTS
| TITLE OF INVENTION: NFTHODS FOR IMMUNOSUPPRESSIVE AGENTS | TITLE OF INVENTION: NFTHORS: US/09/232,346 | CURRENT FILING DATE: 1999-01-15 | CURRENT FILING DATE: 1999-01-15 | PRIOR PLILING DATE: 1994-04-18 | PRIOR APPLICATION NUMBER: 08/228,944 | PRIOR PLILING DATE: 1994-04-18 | PRIOR PLILING DATE: 1994-04-18 | PRIOR PLILING DATE: 1994-04-18 | PRIOR PLILING DATE: 1994-06-13 | PRIOR PLILING DATE: 1994-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE: OTHER INPORMATION: Description of Unknown Organism: putative NF-AT OTHER INPORMATION: binding site US-027-232-346-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 11.4%; Score 14.8; DB 1; Length 20; Best Local Similarity 88.9%; Pred. No. 6; Matches 16; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.9%; Pred. No. 6;
Matches 16; Conservative 0; Mismatches 2; Indels
                                                                                     NAME/KEY: misc_feature

| NAME/KEY: misc_feature

| COATION: 1..20

| OTHER INFORMATION: /note= "Purine Rich Core Sequence"

US-08-507-032-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1394 AAAGGAGGTAAAATTGTT 1411
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       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
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US-06-507-032-3

US-06-507-032-3

Sequence 3, Application US/08507032

Patent No. 599810

REREAL INFORMATION:
APPLICANT: Flanagan, William A. APPLICANT: Crabtree, Geraid R.
TITLE OF INVENTION: Agents

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco
CITY: San Francisco
STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco
STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco
STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco
STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco
STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco
STREET: ADPRESSE:
ADPLICATION NUMBER: PCDOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CLASSIFICATION NUMBER: US/08/228,944

PILING DATE: 22-AUG-1991

RELEVANCE CARRACTERISTICS:
RERERENCE/DOCKET NUMBER: 30,223

REGISTRATION FOR SEC ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 Dase Pairs

TTELETAX: ALSO-1901

TTELETAX: ALSO-1901

TTELETAX: ALSO-1001

TTELETAX: ALSO-10
US-09-527-154-21/C
US-09-527-154-21/C
Sequence 21, Application US/09527154
| Petent No. 6228648
| GENERAL INFORMATION:
| APPLICANT: Phomas P. Condon
| APPLICANT: Thomas P. TITLE OF INVENTION: APPLICANT: Thomas P. Condon
| APPLICANT: Thomas P. Con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
11.7%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.8;
Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTHER INFORMATION: Antisense Oligonucleotide US-09-527-154-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1424 TCGTTCTATGCAGACATATA 1443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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US-09-422-978-5909/c
US-09-422-978-5909/c
US-09-422-978-5909/c
Sequence 5909, Application US/09422978
Sequence 5909, Application US/09422978
Sequence 5909, Application US/09422978
Sequence 5909, Application US/09422978
APPLICANT: Chanker Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chunakov, 112, 020001
TITILE OF INTENDITYON Biallelic markers for use in constructing a high density...
TITILE OF INTENDITYON UNMER: US/09/422,978
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
SEARLIER APPLICATION NUMBER: US 60/109,732
SARLIER PILING DATE: 1998-11-23
SEARLIER FILING DATE: 1998-12-23
SEARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 5909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: upstream amplification primer 99-7737 for SEQ 1975, US-09-422-978-5909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.8%; Score 14; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 7.9; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                      CITY: Seattle
CINNTRY: Seattle
CONTRY: Mashington
CONTURY: Us
ZIP: 98104-7092
COMPUTER: FLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pacentin Release #1.0, Version #1.25
SOFTWARE: Pacentin Release #1.0, Version #1.25
SOFTWARE: PACENTIN DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/270,956
FILING DATE: 17-MAR-1999
CLASSIFICATION: NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 33,963
REJERENCE/DOCKET NUMBER: 24005
TELECOMMUTICATION NUMBER: 2400
TELEFAX: (206) 622-490
TELEFAX: 7323836
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1,
                 ORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 13.8; DB
Pred. No. 9.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.6%;
88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid

STRANDENES: single

TOPOLOGY: linear

US-09-270-956-31
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: primer_bind
LOCATION: 1..19
TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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10.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 8.1;
Matches 16; Conservative 0; Mismatches 3; Indels
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10.8%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-08-432-971C-31

Sequence 31, Application US/08432871C

Patent No. 5877010

GENERAL INFORMATION:
APPLICANT: Loeb, Lawrence A.
APPLICANT: Black, Margaret E.
TITLE OF INVENTION: 114YMIDINE KINASE MUTANTS
NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:
ADDRESSE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: Bashington
COUNTER: Washington
COUNTER: Washington
COUNTER: TEMP FC compatible
OFFRATISH SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM:
MEDIUM TYPE: Flupy disk
OFFRATISH SYSTEM: PC-DOS/MS-DOS
COMPUTER: PatentIn Release #1.0, Version #1.25
COMPUTER: APPLICATION NUMBER: US/08/432,871C
TELECOMMUTICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 31, Application US/09270956
Patent No. 6451571
GENERAL INFORMATION:
APPLICANT: Loeb, Lawrence A.
APPLICANT: Black, Margaret E.
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
                                                                                                                                                                                                                                                              1354 GAAAATATTCCACGCATC 1372
                                                                                                                                                                                                                                                                                                               20 GAAAAAATGCGACGCATC 2
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                                                         TYPE: DNA
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GTTAATGATGACCA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: 18 base pairs
nucleic acid
DEDNESS: single
XGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic
STRANDEDNESS:
                                                                                               ; UKGANISH: CHILLING US-09-198-452A-3773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-432-871C-31
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US-09-270-956-31
        ; SEQ ID NO 3773
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Gaps
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Sequence 113, Application US/08998099A;
Facent No. 6103890.
GENERAL INFORMATION:
APPLICANT: JARVIS, THALE
APPLICANT: MCSWIGGEN, JAMES A.
TILLE OF INVENTION: BNZYMATIC NUCLEIC ACID TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
TITLE OF INVENTION: 231/175
CURRENT PELLING DATE: 1997-12-24
EARLIER APPLICATION NUMBER: 60/037,658
EARLIER APPLICATION NUMBER: 60/037,658
EARLIER PILING DATE: 1995-01-13
EARLIER FILING DATE: 1995-01-13
EARLIER FILING DATE: 1995-01-13
EARLIER FILING DATE: 1994-05-18
NUMBER OF SEQ ID NOS: 375
SOFTWARE FEATSER FUNDANCE: 375
LENGTH 17
LENGTH 17
LENGTH 17
                          GREAL INCOMPATION:
GREAL INCOMPATION:
GREAL INCOMPATION:
APPLICANT: JORGAN JAMES A.
APPLICANT: MCSNIGGEN, JAMES A.
APPLICANT: MCSNIGGEN, JAMES A.
APPLICANT: STINCHCOME, JAM T.
TITLE OF INVENTION: CR CONDITIONS RELATED TO LEVELS OF C-FOS
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
FILE REPERENCE: 231/172
CURRENT APPLICATION NUMBER: US/08/998, 099A
CURRENT APPLICATION NUMBER: 06/037,658
EARLIER APPLICATION NUMBER: 08/037,658
EARLIER APPLICATION NUMBER: 08/037,124
EARLIER APPLICATION NUMBER: 08/037,124
EARLIER APPLICATION NUMBER: 08/037,134
EARLIER APPLICATION NUMBER: 08/037,134
EARLIER PRILING DATE: 1994-01-13
NUMBER OF SEQ ID NOS: 375
SEQ ID NO 112
LENGTH: 17
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9.5%; Score 12.4; DB 1; Length 17;
Best Local Similarity 57.1%; Pred. No. 17;
Matches 8; Conservative 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
9.5%; Score 12.4; Di
Best Local Similarity 57.1%; Pred. No. 17;
Matches 8; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 114, Application US/08998099A, Patent No. 6103890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1423 GTCGTTCTATGCAG 1436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GUCCUUCUAUGCAG 16
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4 GUCCUUCUAUGCAG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Homo sapiens
US-08-998-099-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: RNA
CAGANISM: Homo sapiens
US-08-998-099-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-08-998-099-114
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US-08-998-099-113
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US-09-344-520-37/C
; Sequence 37, Application US/09344520
; Sequence 37, Application US/09344520
; Patent No. 6037176
; Patent No. 6037176
; GENERAL INFORMATION:
; APPLICANT: Breat P. Monia
; APPLICANT: Breat P. Monia
; APPLICANT: Breat P. Monia
; PILE REPRENCES: RTS-0070
; CURRENT APPLICATION NUMBER: US/09/344,520
; CURRENT PELLING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 37
; LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Krailer, Kenneth
APPLICANT: Vogeletein, Bert
APPLICANT: Vogeletein, Bert
APPLICANT: Applicant: Abricant, Wei
TILLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
TILLE OF INVENTION: Cancer Cells
TILLE OF INVENTION: Cancer Cells
FILE REFERENCE: 01107-74664
CURRENT PELLING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: 60/047,352
EARLIER FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 871
SOFTWARE: FastSEQ for Windows Version 3.0
SET ID NO 628
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
10.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 3; Indels
  Indels
  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-344-520-37
  0; Mismatches
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US-08-998-099-112
* ; Sequence 112, Application US/08998099A
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Patent No. 6333152
GENERAL INFORMATION:
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                                               1354 GAAAATATTCCACGCA 1370
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                                                                                       19 GAAAAATAGTACACGCA
     15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-081-646-628
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       Matches
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APPLICANT: Draper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 26.7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
ZIP: 9007
ZIP
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEFAX: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 1637:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: TOPOLOGY: linear
US-08-373-124A-1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1637, Application US/08435628; Patent No. 5817796; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1380 ATCGTCTTCTGATCAAA 1396
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US-08-435-628-1637
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         GENERAL INFORMATION:
APPLICANT: JARLE
APPLICANT: JARLE
APPLICANT: JARLE
APPLICANT: MCSWIGGEN, JAMES A.
APPLICANT: MCSWIGGEN, JAMES A.
APPLICANT: MCSWIGGEN, JAMES A.
APPLICANT: MCSWIGGEN, JAMES A.
TITLE OF INVENTION: ENCYMATIC NUCLEIC ACID TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
FILE REPERBOR: 231/15
CURRENT PELLING DATE: 1997-12-24
EARLIER APPLICATION NUMBER: 60/037,658
EARLIER FILING DATE: 1997-01-13
EARLIER FILING DATE: 1995-01-13
EARLIER FILING DATE: 1995-01-13
EARLIER FILING DATE: 1995-01-13
SARILER FILING DATE: 1994-05-18
NUMBER OF SEQ ID NOS: 375
SOFTWARE: FASISEQ for Windows Version 3.0
ENGINE PASISED TO NO 114
LENGTH: 17
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USECULATOR APPLICATION US/08373124A

SEQUENCE 1637, Application US/08373124A

SEQUENCE 1037, Application US/08373124A

PAPLICANT: Stinchcomb, Dan T.

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Jarvis, Thale

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: TREATMENT OF RESTENCES AND TITLE OF INVENTION: TREATMENT OF RESTENCES.

CORRESPONDENCE ADDRESS:

ANDRESSE: Lyon & Lyon

STREET: Silve 4700

STREET: Galde 4700

STREET: Galde 4700

STREET: Galdenia

COUNTRY: U.S.A.

CONTRY: U.S.A.

MEDIUM TYPE: Storage

OCHUTER READABLE FORM:

MEDIUM TYPE: Storage

OCHUTER: DEM COMPACALION

OCHUTER READABLE FORM:

MEDIUM TYPE: STORAGE

OCHUTER: DEM COMPACALION

OCHUTER: DEM COMPACALION

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/373,124A

FILING DATE: MAY 13, 1994

APPLICATION NUMBER: US/986,422

FILING DATE: PED-TARY 7, 1992

APPLICATION NUMBER: US/936,422

FILING DATE: DATE: AUGUST 10,994

APPLICATION NUMBER: US/936,422

FILING DATE: PED-TARY 7, 1992

APPLICATION NUMBER: US/936,422

FILING DATE: PED-TARY 7, 1992

APPLICATION NUMBER: US/936,422

FILING DATE: US D
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1 GUCCUUCUAUGCAG 14
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; ORGANISM: Homo sapiens
US-08-998-099-114
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Query Match 9.4%; Score 12.2; DB 1; Length 17; Best Local Similarity 64.7%; Pred. No. 18; Matches 11; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                        RESULT 16
US-08-584-040-5557
Sequence 5557, Application US/08584040
Fatent No. 634638
GENERAL INFORMATION:
APPLICANT: Pavoo, Pamela
APPLICANT: Revigen, James
APPLICANT: Estochecomb, Dan T.
APPLICANT: Estochecomb, Dan T.
APPLICANT: Estochedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: OR UNSCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWIT PACTOR
ANDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: 0.5.A.

IPP: 90071-2066

COMPUTER READABLE FORM:
WEDLUM TYPE: 3.5." Diskette, 1.44 Mb
MEDLUM TYPE: Storage
COMPUTER: IBM Compatible
OCHUPITER: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U996
FILING DATE: January 11, 1996
CLASSIPICATION NUMBER: U996
FILING DATE: January 11, 1996
FILING DATE: January 11, 1996
ATORNEY/AGENT INFORMATION:
MAME: WALDAIG ALCOMER 32, 327
REPERSENCE/OCET NUMBER: 32, 327
REPERSENCE/
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US-08-584-040-5854/c
; Sequence 5854, Application US/08584040
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                                                                                                                                                                1395 AAGGAGGTAAAATTGTT 1411
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Best Local Similarity 70.61
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
1 TOPOLOGY: linear
US-08-584-040-5557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
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Sequence 208, Application US/0875587
Sequence 208, Application US/0875587
Sequence 208, Application US/0875587
Sequence 208, Application US/0875587
Septicont: Futual, Finilip A
APPLICANT: Mooster, Michael R
APPLICANT: Ashorth, Alan
APPLICANT: Ashorth, Alan
APPLICANT: Stratton, Michael R
TITLE OF INVENTION: Identification and sequencing of the ERCA canc
TITLE OF INVENTION: Association of the ERCA canc
TITLE OF INVENTION DATA:
COMPUTER REadbale FORM:
COMPUTER READBALE FORM:
SOFTWARY: USA
COMPUTER: Ploppy disk
COMPUTER: Ploppy
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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9.4%; Score 12.2; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 18;
Matches 9; Conservative 5; Mismatches 3; Indels
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OTHER INFORMATION: /note= "N is i"
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LOCATION: 9
COTHER INFORMATION: /note= "N is i"
US-08-755-587-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1380 ATCGTCTTCTGATCAAA 1396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | INFORMATION FOR SEQ ID NO: 1 | SEQUENCE CHARACTERISTICS: | LENGTH: 17 base pairs | TYPE: mucleic acid | TYPE: mucleic acid | STRANBEDRESS: single | TOPOLOGY: linear US-08-435-628-1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
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RESULT 19
US-09-371-772B-2713/c
is Gequence 2713, Application US/09371772B
sequence 2713, Application US/09371772B
sequence 2713, Application US/09371772B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Barco, Pam
APPLICANT: Brinchowh, Dan
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION NUMBER: US/09/371.772B
TITLE REPERENCE: MBHB00,976-08-10
FILE REPERENCE: 1995-10-26
CURRENT FILING DATE: 1995-10-26
FRIOR FILING DATE: 1995-10-26
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2713
LENGTH: 17
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9.4%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 18;
Matches 12; Conservative 2; Mismatches 3; Indels
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Sequence 105, Application US/08319492B

Patent No. 561468

GENERAL INFORMATION:
APPLICANT: Stinchoub, Dan T.
TITLE OF INVENTION: RIGHCAME TREATMENT OF DISEASES

TITLE OF INVENTION: R. ROCYME TREATMENT OF DISEASES

TITLE OF INVENTION: OF CONDITIONS RELATED TO LEVELS

TITLE OF INVENTION: OF IL-5

NUMBER OF SEQUENCES: 751

NUMBER OF SEQUENCES: 751

STREET: 633 West Fifth Street
                          PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-110-26
PRIOR PELICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1396-01-08
NUMBER OF SEQ ID NOS: 14225
SEQ ID NO 2447
LENGTH: 17
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Best Local Similarity 82.49
Matches 14, Conservative
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; ORGANISM: Mus sp.
US-09-371-772B-2713
                                                                                                                                                                                                                                                            ; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2447
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US-003-371-772B-2447
US-003-371-772B-2447
Sequence 2447, Application US/09371772B
Fatent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, Jim
APPLICANT: Escobed, Dan
APPLICANT: Escobed, Jaime
TITLE OF INVENTION: Method of Vascular Endothelial Growth Factor Receptor
FILE REPERBRECE: MBHB00, 976-07 (2377/198)
FILE REPERBRECE: WHBH00, 976-07 (2377/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
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PATENT NO. 6346398

GENERAL INFORMATION:
APPLICANT: Bavoo. Pamela
APPLICANT: Stinchcomb, Dan T.
APPLICANT: CHINENTION: TREATMENT OF INSEASES OR
TITLE OF INVENTION: TREATMENT OF INSEASES
TITLE OF INVENTION: OF VASCULAR ELATED TO LEVELS
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 6502
CORRESPONDENCE ADDRESSS:
ADDRESSE: Lyon & Lyon
STREET: 631 West Fifth Street
COMPUTER: ELONGARIAE FORM:
MEDIUM TYPE: 31.5" Diskette, 1.44 Mb
MEDIUM TYPE: 10071-2066
COMPUTER: PREFICATION DATA:
COMPUTER: PREFICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: OCCOBER 26,1995
ATTORNEY ARBITCATION DATA:
APPLICATION NUMBER: 05/005,974
FILING DATE: OCCOBER 26,1995
ATTORNEY AGREY INFORMATION:
NAME: Warberg, Richard J.
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.4%; Score 12.2; DE
Best Local Similarity 82.4%; Pred. No. 18;
Matches 14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1346 CAGGGGAAGAAAATAT 1362
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US-08-584-040-5854
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Gaps
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                                                                                                                                                   Sequence 7, Application US/07906930E

Patent No. 5534631

GENERAL INFORMATION:
APPLICANT: GAYOR, Richard B.
APPLICANT: Nirula, Ajay
APPLICANT: Li, Ching
TITLE OF INVENTION: PACTOR (ILF)
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CONTRET: P. O. Box 4433
COUNTRY: USE
COUNTRY: TAXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

8.8%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 23;
Matches 12; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 23
US-08-363-240A-72
Sequence 72, Application US/08363240A
PALENE NO. 5705388
GENERAL INFORMATION:
APPLICANT: COULULE. Larry
APPLICANT: McSwiggen, James
APPLICANT: Biggaier, Charles
APPLICANT: Biggaier, Charles
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: PROGRESSION AND REGRESSION
TITLE OF INVENTION: OF VASCULAR DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-07-906-930E-7
                           1433 GCAGACATATACATG 1447
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                                                              15 Gradacagaracard 1
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                                                                                                                               RESULT 22
US-07-906-930E-7
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US-09-081-646-267/c
| Sequence 267, Application US/09081646
| Patent No. 6333152
| GRNERAL INFORMATION
| APPLICANT: Kinzler, Kenneth
| APPLICANT: Zhang, Lin
| APPLICANT: Zhang, Lin
| APPLICANT: Zhang, Lin
| TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
| TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
| TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
| TITLE OF INVENTION: Gene Cells
| TITLE OF INVENTION: Cancer Cells
| TITLE PERPLICATION NUMBER: 60/047,352
| EARLIER FILING DATE: 1997-05-20
| BARLIER FILING DATE: 1997-05-21
| SOFTWARE: Factor Onco: 471
| SOFTWARE: Factor Onco: 471
| SOFTWARE: Factor Onco: 471
| SOFTWARE: Factor Mindows Version 3.0
| SEQ ID NO 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER: READALE FORM:
MEDIUM TYPE: Storage
COMPUTER: READALE FORM:
MEDIUM TYPE: BROCAGE S.0
SOFWATER: MACOMPATION DATA:
SPELICATION NUMBER: U.S.08 5.0
SOFWATER: October 7, 1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 05/08/989
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989, 849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WAIDING: RICHARD
REFERENCE/DOCKET NUMBER: 209/276
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELERA: 67-3510
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LEMOTH: 15 base pairs
TYPE: nucleic acid
STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
9.1%; Score 11.8; Distriction 11.8; Distriction Similarity 60.0%; Pred. No. 19; Maraches 9; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1357 AAATATTCCACGCAT 1371
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1 AAAUAUUUCAGGCAU 15
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; ORGANISM: Homo sapiens
US-09-081-646-267
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US-08-319-492B-105
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Gaps
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US-08-74-829-1
Sequence 1, Application US/08744829
Sequence 1, Application US/08744829
Sequence 1, Application US/08744829
Sequence 1, Application US/0874829
Sequence 1, Application Galli, Gullano
APPLICANT: GALLI, GILLIANO
APPLICANT: CARPANTINI, RENATA
APPLICANT: CARPANTINI, GILDO
TITLE OF INVENTION: D-ALPHA-AMINO ACIDS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: D-C.
ADDRESSEE: D-C.
ADDRESSEE: P-C.
AD
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8.8%; Score 11.4; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 23;
Matches 8; Conservative 4; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER. IEBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Parcentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,829
FILING DATE: 06-NOV-1996
CLASSIFICATION NUMBER: IT 002432 95/A
FILING DATE: 23-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 22,418
REGISTRATION NUMBER: 22,418
REGISTRATION NUMBER: 22,418
REGISTRATION NUMBER: 22,418
REFERENCE/DOCKET NUMBER: 2264-142-0
TELECHOMINICATION INFORMATION:
TELECHOMINICATION INFORMATION:
TELECHOMINICATION INFORMATION:
TELECHOMINICATION INFORMATION:
SOFTWARE: WORD FELL.
CURRENT APPLICATION DATA:
APPLICATION NAMES: US/08/363,240A
FILING DATE: December 23, 1994
FILING DATE: December 23, 1994
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WARDING RICHARD 32,327
REGERRANCE/DOCKET NUMBER: 210/096
TELECHONICATION INFORMATION:
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELBFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1446 TGGAAGATGGGTT 1458
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US-08-363-240A-246
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Batent No. 5706388

GENERAL INFORMATION:
APPLICANT: Coutture, Larry
APPLICANT: Biggaier, Charles
APPLICANT: De INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: PROGRESSION AND REGRESSION
TITLE OF INVENTION: OF VASCULAR DISEASES
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
CHARLESEE LYON & LYON
                                     NUMBER OF SEQUENCES:

ONDRESSEE: Lyon & Lyon STREET: 633 West Fitch Street STREET: 632 West Fitch Street STREET: 631 West Fitch Street STREET: 631 Mest Fitch Street STREET: 631 Mest Fitch Street STREET: 631 Mest Fitch Street STREET: 630 West Fitch STREET: 631 West Fitch STREET: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1455 GGTTGATCAAGCA 1467
                               NUMBER OF SEQUENCES: 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGUGGAUCAAGCA 13
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Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-363-240A-246
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US-08-363-240A-72
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Sequence 75, Application US/09580794C

Sequence 75, Application US/09580794C

Patent No. 6331389

GRERAL INFORMATION:
APPLICANT: Louwerie, Joost

APPLICANT: Louwerie, Joost

APPLICANT: Louwerie, Joost

APPLICANT: Louwerie, Joost

TITLE OF INVENTION: METHOD FOR DETECTION OF DRUG-INDUCED MUTATIONS IN THE REVERSE

TITLE OF INVENTION: TRANSCRIPTASE GENE

TITLE OF INVENTION: PARACRIPTASE GENE

TITLE OF INVENTION: TRANSCRIPTASE GENE

TITLE OF INVENTION: TOOP 05-13

PRIOR APPLICATION NUMBER: 08/913

PRIOR PILING DATE: 1997-00-17

PRIOR PILING DATE: 1997-01-17

PRIOR PILING DATE: 1996-01-26

PRIOR PILING DATE: 1996-01-26

PRIOR PILING DATE: 1996-01-26
APPLICANT: LOUWAGIE, JOOST
APPLICANT: LOUWAGIE, JOOST
ATTLE OF INVENTION: METHOD FOR DETECTION OF DRUG-INDUCED
TITLE OF INVENTION: MUTATIONS IN THE REVERSE TRANSCRIPTASE GENE
NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                  ADDRESSE:
ANDLEAM
ADDRESSE:
ANDLOL, WHITE & DURKEE
ADDRESSE:
ANDLOL, WHITE & DURKEE
CITY: HOUSTON
STRATE: PEAAS
COUNTER: TEAAS
COUNTER: TEAAS
COUNTER: TEAAS
COUNTER: TABA PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: POT/89913,833
APPLICATION NUMBER: USP 96913,833
PRIOR APPLICATION NUMBER: EP 96870005.4
FILING DATE: J7 Jan 1997
PRIOR APPLICATION NUMBER: EP 9687001
PRIOR APPLICATION NUMBER: BP 9687001.5
FILING DATE: Z5 Jan 1996
ATTORNEY/AGENT INFORMATION:
NAME: KARMERER, PATRICIA A.
REGISTRATION NUMBER: BP 9687008.5
FILING DATE: S Jun 1996
ATTORNEY/AGENT INFORMATION:
NAME: KARMERER, PATRICIA A.
REGISTRATION NUMBER: BP 9687008.5
FILING DATE: S Jun 1996
ATTORNEY/AGENT INFORMATION:
NAME: KARMERER, PATRICIA A.
REGISTRATION NUMBER: BP 9687008.5
FILING DATE: BASE DATE
TING BATTORNERE, PATRICIA A.
REGISTRATION NUMBER: BP 9687008.5
FILING DATE: LS DAS PATRICIA A.
REGISTRATION NUMBER: BP 9687008.5
FILING DATE: BASE PATRICIA A.
REGISTRATION NUMBER: BP 9687008.5
FILING DATE: BASE PATRICIA A.
REGISTRATION NUMBER: BP 9687008.5
FILING DATE: BASE PATRICIA A.
REGISTRATION NUMBER: BP 9687008.5
FILING DATE: BASE PATRICIA A.
REGISTRATION NUMBER: BP 9775
REFERENCE CHARACTERISTICS:
LENGTH: LENGTH: LUCLEIC ACIA
CTPERATING DATE: BASE PATRICIA A.
REFERENCE CHARACTERISTICS:
LENGTH: LS DAS PATRICIA A.
REPERENCE CHARACTERISTICS:
LENGTH: LS DAS PATRICIA A.
REPRENCE PATRICIA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
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Best Local Similarity 92.33
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 ATACATGGACGAT 15
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MOLECULE TYPE: DN
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 28
US-09-580-794C-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
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US-08-364-246-1
Sequence 1, Application US/08364246
Factor No. 5872104
GENERAL INFORMATION:
APPLICANT: Schwartz, Dennis
TITLE OF INVENTION: Combinations and Methods For Reducing
TITLE OF INVENTION: Antimicrobial Resistance
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.8%; Score 11.4; DB 1; Length 15; 92.3%; Pred. No. 23; 1; Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                           DB 1; Length 15;
                                                                                                                                                                                                                                                                                                                                                                    Indels
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COUNTRY: United social country of the countr
                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                  Query Match
8.8%; Score 11.4; Dl
Best Local Similarity 92.3%; Pred. No. 23;
Matches 12; Conservative 0; Mismatches
    JENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLAGY: linear
MOLECULE TYPE: other nucleic acid
US-08-744-829-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-913-833-75; Sequence 75, Application US/08913833; Patent No. 6087093; Patent No. GORNATION: APPLICANT: STUYVER, LIEVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1350 GGAAGAAAATAT 1362
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Best Local Similarity 92.3%
Matches 12; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-364-246-1
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RESULT 31
US-09-081-660/c
US-09-081-66. Application US/09081646

Sequence 860, Application US/09081646

Patent No. 6333152

GENERAL INCORATION:
APPLICANT KINZIAD

TITLE OF INVERTION: Gene Expression Profiles in No. 6333152mal and
TITLE OF INVERTION: Gene Cells

TITLE REFERENCE: 0107.74664

CURRENT APPLICATION: Cancer Cells

TITLE REPERINCS: 01107.74664

CURRENT FILING DATE: 1998-05-20

EARLIER PLICATION: 0379-05-21

NUMBER OF SEQ ID NOS: 871-05-21

NUMBER OF SEQ ID NOS: 871-05-21

SEQ ID NO 860

EMBETTION: 155

MANTHER PRINCE: 155
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US-08-913-313-76
JOSEPH TO SEQUENCE 76, Application US/08913833
JEACHT NO. 6087033
JEACHT NO. 6087033
JEACHT NO. 6087033
JEACHT NO. 6087031
JEACHT NO. 6087031
JEACHT NO. 6087031
JEACHT STUDYER, LIEVER
APPLICANT: LOUMAGIE, JOOST
JITLE OF INVENTION: MUTATIONS IN THE REVERSE TRANSCRIPTASE GENE
TITLE OF INVENTION: MUTATIONS IN THE REVERSE TRANSCRIPTASE GENE
MUMBER OF SEQUENCES:
JEACHT NO. BOX 4433
CITY: HOUSTON
STARET: P.O. BOX 4433
CITY: HOUSTON
JEACHT NO. BOX 4433
JEACHT NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6.0 / ASCII text output
CURRENT APPLICATION NUMBER: US/08/913,833
FILING DATE: 15 Sep 1997
PRING DATE: 15 Sep 1997
                                                                                                                                                                   Query Match 8.8%; Score 11.4; DB 1;
Best Local Similarity 92.3%; Pred. No. 23;
Matches 12; Conservative 0; Mismatches 1;
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Best Local Similarity 92.3%; Pred. No. 23;
Matches 12; Conservative 0; Mismatches
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CORGANISM: Homo sapiens
US-09-081-646-860
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-210
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Patent No. 6333152

GENERAL INCRAMITION

APPLICANT: Kinzler, Kenneth

APPLICANT: Zhang, Lin

TITLE OF INVENTION: Gencer Cells

TITLE OF INVENTION: Gencer Cells

FILE REFERENCE: 01107, 7464

CURRENT APPLICANT: 1399-05-20

EARLIER PETLING DATE: 1997-05-21

NUMBER OF SEQ ID NOS: 877

SEQ ID NOS: 100

SEQ ID NOS: 100

ENGINE FASTESEQ for Windows Version 3.0

SEG ID NOS: 100

SERVITE: 1597-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Sequence 1977, Application US/09081646 |
| Sequence 1977, Application US/09081646 |
| Parent No. 6333152 |
| General District Control of Cont
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                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-580-794C-75
     PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 164
SOFTWARE: PatentIn version 3.0
SEQ ID NO 75
LENGTH: 15
                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1444 CATGGAAGATGGG 1456
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; ORGANISM: Homo sapiens
US-09-081-646-197
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US-09-081-646-210/c
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US-09-081-646-197
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US-07-704-288C-26

Sequence 26, Application US/07704288C

Patent No. 5399680

GENERAL INFORMATION:

APPLICANT: LAME, CHRISTOPHER J.

APPLICANT: LAME, CHRISTOPHER J.

TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE

TITLE OF INVENTION: LEMENTS

NUMBER OF SEQUENCES: 26

CORRESSEE: PRETT'S SCHROEDER, BRUEGGEMANN & CLARK

STREET: 444 SOULH Flower Street, Suite 2000

CITY: Los Angeles

COUNTRY: United States

ZIP: 9007-2221

COMPUTER: READABLE FORM:

MEDIUM TYPE: Ploppy disk

COUNTRY: United States

SOFTWARE: PatentIn Release #1.0, Version #1.25

CUMPUTER: PatentIn Release #1.0, Version #1.25

CLASSIFICATION NUMBER: US/07/704,288C

FILING DATE: 22-MAY-1991

CLASSIFICATION NUMBER: 31,192

REGISTRATION NUMBER: 31,192

REGISTRATION NUMBER: 31,193

RESTERRORE/DOCKET NUMBER: 31,193

RESTERRORE/DOCKET NUMBER: 31,193

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION NUMBER: 31,293

TELECOMMUNICATION NUMBER: 31,293
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Sequence 26, Application US/08379259;
Patent No. 565939
GENERAL INFORMATION:
APPLICANT: LAMB, QUN
TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
TITLE OF INVENTION: BLEMENTS
TITLE OF INVENTION: BLEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREFT: 444 SOUTH Flower Street, Suite 2000
CITY: LOS ANGELS
STATE: California
COMPTRY: United States
ZIP: 90071-2921
ZIP: 90071-2921
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INPOLATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
FYPE: nucleic acid
STRANDEDNESS: single
FYPE: TOPOLOGY: linear
MOLECULE TYPE: NO
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-704-288C-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1431 ATGCAGACATATACAT 1446
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US-08-379-259-26
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SEQUENCE 76, Application US/09580794C

Patent No. 6331389

GENERAL INFORMATION:

APPLICANT: SULVEY. Lieven

APPLICANT: LOUWAGIE, JOOST

TITLE OF INVENTION: METHOD FOR DETECTION OF DRUG-INDUCED MUTATIONS IN THE REVERSE

TITLE OF INVENTION: METHOD FOR DETECTION OF DRUG-INDUCED MUTATIONS IN THE REVERSE

TITLE OF INVENTION: METHOD FOR DETECTION OF DRUG-INDUCED MUTATIONS IN THE REVERSE

TITLE OF INVENTION: METHOD FOR DETECTION OF DRUG-INDUCED MUTATIONS IN THE REVERSE

TITLE OF INVENTION: METHOD FOR DETECTION OF DRUG-INDUCED MUTATIONS IN THE REVERSE

TITLE OF INVENTION NUMBER: US/09/580,794C

CURRENT FILING DATE: 1997-09-15

PRIOR FILING DATE: 1997-01-17

PRIOR FILING DATE: 1996-06-25

NUMBER OF SEQ ID NOS: 164

SOFTWARE: PATENTIN VERSION 3.0
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8.8%; Score 11.4; DB 1; Length 16;
Best Local Similarity 92.3%; Pred. No. 25;
Matches 12; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.8%; Score 11.4; DB 1; Length 16; Best Local Similarity 92.3%; Pred. No. 25; Matches 12; Conservative 0; Mismatches 1; Indels
APPLICATION NUMBER: PCT/EP97/00211
FILING DATE: 17 Jan 1997
PRIOR APPLICATION DATE:
APPLICATION NUMBER: EP 96870005.4
FILING DATE: 26 Jan 1996
PRIOR APPLICATION DATE:
APPLICATION NUMBER: EP 9687081.5
FILING DATE: 25 Jan 1996
ATTOREY/AGANT INFORMATION:
NAME: KAWMERER, PATICIA A.
REGISTRATION NUMBER: 29,775
REPERRINCE/DOCKET NUMBER: 3,775
REPERRINCE/DOCKET NUMBER: 3,775
REPERRINCE/DOCKET NUMBER: 1NNS:008
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: NOAECULE TYPE: NOA (genomic)
HYPOTHETICAL: NO
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; ORGANISH: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-580-794C-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1441 ATACATGGAAGAT 1453
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HYPOTHETICAL: NO
JANTI-SENSE: NO
US-08-913-833-76
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Sequence 296, Application US/08173489C
Patent No. 5861244
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1.50-09-479-005A-61

2.50-479-105A-61

2.50-40-479-005A-61

3.50-40-479-005A

3.50-40-479-005A

3.50-40-470-61

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pacentin Release #1.0, Version #1.25
SOFTWARE: Pacentin Release #1.0, Version #1.25
CURRENT APPLICATION NOMBER: US/08/379,259
FILING DATE:
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Relear's Glephen B:
REGISTRATION NUMBER: 91,192
REFERENCE/DOCKET NUMBER: 91,192
REFERENCE/DOCKET NUMBER: 91,192
TELECOMMUNICATION INFORMATION:
TELEFRONE: (619) 546-4337
TELEFRONE: (619) 546-4337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.0%; Pred. No. 28;
Matches 12; Conservative 1; Mismatches
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MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-379-259-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 16 Dase pairs TYPE: nucleic acid STRANDEDNESS: single TOOPLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 37
US-08-173-489C-296/c
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US-09-375-673B-6
Sequence 6, Application US/09375673B
Patent No. 6605431
Sequence BEREAL INFORMATION:
APPLICANT: GOURSE, RICHARD L.
APPLICANT: BSTREM, SHAWN T.
APPLICANT: ROSS, WILMA E.
APPLICANT: GALL, TANAS
ITTLE OF INVENTION: PROMOTER ELEMENTS AND METHODS OF USE
FILE REPERRANCE: 11900130101
CURRENT APPLICATION NUMBER: US/09/375,673B
CURRENT PLING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.5%; Score 11; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 20; Matches 11; Conservative 0; Mismatches 0; Indels
GENERAL INFORMATION:
APPLICANT: HEPBITRN A. G.
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICANT: HEPBITRN A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
COMPUTER READABLE FORM:
MEDIUM TYPE: 15 inch, 1.44Mb storage
CONTRY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
CONFUTER: IBM PC/XT/AT
COMPUTER: IBM PC/XT/AT
OFFRATING SYSTEM: WS.DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
COMPUTER: BORDIAN TYPE: 2. DEC 1993
CONFURENT APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION NUMBER: US/08/173,489C
FILING DATE: 20 CCT 1992
ATTORNEY/ABONT INFORMATION:
NAME: HANGEIMEN, USGEPH H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 26,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from C. psittaci
DESCRIPTION: 16s region in Seq ID No. 5861244295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: no
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 296 :FROM 1 TO 11
US-08-173-489C-296
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STRANDEDNESS: single stranded
TOPOLOGY: linear
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                                                                                        Length 14;
                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                RESULT 41
UG-08-319-492B-104
) Sequence 104 Application US/08319492B
) Patent No. 561648B
) GENERAL INFORMATION:
APPLICANT: SUllivan, Sean M. APPLICANT: Sullivan, Sean M. APPLICANT: Stinchcomb, James
APPLICANT: Stinchcomb, Dan T.
ITILE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
ITILE OF INVENTION: OF IL-5
ITILE OF INVENTION: OF IL-5
INVENTION: ALONESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Sulfet 4700
STREET: California
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ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 15.0 biskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM COMPATIAL
COMPUTER: IBM COMPATIAL
COMPUTER: IBM COMPATIAL
CORRENT APPLICATION DATA: 1994
PRIOR APPLICATION DATA: 100404
PRIOR APPLICATION DATA: 100104
PRIOR APPLICATION DATA: 100104
PRIOR APPLICATION DATA: 100104
PRIOR APPLICATION DATA: 100104
PRIOR APPLICATION DATA: 100799, 949
PRILING DATE: COMPAT: 100799, 949
PILING DATE: DECEMBER: 1993
APPLICATION NUMBER: 08/008, 895
FILING DATE: BECEMBER: 1992
ATTORNEY AGBNIT INFORMATION:
NAWE: WAIDLIG, RICHARD
REGISTRATION NUMBER: 20,9276
TELEPRAX: (213) 955-0440
TELEPRAX: (7-3510
TELEPRAX: (7-35
                                                                                        DB 1;
OTHER INFORMATION: accessory promoter element
                                                                                 Query Match 8.3%; Score 10.8; D
Best Local Similarity 85.7%; Pred. No. 29;
Matches 12; Conservative 0; Mismatches
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STRANDEDNESS: single
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US-08-319-492B-104
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                            US-09-375-673B-27
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US-09-375-673B-27/C
| Joaquence 27, Application US/09375673B
| Patent No. 666541
| GENERAL INFORMATION:
| APPLICANT: GOURSE, RICHARD L.
| APPLICANT: BOYER, SHAWN T.
| APPLICANT: BYTEM, SHAWN T.
| STOREM PRILING DATE: 1999-08-17
| JOHNBER OF SEQ ID NOS: 89
| SOFTWARE: PATENTIN VET. 2.1
| SEQ ID NO 27
| LENGTH. 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANIA: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Distal
                                                                                                                                FEATURE:
JOTHER INFORMATION: Description of Artificial Sequence: Distal
JOTHER INFORMATION: accessory promoter element
US-09-375-673B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

8.3%; Score 10.8; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 12; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                              Query Match

8.5%; Score 11; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 39
US-08-706-945D-86/C
Sequence 66, Application US/08706945D
Parent No. 636907
GENERAL INFORMATION:
APPLICANT: Boyle, William
APPLICANT: Galzone, Frank
APPLICANT: Calzone, Frank
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-79 GCIP
CURRENT PAPLICATION NUMBER: US/08/706,945D
CURRENT FILING DATE: 1996-09-03
PRIOR FILING DATE: 1996-12-22
NUMBER OF SEQ ID NOS: 145
SSOCIENTARE: Patentin version 3.1
SEQ ID NO 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Synthetic Oligonucleotide US-08-706-945D-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1408 TGTTAATGATGACC 1421
                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 TGTTAATGAGGATC 1
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       SEQ ID NO 6
LENGTH: 14
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US-08-452-724A-30
Sequence 30, Application US/08452724A
Sequence 30, Application US/08452724A
Sequence 30, Application US/08452724A
Sequence 30, Application US/08452724A
Sequence 30, Application Secure 30, Mutagenesis
TITLE OF INTENTION: Walk-Through Mutagenesis
TITLE OF INTENTION: Walk-Through Mutagenesis
MUNURER OF SEQUENCES: 59
CONTRESSOUNDERSES:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Amiltia Drive
CIT: Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 15;
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TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS TITLE OF INVENTION: OF IL-5
NUMBER OF SEQUENCES: 751
CORRESPONDENCE ADDRESS:
ADDRESSED: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 8uite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIDM TYPE: 3.5" Diskette, 1.44 Mb
MEDIDM TYPE: 3.5" Diskette, 1.44 Mb
MEDIDM TYPE: 3.5" Diskette, 1.44 Mb
MEDIDM TYPE: 5.0" Diskette, 1.44 Mb
MEDIDM TYPE: 1EM Compatible
COMPUTER: 1EM Compatible
COMPUTER: 1EM Compatible
COMPUTER: 1EM Compatible
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA: 109.44
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION NUMBER: 07/89,89
FILING DATE: December 7, 1992
ATTORNEY ADAIT: December 7, 1992
ATTORNEY ADAIT: December 7, 1992
ATTORNEY ADAIT: NUMBER: 209/276
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.3%; Score 10.8; D
85.7%; Pred. No. 31;
tive 0; Mismatches
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-319-492B-423
                                                                                                                                                                                                                                                                                                                                                                      90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                US-10:-119:-4924-106
Sequence 106, Application US/08319492B
Sequence 106, Application US/08319492B
Setent No. 561648
GENERAL INFORMATION:
SHILLY SHILLYAM, Sean M.
APPLICANT: SHILLYAM, Sean M.
APPLICANT: SHILLYAM, Sean M.
APPLICANT: SHICKNOW, Dan T.
TITLE OF INVENTION: RELOCATE TREATMENT OF DISEASES
TITLE OF INVENTION: OF IL-5
NUMBER OF SECUENCES: 751
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 613 Weat Fifth Street
STREET WORD PATE: 01993
FILING DATE: 01004 FIFTH STREET
FILING DATE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 43
US-08-319-492B-423/c
US-08-319-492B-423/c
Sequence 4123, Application US/08319492B
Parent No. 561648B
GENERAL INFORMATION.
APPLICANT: Sullivan, Sean M.
APPLICANT: McSwiggen, Zames
APPLICANT: McSwiggen, Zames
APPLICANT: Richardgen, Dan T.
APPLICANT: Sinchcomb, Dan T.
APPLICANT: Sinchcomb, Dan T.
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1358 AATATTCCACGCAT 1371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WORD PETECT 5.1
CURSENT APPLICATION DATA:
PILING DATE: AUGUST 17, 1994
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: December 7, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: DECEMBER: 7, 1992
ATTORNEY/AGENT INFORMATION:
NAMME: WARDLYS, AGCHART ON:
NAMME: WARDLYS, ACCHART ON:
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-292-52ACA PAPPICATION US/08292620A
| Patent No. 5837542
| GENERAL INFORMATION:
| APPLICANT: Susan Grimm APPLICANT: Susan Grimm APPLICANT: Sean Sullivan APPLICANT: General Stinchomb APPLICANT: General Stinchomb APPLICANT: General Stinchomb APPLICANT: General Sullivan APPLICANT: APPLICANT: NOTECTION: TITLE OF INVENTION: INTRACELLULAR ADHESION TITLE OF INVENTION: INTRACELLULAR ADHESION AUMBER OF SEQUENCES: 2390
| CORRESPONDENCE ADDRESS: ALYON APPRESSES: LAYON & LYON APPRESSES: LAYON & LYON APPRESSES: LAYON & LYON APPRESSES: STREET: Galifornia STREET: Galifornia STREET: Callifornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 30071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 35" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WOrld Perfect 5.1
APPLICATION NUMBER: Uo/vcc;
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY, GABTT INFORMATION:
NAME: Warburg, Richard J
REGISTRATION NUMBER: 208/145
FERERENGE/DOCKET NUMBER: 208/145
TELECOMMUNICATION INFORMATION:
TELECHOME: (213) 855-6440
TELEX: 67-310
TELEX: 67-310
TELEX: 67-310
INFORMATION FOR SEQ ID NO: 3889:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: TOPOLOGY: linear
US-08-292-620A-388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1421 CAGTCGTTCTATGC 1434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CAGUGGUUCUCUGC 14
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Best Local Similarity 50.0%
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.3%; Score 10.8; DB 1; Length 15; Best Local Similarity 85.7%; Pred. No. 31; Matches 12; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WESULT 45-
US-08-298-620A-388
i Sequence 388, Application US/08292620A
i Setent No. 5837542
i GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: James McGwiggen
APPLICANT: James McGwiggen
APPLICANT: James McGwiggen
APPLICANT: Sen Sullivan
APPLICANT: Renneth G. Draper
TITLE OF INVENTION: RIBCYME TREATMENT OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
ITILE OF INVENTION: INTRACELLULAR ADHESION
ITILE OF INVENTION: INTRACELLULAR ADHESION
STREED: SOUTHONESS: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Solite 4700
CTTW. IS AND ADDRESSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          including application described below:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUBBER: US/08/292,620A
FILING DATE: August 17, 1994
                           APPLICATION NUMBER: US/08/452,724A
FILING DATE: 30-MAY-1995
CLASSIFCATION: 435
PRIOR APPLICATION DATR:
APPLICATION NUMBER: US 07/930,600
FILING DATE: 05-ARR-1991
PRIOR APPLICATION DATR: PCT/US91/02362
FILING DATE: 05-ARR-1991
PRIOR APPLICATION DATR: SCARR-1991
PRIOR APPLICATION NUMBER: US 07/505,314
PRIOR APPLICATION NUMBER: US 07/505,314
PRIOR APPLICATION NUMBER: US 07/505,314
FILING DATE: 05-ARR-1990
ATTORNEY/AGRNT INFORMATION:
FILING DATE: (617) 801-6240
TELECHMONE: (617) 861-6240
TELECHMONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: uncled acid
STYPE: uncled acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1436 GACATATACATGGA 1449
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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US-08-452-724A-30
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Gaps
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                                                                                                                                                                                                                                     DB 1; Length 15;
                                                                                                                                                                                                                                                                                                                 Indels
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Sequence 699, Application US/09071845

Patent No. 6132967

GENERAL INFORMATION:
APPLICANT: Susan Grimch APPLICANT: Same Sulivan APPLICANT: Same Sulivan APPLICANT: Same Sulivan APPLICANT: Sean Sulivan APPLICANT: Susan Sulivan APPLICANT: Susan Sulivan APPLICANT: Susan Sulivan APPLICANT: Susan Sulivan APPLICANTON: NUTRACELLULAR ADHESION ITLE OF INVENTION: NUTRACELLULAR ADHESION ITLE OF INVENTION: MOLECULE-1 (I-CAM-1) NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS: 2390
CORRESPONDENCE ADDRESS: 2390
CORRESPONDENCE ADDRESS: 2390
STREET: Suite 4700
CONTRY: LOS ANGELE FORM: STREET: Galifornia COMPUTER: IBM COMPATIBLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" DISKETS: COMPUTER: IBM COMPATIBLE COMPUTER: IBM COMPUTER: IBM COMPATIBLE COMPUTER: IBM CO
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8.3%; Score 10.8; D

Best Local Similarity S0.0%; Pred, No. 31;
Matches 7; Conservative 5; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/999,849
FILING DATE: DECember 7, 1992
ATYORNEY/AGENT INFORMATION:
NAME: WAZDALICA, INFORMATION:
REGISTRATION NUMBER: 32,327
REGERENCE/DOCKET NUMBER: 208/149
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    669
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-845-699
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                           TOPOLOGY:
US-09-071-845-388
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8.3%; Score 10.8; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 7; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-071-046-388, Application US/09071845
| Sequence 388, Application US/09071845
| Patent No. 613267
| GENERAL INFORMATION:
| APPLICANT: Susan Grimm APPLICANT: James McSaviggen APPLICANT: Sean Sullivan APPLICANT: NUMBER OF SURPERION INTRACELLULAR ADHESION TITLE OF INVENTION: INTRACELLULAR ADHESION TITLE OF INVENTION: MOLECULE-1 (1-CAM-1) NUMBER OF SEQUENCES:
| ADDRESSEE: Lyon & Lyon STREET: Sall West Fifth Street STREET: Sulle 4700 CITY: Los Angeles STREET: Sulle 4700 CITY: CONTREET: Sull
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIE: 90071-2066
COMPUTER READABLE FORM:
NEDIUM TYPE: 3.5" Diskette, 1.44 Mb
WEDIUM TYPE: strongering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
             REFERENCE/DOCKET NUMBER: 208/149;
TELECOMMUNICATION IRPCRMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 699:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPACNE: (213) 489-1600
TELEFAX: (213) 955-0440
TELERX: 67-3510
INFORMATION FOR SEQ ID NO: 388:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1421 CAGTCGTTCTATGC 1434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                    ,
US-08-292-620A-699
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DESCRIPTION: third strand derived from Hepatitis B
DESCRIPTION: isolate adw2 sequence region in Seq ID No. 5861244189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
8.3%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 12; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NESOLI 3-489C-190/C
1Sequence 190, Application US/08173489C
1Sequence 190, Application US/08173489C
1Sequence 190, Application US/08173489C
1Sequence 100, Application US/08173489C
1SEQUENCE NOTE: CONTINUENCE OF USERIAL INFORMATION: CONTINUENCE OF INVENTION: TRIPLE-STRAND FORMATION: TITLE OF INVENTION: TRIPLE-STRAND FORMATION: NUMBER OF SEQUENCES: 365
1 CORRESPONDENCES: 365
1 CARBERT: 510 EAST 73RD STREET; STREET;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARTI-SENSE: no
PUBLICATION INFORMATION:
PUBLICATION INFORMATION: 190 :FROM 1 TO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: SIG EAST TARD STREET,
STREET: NEW YORK
STATE: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER IBM PC/XT/AT
COMPUTER IBM PC/XT/AT
COMPUTER IBM PC/XT/AT
COMPUTER: 1BM PC/XT/AT
COMPUTER: 2.5 inch, 1.44Mb storage
COMPUTER: 2.2 inc, 193
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 2.9 OCT 1992
FILING DATE: 2.9 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAMM: HANGELMEN ORGER
NAMM: HANGER
NAMM: HANGELMEN ORGER
NAMM: HANGELMEN 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNET, WALEN I INTORNET, ON THE REGISTRATION WINDER: 26,179
REGISTRATION WINDER: 26,179
REFERENCE/DOCKET NUNBER: 19518-6
TELECOMMUNICATION INFORMATION:
TELEPONE: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 190: 280UENCE CHARACTERISTICS:
LENGTH: 12 bases
TYPE: nucleic acid
STRANDENNES: single stranded
TOPPL: nucleic acid
STRANDENNES: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
NAME: BLOOK, David E.
REGISTRATION INDEER: 22,592
REPERRICZ/DOCKET NUMBER: RC90-
TELECOMMUNICATION INPORMATION:
TELEPROME: (617) 861-9540
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STREED TYPE: Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1436 GACATATACATGGA 1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GACTICTACATGGA 14
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sequence 657 Application US/09081646
patent No. 6333152
GENERAL INFORMATION
APPLICANT: Kinzler, Kenneth
APPLICANT: Zhang, Lin
APPLICANT: Zhang, Lin
APPLICANT: Zhang, Lin
APPLICANT: Zhang, Lin
TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
TITLE OF INVENTION: Gene Calls
FILE REPRIENCE: 01107.74664 US/09/081,646
CURRENT PILING DATE: 1998-05-20
EARLIER PILING DATE: 1998-05-20
EARLIER PILING DATE: 1997-05-21
NUMBER OF SEQ ID NOS: 817
SOFTWARE: FastSEQ for Windows Version 3.0
                                                          Gaps
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; Patent No. 6649340
; GENEAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Walk-Through Mutagenesis
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
STREET: 2 MAIltia Drive
STREET: 2 Millia Drive
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COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DETERMINE STATEMENT PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION UNDERS: US/08/453,623
FILING DATE: 30-May-1995
CLASSIFICATION: CURROWN>
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8.3%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 12; Conservative 0; Mismatches 2; Indels
                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,600
FILING DATE: 05-APR-1991
APPLICATION NUMBER: PCT/US91/02362
FILING DATE: 05-APR-1991
APPLICATION NUMBER: US 07/505,314
FILING DATE: 05-APR-1990
ATTORNEY/AGENT INFORMATION:
                    Best Local Similarity 50.0%; Pred. No. 31; Matches 7; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1346 CAGGGGAAGAAAA 1359
                                                                                                                                      1421 CAGTCGTTCTATGC 1434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRGANISM: Homo sapiens US-09-081-646-657
                                                                                                                                                                                                                                                                                                                          RESULT 49
US-09-081-646-657
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                                       Gaps
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                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 279, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
ITILE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
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                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC., STREET: 510 EAST 73RD STREET, CITY: NEW YORK CITY: NEW YORK COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: 3.5 inch, 1.44Mb storage
COMPARE: 3.5 inch, 1.44Mb storage
COMPARE: 3.5 inch, 1.44Mb storage
SOFTWARE: 3.5 inch, 1.44Mb storage
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION NUMBER: US 07/968,436
FILING DATE: 22 DCT 1992
ATTONEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
NAME: Handelman, Joseph H.
NAME: Handelman, Joseph H.
TRLEFONMUNICATION INFORMATION:
TRLEFONEY: (attorney) (212) 708-1880
TRLEFONEY: (attorney) (212) 708-1880
TRLEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 279:
CENGUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acidir
TYPE: nucleic acidir
Best Local Similarity 84.6%; Pred. No. 33; Matches 11; Conservative 0; Mismatches
                                                                                                                                      1409 GTTAATGATGACC 1421
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US-08-173-489C-279
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| Sequence 9, Application US/08927219
| Sequence 1, Sequence 1, Sequence 2, Sequence 3, S
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                                                                                              Score 10.4; DB 1; Length 12; Pred. No. 30; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Houston
STATE: Texas
CUNNIX: USA
ZIP: T7210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATION TYPE: PC-DOS/MS-DOS
SOFWARE: PREDICATION DATA:
APPLICATION NUMBER: US/08/927,219
FILING DATE: CONCURTENTLY HERWITH PRICE APPLICATION NUMBER: US 60/029,679
FILING DATE: 02-CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,679
FILING DATE: 02-CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,056
FILING DATE: 02-CT-1996
FILING DATE: 10-SEP-1996
FILING DATE: 10-
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                                                                                                             8.0%;
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                                                                                                                                                                                                                                                                                      1348 GGGGAAGAAAA 1359
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                          Best Local Similarity 91.79
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                           12 GGGCAGAAAA 1
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                        US-08-173-489C-190
                                                                                                                       Query Match
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REFERENCE/DOCKET NUMBER: U9518-6
TELECOMUNICATION INFORMATION:
TELEPRAN: (attorney) (212) 708-1880
TELEPRAN: (attorney) (212) 246-8959
TELEPRAN: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
EMUTH: 11 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
DESCRIPTION: dystrophin gene (Accession # M18533, DESCRIPTION: Mystrophin gene (Accession # M1853), DESCRIPTION: Mystrophin gene (Accession # M1853), HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 56
US-08-173-489C-132/C
US-08-173-489C-132/C
US-08-173-489C-132/C
US-08-173-489C-132/C
US-08-174-4

GENERAL INFORMATION:
APPLICANT: MENGY. C. -G.
APPLICANT: MANGY. C. -G.
APPLICANT: MENGY. C. -G.
APPLICANT: MENGY. C. -G.
APPLICANT: MANGY. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.7%; Score 10; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 33; Matches 10; Conservative 0; Mismatches 0; Indels
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORANISM: Home sapiens
ORGANISM: Home sapiens
ORGANISM: Home sapiens
CHROWIGSOME/SEGMENT: X-chromosome
MAP POSITION: Xp21.3-p21.1
PUBLICATION: Xp21.3-p21.1
PUBLICATION: NFORMATION:
AUTHORS: Koenig, M. Hoffman, E P, Bertelson, C J,
AUTHORS: Koenig, M. Hoffman, E P, Bertelson, C J,
TITLE: Complete cloning of the
TITLE: Complete cloning of the
TITLE: Duchenne muscular dystrophy (DMD) cDNA and
TITLE: preliminary genomic organization of the DMD
TITLE: greei in normal and affected individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DATE: 1987

WHTHORS: Koonig, M, Monaco, A P, Kunkel, L M.

TITLE: The complete sequence of

TITLE: dystrophin predicts a rod-shaped cytoskeletal

TITLE: protein

JOURNAL: Cell

VOLUME: 53

PAGES: 219-28

PAGES: 19-28

PARE: 1988

RELEYANT RESIDUES IN SEQ ID NO: 25 :FROM 1 TO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS: Hoffman, E P, Monaco, A P, Feener, C C, AUTHORS: Kunkel, L M.
TITLE: Conservation of the Duchenne
TITLE: muscular dystrophy gene in mice and humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1347 AGGGGAAGAA 1356
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11 AGGGGAAGAA 2
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238
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1987
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JOURNAL:
VOLUME: 2
PAGES: 34
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PAGES: 5
DATE: 19
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                                                                                                                                                                                                                                                                                                                                                                             | Sequence | 13. Application US/09508753B | Sequence | 13. Application US/09508753B | Sequence | 13. Application US/09508753B | Sequence | Sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FRATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
VS-09-508-753B-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 55
US-08-173-489C-25/C
US-08-173-489C
Sequence 25, Application US/08173489C
Sequence 25, Application US/08173489C
Sequence 25, Application US/08173489C
Sequence 26, Application US/08173489C
Sequence 26, Application US/08173489C
SEQUENCE OF USOR TION
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS: ADDRESSEE: ADDRESSEE: STREET: 510 BAST 73RD STREET,
CITY: NEW YORK
STREET: NEW YORK
COUNTRY: USA
ZIP: 10021.
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Best Local Similarity 100.0%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 0; Indels
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ZIP: 10021.
MEDIUM TYPE: 3.5 inch, 1.44Mb storage COMPUTER: IBM PC/XT/AT COMPUTER: IBM PC/XT/AT COMPUTER: IBM PC/XT/AT COMPUTER: IBM PC/XT/AT COMPUTER: Wordperfect Version 5.1 CURRENT APPLICATION DATA: US/08/173,489C FILING DATE: 22 DEC 1993 CLASSIFICATION: 435
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/968,436

FILING DATE: 29 OCT 1992

ATTORNEY/AGENT INFORMATION:

RADG: Handelman, Joseph H.

REGISTRATION NUMBER: 26,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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US-08-458-372-3/C
Sequence 3, Application US/08458372
Sequence 3, Application US/08458372
Sequence 3, Application US/08458372
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD FOR COAMPLIFICATION OF HUMAN
TITLE OF INVENTION: PROTEIN C GENES IN HUMAN CELLS
NUMBER OF SEQUENCES: 21
SURBESSEE: Blilly and Company
STREET: Lilly Corporate Center/Patent Division
CITY: Indianapolis
STREET: NS
COUNTRY: US
COUNTRY: US
COUNTRY: DS
CITY: FA285
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7.7%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.7%; Score 10; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 36; Matches 10; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPTRARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,372
FILING DATE: 02-UNN-1995
CLASSIFICATION: 435
FILING DATE: 02-JUN-1995
ATTORNEY/AGRAT INRORAWITON:
NAME: No. RE37806man, Douglas K.
REGISTRATION NUMBER: 33,267
REFERENCE/STOCKTON NUMBER: 33,267
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2958
TELEPHONE: 317-2776-2958
INFORMATION FOR SEG ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: SINGLE
TOPOLOGY: Ilnear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-384-327-3
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NAME: NO. 564932man, Douglas K.
REGISTRATION NUMBER: 33,267
REFERENCE/DOCKET NUMBER: X-66061
TELEPCOMMUNICATION INFORMATION:
TELEPKN: 317-277-1917
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1388 CTGATCAAAG 1397
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DESCRIPTION: third strand derived from Hepatitis B
DESCRIPTION: isolate adr sequence region in Seq ID No. 5861244131
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US-09-384-327-3/C
US-09-384-327-3/C
Sequence 3. Application US/09384327
; Sequence 3. Application
Patent No. RE37806
; GENERAL INFORMATION:
; APPLICANT: Grinnell, Brian W.
; APPLICANT: Grinnell, Brian W.
; TITLE OF INVENTION: METHOD FOR COAMPLIFICATION OF HUMAN
TITLE OF INVENTION: PROTEIN C GENES IN HUMAN CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPATION STATES OF THE STATES
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Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli 1,111y and Company
STREET: Lilly Corporate Center/Patent Division
CITY: Indianapolis
STATE: IN
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: yes
MITI-SENSE: no
PUBLICATION INFORMATION:
RELEATION INSENDES IN SEQ ID NO: 132 :FROM 1 TO 11
US-08-173-489C-132
                                                                                                                    COMPUTER READALLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 26,179
REFISCHOWNUK-ALTON INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 bases
TYPE: nucleic acid
STRANDENBESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1347 AGGGGAAGAA 1356
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                                     STATE: NEW YORK
                                                                           USA
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APPLICANT: Afar, Daniel E.
APPLICANT: Afar, Daniel E.
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rahan
APPLICANT: Eastenon, Arthur E.
APPLICANT: Jenogy, Kahan
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: BFC-11 A SECRETED BRAIN-SPECIFIC PROTEIN EXPRESSED AND
TITLE OF INVENTION: SECRETED BY PROSTATE AND BLADDER CANCER CELLS
TITLE OF INVENTION: SECRETED BY PROSTATE AND BLADDER CANCER CELLS
TITLE OF INVENTION: SECRETED BY PROSTATE AND BLADDER CANCER CELLS
TITLE OF INVENTION: 1999-08-10
FRICK APPLICATION NUMBER: 60/095,982
PRICK APPLICATION NUMBER: 60/095,982
PRICK APPLICATION NUMBER: 60/095,982
NUMBER OF SEQ ID NOS: 20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: cDNA synthesis is OTHER INFORMATION: primer US-09-374-135-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 61
US-09-410-112-5
Sequence 5, Application US/09410132
Sequence 5, Application US/09410132
Patent No. 6609458
GENERAL INFORMATION:
APPLICANT: Atar. Daniel E.
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
TITLE OF INVENTION: NOVEL GENE EXPRESSED IN PROSTATE CANCER FILE REPRENCE: 1/09-021.031
CURRENT APPLICATION NUMBER: US/09/410,132
CURRENT FILING DATE: 1999-09-30
EARLIER PILING DATE: 1999-09-30
BARLIER PILING DATE: 1999-09-30
BARLIER PILING DATE: 1999-09-30
BARLIER PILING DATE: 1999-09-30
BARLIER PILING DATE: 1999-09-30
SALLIER PILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 5
LEARLING DATE: PALENTING DATE: 1999-07-28
SEQ ID NO 5
LEARLING DATE: 1999-07-28
SEQ ID NO 5
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                                                                                      RESULT 60
US-09-374-135-9
; Sequence 9, Application US/09374135
; Patent No. 6277972
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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2 GGGAAGAAA 11
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                                                                                                                       US-08-173-489C-333
Sequence 333, Application US/08173489C
Sequence 333, Application US/08173489C
SEGURRAL NO. $861210
SEGURRAL SEGURAL A. G
STITLE OF INVENTION: GENERIC SEGURATE ASSAY USING DNA. TITLE OF INVENTION: GENERIC SEGURATE ASSAY USING DNA. TITLE OF INVENTION: TALPLE-STRAND PORMATION.
STREET: $10 EAST 73RD STREET,
STREET: $10 EAST 7
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; BALEVANT RESIDUES IN SEQ ID NO: 333 :FROM 1 TO 13
US-08-173-489C-333
                  12 CTGATCAAAG 3
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1457 TTGATCAAGC 1466

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FOURTHE INFORMATION: Description of Artificial Sequence: Distal
FOURTHE INFORMATION: accessory promoter element
FOURTHER INFORMATION: Accessory promoter element
                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SCHTER, SHAWN T.
APPLICANT: SCHTER, SHAWN T.
APPLICANT: ROSS, WILWA E.
APPLICANT: ROSS, WILWA E.
APPLICANT: ROSS, WILWA E.
FILE OF INVENTION: PROMOTER ELEMENTS AND METHODS OF USE
FILE REPERENCE: 11900130101
CURRENT APPLICANTON NUMBER: US/09/375,673B
CURRENT FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO.
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US-09-409-938-9
Sequence 9. Application US/09409938
Patent No. 6652859
GENERAL INFORMATION:
APPLICANT: Afar. Daniel E.H.
APPLICANT: Afar. Daniel E.H.
APPLICANT: Atastano, Arthur B.
APPLICANT: Micchell, Stephen C.
TITLE OF INVENTION: EXPRESSED IN PROSTATE CANCER
FILE REPERBUCE: 129.26-US-U4
CURRENT PAPLICATION UNMERR: US/09/409,938
CURRENT APPLICATION NUMBER: 60/102,556
PRIOR FILING DATE: 1998-09-30
PRIOR FILING DATE: 1998-09-30
PRIOR FILING DATE: 1998-09-10
PRIOR FILING DATE: 1998-09-10
PRIOR FILING DATE: 1998-09-10
PRIOR FILING DATE: 1998-10-12
PRIOR FILING DATE: 1998-10-12
PRIOR FILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FASTERQ for Windows Version 4.0
SEQ ID NOS: LENGTH: 14
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CTHER INFORMATION: CDNA Synthesis Primer
US-09-409-938-9
US-09-375-673B-10
; Sequence 10, Application US/09375673B
; Patent No. 6605431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1457 TTGATCAAGC 1466
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US-09-688-203-11
Sequence 11, Application US/09638203
Sequence 11, Application US/09638203
Patent No. 6605501
Sequence 11, Abplication US/09638203
Sequence 11, Application US/09638203
Sequence 11, Application NUMBER 105, Application Sequence 11, Application Sequenc
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7.7%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

7.7%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                         US-09-702-114A-3

US-09-702-114A-3

US-09-702-114A-3

Patent No. 6566078

GENERAL INPORMATION:
APPLICANT: Arthur B. Raitano
APPLICANT: Arthur B. Raitano
APPLICANT: Arthur B. Hubert
APPLICANT: Daniel B.H. Afar
APPLICANT: Rene S. Hubert
GURRENT PAPLICATION WHERE: US/09/702,114A
CURRENT APPLICATION NUMBER: US/09/702,114A
PRICR PILING DATE: 1999-10-28

NUMBER OF SEQ ID NOS: 28

NUMBER OF SEQ ID NOS: 28

SOFTWARR: FastSEQ for Windows Version 4.0

SEROID NO. 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Primer US-09-702-114A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1457 TTGATCAAGC 1466
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CORGANISM: Homo Sapiens
US-09-638-203-11
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APPLICANT: Forme, Barry M.
APPLICANT: Forme, Barry M.
APPLICANT: Forme, Barry M.
APPLICANT: Formen, Barry M.
APPLICANT: Weinberger, Cary A.
TITLE OF INVENTION: METHOD FOR MODILATING PROCESSES MEDIATED
TITLE OF INVENTION: BY FARNESOID ACTIVATED RECEPTORS
TITLE OF INVENTION: BY FARNESOID ACTIVATED RECEPTORS
TITLE OF INVENTION: BY FARNESOID ACTIVATED RECEPTORS
TORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: Clark
STREET: 444 South Flower Street, Suite 2000
COUNTRY: LOS Angeles
STATE: CA
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MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PRINCED APPLICATION NUMBER: US/09/469,721
FILING DATE:
PRINCE APPLICATION:
APPLICATION NUMBER: US/08/372,183
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REGISTRATION NUMBER: 31,192
REGISTRATION INFORMATION:
TELEPHONE: 619-546-4737
TELEPHONE: 619-546-4737
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.5%; Score 9.8; DB Best Local Similarity 84.6%; Pred. No. 43; Matches 11; Conservative 0; Mismatches
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOCHWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,078
FILING DATE: February 26, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 19,726
REGISTRATION NUMBER: 39,726
REGISTRATION NUMBER: 30,726
REGISTRATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09469721; Patent No. 6184353; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1431 ATGCAGACATATA 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATATAGACATATA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , TOPOLOGY: linear
US-08-607-078-3
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US-09-469-721-5
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                                                                                                                                               Sequence 5, Application US/08372183

Sequence 5, Application US/08372183

Sequence 6, Application US/08372183

SEQUENCE 1 INFORMATION:

PAPLICANT: Evans, Ronald M. APPLICANT: Forman, Barry M. APPLICANT: Waitherger, Cary M. APPLICANT: Waitherger, Cary M. APPLICANT: Waitherger, Cary M. APPLICANT: Waitherger, S. CARY M. MITTE OF INVENTION: BY FARNESOID ACTIVATED RECEPTORS

TITLE OF INVENTION: BY FARNESOID ACTIVATED RECEPTORS

NUMBERS OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSE: Pretty, Schroeder, Brueggemann & Clark

STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles

STREET: 445 South Flower Street, Suite 2000

CITY: Los Angeles

COUNTRY: USA

ZIP: 90071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-607-078-3

Sequence 3, Application US/08607078

Sequence 3, Application US/08607078

Patent No. 6090847

PAPLICANT: California Institute of Technology
TITLE OF INVENTION: and Imidazole Carboxamides on a TITLE OF INVENTION: Solid Support
NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESSE

ADDRESSEE: Swanson & Bratschun, L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin NATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION TAMBER: US/08/372,183
FILING DATE:
FLASSIFICATION THORMATION:
NAME: Relear, Stephen E.
REGIGTRATION WIMBER: P41 9844
TELECOMUNICATION WIMBER: P41 9844
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHRACTERISTICS:
LENGRATION FOR SEQ ID NO: 5:
SEQUENCE CHRACTERISTICS:
LENGRATION TO THE STEPHEN THE 
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COMPUTER READBLE FORM: 1/2 diskette, 1.44 MG WBDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Golorado
STATE: Colorado
STATE: USA
STATE: USA
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MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1425 CGTTCTATGCAGA 1437
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nucleic acid
DEDNESS: single
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RESULT 71
US-09-360-344-3
US-09-360-344-3
Sequence 3, Application US/09360344
Sequence 3, Application US/09360344
Sequence 3, Application US/09360344
Sequence 3, Application US/09360344
SERENT NOWERINGON BETER B.
APPLICANT: BERVAN, PETER B.
TITLE OF INVENTION: METHOD FOR THE SYNTHESIS OF PYRROLE AND IMIDAZOLE
TITLE OF INVENTION: CARBOXAMIDES ON A SOLID SUPPORT
TITLE OF INVENTION: CARBOXAMIDES ON A SOLID SUPPORT
CURRENT APPLICATION UNMER: US/09/360,344
CURRENT FILING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 31
SOUTHWARE: PATENTIN Ver. 2.1
SEQ ID NO 3
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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   RESULT 70
US-09-359-921-3
US-09-359-921-3
Sequence 3, Application US/09359921
Sequence 3, Application US/09359921
Sequence 3, Application
Sequence 3, Application
Sequence 3, Application
Sequence 3, Application
GENERAL INFORMATION:
APPLICANT: DERVAN, PETER B.
APPLICANT: BAIRD, ELDON B.
TITLE OF INVENTION: MITHOD FOR THE SYNTHESIS OF PYRROLE AND IMIDAZOLE
TITLE OF INVENTION: ACREOXAMIDES ON A SOLID SUPPORT
TITLE OF INVENTION NUMBER: US/09/359,921
CURRENT APPLICATION NUMBER: US/09/359,921
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: Description of Artificial Sequence: Synthetic // CTHER INFORMATION: Oligonucleotide US-09-360-344-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application PC/TUS9517023
Sequence 5, Application PC/TUS9517023
GENERAL INFORMATION:
APPLICANT: Evans, Ronald M.
APPLICANT: Forman, Pariberger, Cary A.
APPLICANT: Maiberger, Cary A.
TITLE OF INVENTION: METHOD FOR MODULATING PROCESSES MEDIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.5%; Score 9.8; DB Best Local Similarity 84.6%; Pred. No. 43; Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1431 ATGCAGACATATA 1443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEO ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 72
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                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Evans, Ronald M.
Forman, Barry M.
Wainberger, Cary A.
TITLE OF INVENTION: BY FARNESOID ACTIVATED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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STATE: CA
COUNTER: CA
ZOUNTER: CA
ZOUNTER: CA
ZOUNTER: USA
ZIP: 90071
COMPUTER: IBAPORDELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBAP FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/696,443
FILING DATE: 24-OCL-2000
CLASSIFTCATION: CURROWN:
PRIOR APPLICATION NUMBER: US/09/696,443
FILING DATE: CALCATON: CHROWN:
APPLICATION NUMBER: US/09/696,443
FILING DATE: CALCATON: CHROWN:
APPLICATION NUMBER: S1,192
REGISTRATION NUMBER: 31,192
REGISTRATION NUMBER: P41 9844
TELECOMMUNICATION INFORMATION:
TELECOMMUNICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.5%; Score 9.8; DB 1; Length 13; Best Local Similarity 84.6%; Pred. No. 43; Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSS:
SINGESSEE: Pretty, Schroeder, Brueggemann & Clark
SIREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
SITHE: CA
                                                                                                                                                                                                                                             Query Match 7.5%; Score 9.8; DB 1; Length 13; Best Local Similarity 84.6%; Pred. No. 43; Matches 11; Conservative 0; Mismatches 2; Indels
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                                                                                                TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Oligonucleotide
US-09-469-721-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09696443
Patent No. 6416957
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1425 CGTTCTATGCAGA 1437
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGTTCAATGCACA 13
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-696-443-5
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US-09-696-443-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.5%; Score 9.8; DB 1; Length 14; Best Local Similarity 84.6%; Pred. No. 47; Matches 11; Conservative 0; Mismatches 2; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INCRMATION:
APPLICANT: Trustees of the University of Pennsylvania APPLICANT: Trustees of the University of Pennsylvania APPLICANT: Fisher, Krishna J.
APPLICANT: Fisher, Krishna J.
APPLICANT: Chen, Shu-Jen
APPLICANT: Meltramn, Matthew
TITLE OF INVENTION: Improved Adenovirus Virus and NUMBER OF SEQUENCE: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
CITY: Spring House
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIOW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Ploppy disk
COMPUTER: Pacentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,022A
FILING DATE: US/08/835,022A
FILING DATE: 28-CT-1994
ATTORNEY APPLICATION NUMBER: US 08/331,381
FILING DATE: 28-CT-1994
ATTORNEY AGBNT INFORMATION:
NAME: Bak, Mary E.
REGISTARTION NUMBER: 31,215
REFREENCE/MOUNT CATION INFORMATION:
TELEPOMOUNICATION INFORMATION:
TELEPOMOUNICATION INFORMATION:
TELEPHONE: 215-540-9200
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: UPWH1254USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-836-022A-8/c
; Sequence 8, Application US/08836022A
; Patent No. 6001557
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; MOLECULE TYPE: DNA (genomic)
US-08-836-022A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-393-734-8
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                                                                                                                                                                                                                               TELEPAX: 215-540-5918
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 14 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 base pairs
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 AGACAAATATTAC 2
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Best Local Similarity
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US-08-393-73
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7.5%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 43;
Matches 11; Conservative 0; Mismatches 2; Indels
               TITLE OF INVENTION: BY FARNESOID ACTIVATED RECEPTORS NUMBER OF SEQUENCES: 7
CORRESPONDENCES: 7
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WHERE: PCT/US95/17023
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Release #1.92
REGISTRATION UNMBER: P41 9844
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PetentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Oligonucleotide
PCT-US95-17023-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1425 CGTTCTATGCAGA 1437
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STRANDEDNESS: single
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APPLICANT: Strauss, Jerome F.

TITLE OF INVENTION: Methods and Compositions for Gene
TITLE OF INVENTION: Methods and Compositions
TITLE OF INVENTION: Methods for the Treatment of Defects in Lipoprotein
TITLE OF INVENTION: Methods and
NUMBER OF SEQUENCES:
ADDRESSER: Howson and Howson
STREET: Spring House Corporate Cutr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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US-09-427-048A-8/C
US-09-427-048A-8/C
Sequence 8, Application US/09427048A
Sequence 8, Application US/09427048A
Sequence 8, Application US/09427048A
GENERAL INFORMATION:
APPLICANT: Trustees of the University of Pennsylvania
APPLICANT: Trustees of the University of Pennsylvania
Fisher, Krishna J.
Chen, Shu-den
Heitsman, Matchew
Heitzman, Matchew
TITLE OF INVENTION: Improved Adenovirus Virus and
Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howeon and Howson
STREET: Spring House Corporate Cntr, P O Box 457
STRIET: Spring House
STRIE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
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ZIP: 19477

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: Eloppy disk
CLASTICATION NUMBER: US/08/994,489
FILING DATE: 24 FEB-1995
ATTORNEY/AGBNT INFORMATION:
REGISTRATION NUMBER: 31,215
REGISTRATION POWERTING: 115-40-9200
TELEPROME CLARACTERISTICS:
LENGMATION FOR ESCI ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGMATION FOR ESCI ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGMATION FOR ESCI ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGMATION FOR ESCI ID NO: 8:
STREAMEDINESS: Goodule
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7.5%; Score 9.8; DB
Best Local Similarity 84.6%; Pred. No. 47;
Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic) US-08-894-489-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1353 AGAAAAATATTCC 1365
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Sequence 78, Application US/08913833

Sequence 78, Application US/08913833

Sequence 78, Application US/08913833

SEQUENCE STUVENTON: LIEVEN
APPLICANT: LOUMAGILE, JOCST
APPLICANT: ROSSAU, NEUDI
TITLE OF INVENTION: MUTATIONS IN THE REVERSE TRANSCRIPTASE GENE
ITTLE OF INVENTION: MUTATIONS IN THE REVERSE TRANSCRIPTASE GENE
ITTLE OF INVENTION: MUTATIONS IN THE REVERSE TRANSCRIPTASE
COUNTRY: USA

CITY: HOUSTON WAS ABOUT A STATE
CONDITION: USA
COUNTRY: USA
COUNTRY
COUNTRY: USA
COUNTRY: USA
COUNTRY
COUNTRY: USA
COUNTRY
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                                                                                                            2; Indels
                                                                                                            Mismatches
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US-008-894-489-8/C
US-008-894-489-8/C
Sequence 8, Application US/08894489
Patent No. 6174527
GENERAL INFORMATION:
APPLICANT: Wilson, James M.
APPLICANT: Kozarsky, Karen F.
                                                                                                                   .;
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                                                                                                                   Matches 11; Conservative
                                                                                                                                                                                                                                      14 AGACAAATATTAC 2
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US-08-913-833-78
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Best Local S:
Matches 11
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US-UY-8/4-601-123/C
| Sequence 123, Application US/09874601
| Sequence 123, Application US/09874601
| Patent No. 6632057
| GENERAL INFORMATION:
| APPLICANT: LEMIN, ALFRED S.
| APPLICANT: GRANT, MARIA B.
| TITLE OF INVENTION: APRIA B.
| TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
| TITLE OF INVENTION: APRIA B.
| TITLE OF INVENTION: APRIA B.
| TITLE OF INVENTION: APPLICANTON NUMBER: US/09/874,601
| CURRENT FILING DATE: 1000-05-01
| PRIOR FILING DATE: 1998-04-21
| PRIOR FILING DATE: 1998-04-21
| PRIOR FILING DATE: 1997-05-09
| PRIOR PLING DATE: PARCHIN VERSION 3.0
| SEQ ID NO 123
| LENGTH: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.5%; Score 9.8; DB 1; Length 14; Best Local Similarity 84.6%; Pred. No. 47; Matches 11; Conservative 0; Mismatches 2; Indels
                        RESULT 79
US-09-475-947A-6/C

Sequence 6, Application US/09475947A
Patent No. 6472154
GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REPERENCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFWMARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 14
TIPE: DNA
COGANISM: human
US-09-475-947A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: RNA
SOGANION: Artificial Sequence
FRATURE:
NAME/KEY: misc_feature
| COGATION: () ... ()
| OTHER INFORMATION: SYNTHEFIC OLIGONUCLEOTIDE
US-09-874-601-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1380 ATCGTCTTCTGAT 1392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 TATGCACACACAT 2
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;Patent No. 5223407
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US-09-874-601-123/c
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NS-05-580-794C-78

NS-05-580-794C-78

Sequence 78, Application US/09580794C

Patent No. 631389

GENERAL INFORMATION:

APPLICANT: Studyer, Lieven

APPLICANT: Louwagie, Joost

APPLICANT: NOSSAU, Rudi

TITLE OF INVENTION: PRADELTATION OF DRUG-INDUCED MUTATIONS IN THE REVERSE

TITLE OF INVENTION: PRADEL SECOND

TITLE OF INVENTION WINDRES: 08/913,833 now US/6,087,093

PRIOR FILING DATE: 1997-09-15

CURRENT FILING DATE: 1997-09-15

PRIOR PELING DATE: 1997-00-15

PRIOR APPLICATION NUMBER: EP 96870005.4

PRIOR APPLICATION NUMBER: EP 96870005.4

PRIOR APPLICATION NUMBER: EP 96870005.4

PRIOR PILING DATE: 1996-06-25

NUMBER OF SEQ ID NOS: 164

SEQ ID NOS: 164

SEQ ID NOS: 164
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/427,048A
FILING DATE: 21-Oct-1999
CLASSIFOATION: «Unknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/936,022
FILING DATE: «Unknown>
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNVPN.008PCT
TELEPHONE: 215-540-9200
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.5%; Score 9.8; DB 1; Length 14; Best Local Similarity 84.6%; Pred. No. 47; Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.5%; Score 9.8; DB 1; Length 14; Best Local Similarity 84.6%; Pred. No. 47; Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  | LENGTH: 14 Dase pairs | LENGTH: 14 Dase pairs | TENGTH: 14 Dase pairs | TYPE: nucleic acid | STRANDEDNESS: double | TOPLOGY: UNKNOWN | MOLECULE TYPE: UNA (Genomic) | SEQUENCE DESCRIPTION: SEQ ID NO: 8: US-09-427-048A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-580-794C-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1441 ATACATGGAAGAT 1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1353 AGAAAATATTCC 1365
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US-US-146-613-15

PATENT NO. 5686264

PAPLICANT: GANNOR, RICHARD B.
APPLICANT: GANNOR, RICHARD B.
APPLICANT: GANNOR, RICHARD B.
APPLICANT: GANNOR, THRREDE A.
TITLE OF INVENTION: THRREDE B.
TITLE OF INVENTION: WHITE & DURKEE B.
STREET: D.O. BOX 4433
CITY: HOUSTON STREET

COUNTRY: USA
STREET TEXAS
COUNTRY: USA
TILING DATE:
CLASSIFICATION: 435
ATTORNEY AGENT THROMATH:
THE COUNTRY: USA DELICATION: 435
ATTORNEY APELICATION NUMBER: 07/910,867
FILING DATE:
CLASSIFICATION: 435
ATTORNEY APELICATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSD:263/MAY
TELECOMMUNICATION INFORMATION:
TELECOMUNICATION INFORMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.2%; Score 9.4; DB 1; Length 11; Best Local Similarity 90.9%; Pred. No. 44; Matches 10; Conservative 0; Mismatches 1; Indels
             APPLICATION NUMBER: US/07/910,867B
PILIGO DATE: 02-JUL-1992
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSD:263/WAY
TELECOMMUNICATION INFORMATION:
TELECHONE: 512/418-3000
                                                                                                                                                                                                                                                                                      TELERAX: 512/474-7577

INFORMATION FOR SEQ 1D NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
NOLECTULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-07-910-8678-15
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TELEX: NOT APPLICABLE
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1449 AAGATGGGTTG 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAGATGGGTGG 11
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US-07-910-867B-15
Sequence 15. Application US/07910867B
Patent No. 5597895;
GENERAL INFORMATION:
APPLICANT: GAYDOX: Richard B.
APPLICANT: GAYDOX: Transdominant Tat Mutants and Uses
TILLE OF INVENTION: Thereof
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: ATMODIA, White & Durkee
GTRATE: Texas
CONTRY: US
ZIP: Texas
COUNTY: US
ZIP: TY210
COMPUTER PPPROTE
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.5%; Score 9.8; DB 1; Length 14; Best Local Similarity 84.6%; Pred. No. 47; Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.5%; Score 9.8; DB 1; Length 14; Best Local Similarity 84.6%; Pred. No. 47; Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 82
5223407-6
; Patent No. 5223407
** APPLICANT: WONG, RAYMOND W.K.;SUTHERLAND, MARGARET L.
; TITLE OF INVENTION: EXCRETION OF HETEROLOGGOUS PROTEINS
APPLICANT: WONG, RAYMOND W.K.; SUTHERLAND, MARGARET L.
FROM E.COLI
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
RILING DATE: 18-AUG-1989
PRIOR APPLICATION NUMBER: US/07/395,797
FILING DATE: 18-AUG-1989
PRIOR APPLICATION NUMBER: 239,145
PRILING DATE: 31-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM E.COLI

NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/395,797
FILLING DATE: 18-AGC-1889
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 239,145
FILING DATE: 31-AUG-1988
SEQ ID NO: 6:
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1396 AGGAGGTAAATT 1408
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LENGTH: 14
5223407-5
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Sequence 2, Application US/08929856

Sequence 2, Application US/08929856

Patent No. 6136568

GENERAL INFORMATION:

APPLICANT: Hiatt, Andrew
APPLICANT: Hiatt, Andrew
TITLE OF INVENTION: DE NOVO POLYNUCLEOTIDE SYNTHESIS USING
TITLE OF INVENTION: ROLLING TEMPLATES
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSE: HENRE, DAVID, LITTENBERG, KRUMHOLZ &
ADDRESSE: MENTILIK
STREET: 600 South, Avenue West
CITY: Westfield
STATE: New Jersey
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
MONEUTER READABLE FORM:
MONEUTER READABLE FORM:
OOPERAITING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: PS-ENICATION NOMBER: US/08/929,856
FILING DATE: 15-8EP-1997
CLASSIFICATION: 3.46
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REGISTRATION NUMBER: 33,071
REGISTRATION NUMBER: 33,071
REGISTRATION NUMBER: ROSE 3.0-057
TELECOMMUNICATION: INFORMATION:
                                                 ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
MENTILIK

CITY: Westfield
STATE: New Jersey
COUWIRY: USA
ZIP: 07090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1373 ACGAGCGATCG 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ACGATCGATCG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-929-856-2
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                                                                                                                                                                                                                                                                                                                                                                                                                       us-vas-108-24/c
; Sequence 24, Application US/08983108
; Patent No. 5972612
; GRNEAAL INFORMATION:
    TITLE INFORMATION:
    TITLE OF INVURITION: METHOD FOR NUCLEIC ACID SEQUENCING
    TITLE OF INVURITION: METHOD FOR NUCLEIC ACID SEQUENCING
    CORRESPONDENCE ADDRESS:
    ADDRESSE: SEED and BERRY
    STREET: Seattle
    COUNTRY: Geattle
    STRATE: Washington
    COUNTRY: USA
    ZIPP 98104
    COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER PRADABLE FORM:
    MEDIUM TYPE: TIM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Detentin Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
    REPLICATION NUMBER: US/08/983,108
    FILING DATE: LS-MAY-1998
    CLASSIFICATION NUMBER: 41,181
    REDISTRATION NUMBER: 41,181
    REDISTRATION NUMBER: 41,181
    REDERROWEN FORMATION:
    NAME: LOOP, Thomas E:
    RECIENTATION NUMBER: 41,181
    RELECOMMUNICATION INFORMATION:
    TELECOMMUNICATION INFORMATION:
    TELECO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08929856
Patent No. 6136568
Patent No. 6136568
Patent No. 6136568
PapilCANT: Hiatt, Andrew
APPILCANT: Rose, Floyd
TITLE OF INVENTION: DE NOVO POLYNUCLEOTIDE SYNTHESIS USING
TITLE OF INVENTION: ROLLING TEMPLATES
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.2%; Score 9.4; DB 1; Length 11; 90.9%; Pred. No. 44; tive 0; Mismatches 1; Indels
                                                                                                                                                DB 1; Length 11;
                                                                                                                                                                                                       1; Indels
                                                                                                                                         Query Match 7.2%; Score 9.4; DB Best Local Similarity 90.9%; Pred. No. 44; Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                  1449 AAGATGGGTTG 1459
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                             1 AAGATGGGTGG 11
                                    ; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-346-613-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 AAATATTCTAC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                  RESULT 85
US-08-983-108-24/c
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US-08-929-856-2
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APPLICANT: Divaco, Mabel P.
APPLICANT: Divaco, Mabel P.
APPLICANT: Divaco, Macry E.
APPLICANT: MacDonald, Marcy E.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: A No. 5538844el Transport Protein Gene from TITLE OF INVENTION: Lhe Huntington's Disease Region
CORRESPONDENCE ADDRESS: 2
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13. Application US/08214603
Sequence 13. Application US/08214603
Fatent No. 5596031
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL ANTISENSE OLIGONUCLEOTIDES
NUMBER OF EXCURNES: 13
CORRESPONDENCES: 13
CORRESPONDENCES: 13
CORRESPONDENCES: 15
CORRESPONDENCES: 15
CORRESPONDENCES: 15
CORRESPONDENCES: 15
CORRESPONDENCES: 15
COURTY: San Francisco
CITY: San Francisco
COURTRY: US.
                                                                                                                                                                                                                                                                                                                           CITY:

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM FOC compatible

OPERATING SYETM: PC-DOS/MS-DOS

OPERATING SYETM: PC-DOS/MS-DOS

OPERATING SYETM: DATA:

APPLICATION NUMBER: U9930323

FILING DATE: 19930323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIF: 94105-1493

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/214,603
FILING DATE: 18-MAR-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
     RESULT 89
US-08-035-928-8
Sequence 8, Application US/08035928
Patent No. 553864
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19930323
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : (202) 466-0800
(202) 833-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX:
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1447 GGAAGATGGGT 1457
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US-08-035-928-8
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                                                                                                                                                                                                                                           7.2%; Score 9.4; DB 1; Length 11; 90.9%; Pred. No. 44; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 88
PCT-US96-09430-19
| Sequence | Application PC/TUS9609430 | |
| GENERAL INFORMATION: | APPLICANT: | GALACE |
| APPLICANT: | GALACE |
| APPLICANT: | GALACE |
| TILL OF INVENTION: | TREATMENT OF HEMOGLOBINOPATHIES |
| NUMBER OF SEQUENCES: 23 |
| CARRESPONDENCES: 23 |
| ADDRESSEE: OncorPharm, Inc. |
| STREET: 200 Perry Parkway |
| CITY: Galthersburg |
| COUNTRY: Maryland |
| COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/M9-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: PCT/US96/09430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.2%; Score 9.4; DB Sest Local Similarity 90.9%; Pred. No. 44; Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFCATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/473,845
FILING DATE: O7-UTN-1995
ATTOMNEY/AGENT INFORMATION:
NAME: KATTA GIGIN E.
REGISTRATION NUMBER: 30,649
REFERENCE/COCKET NUMBER: PA-0040
TELECOMMUNICATION INFORMATION:
TELECHONE: 301-527-2088
TELEFAX: 011-208-6997
            TELEFAX: 908-654-7866
| INPORMATION FOR SEQ ID NO: 2: 1EBNGTH: 11 base pairs | TYPE: mullel acid | TYRANDEDNESS: single | TYPE: TYPE: DNA | US-08-929-856-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 11 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                  1374 CGAGCGATCGT 1384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SENSE: NO PCT-US96-09430-19
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
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                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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                                                                                                                                                                               Best Local Similarity 90.9%; Score 9.4; DB 1; Length 12; Matches 10; Conservative 0; Mismathhar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 86, Application US/08173489C
| Sequence 86, Application US/08173489C
| Patent No. 5661244
| Patent No. 5661244
| Title OF INVENTION: RAPLICANT: RANG, C. -G.
| APPLICANT: REPURN, A. G.
| TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA TITLE OF INVENTION: TRIPLE-STRAND FORMATION. NUMBER OF SEQUENCES. 365
| CORRESPONDENCE ADDRESS: ADDRESSE: ROPILE DIAGNOSTIC SCIENCES, INC., STREET; SIO EAST 73RD STREET,
| COUNTRY: USA YORK COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 86 :FROM 1 TO 12
US-08-13-469C-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch;
COMPUTER: IBM PC/XT/AT
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIPPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELEPHONE: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 86: SEQUENCE CHARACTERISTICS:
LENGTH: L2 Dases
TYPE: Nucleic Acid
STRANDENNESS: single stranded
                                                                                                                 ; TOPOLOGY: linear;
; MOLECULE TYPE: DNA (probe)
US-08-441-887A-119
                                                                                                                                                                                                                                                                                                              1429 CTATGCAGACA 1439
           SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 119, Application US/08441887A
Patent No. 5837832
GENERAL INFORMATION
APPLICANT: Chee, Mark
APPLICANT: Choin, Maureen T.
APPLICANT: Huang, Xiachua X.
APPLICANT: Hubbell, Earl A.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Sheldon, Peter E.
APPLICANT: Sheldon, Raward L.
ITILE OF INVENTION: Aniays of Nucleic Acid Probes on TITLE OF INVENTION: Aslogical Chips
NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 9411

COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPOPO disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWART: PatentIn Release #1.0, Version #1.25
SOFTWART APPLICATION DATA:
APPLICATION NUMBER: US/08/41,887A
FILING DATE: 16-MAY-1995
CLASSIFICATION DATA:
APPLICATION DATE: 35
FRIOR APPLICATION DATA:
APPLICATION DATE: 25-UNA-1993
ATTORNEY/AGENT IRPORMATION:
NAME: Liebeschuetz, Joseph O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                               TOPOLOGY: linear ...
NOLECULE TYPE: other nucleic acid
.: DESCRIPTION: /desc = "Oligodeoxynucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-004160US
TELECOMMUNICATION INPORMATION:
TELEPHONE: 650-326-2400
NAME: Kezer, William B.
REGISTRATION NUMBER: 37,369
REFRENCE/DOCKET NUMBER: 2307B-052100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-9603
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650-326-2422
INFORMATION FOR SEQ ID NO: 119:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1347 AGGGGAAGAA 1357
                                                                                                                                                                                                   LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGGGAAAGAAA 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Facteut No. 202/824.

APPLICANT: Chee, Mark
APPLICANT: Chee, Mark
APPLICANT: Fodor, Stephen P. A.
APPLICANT: Fodor, Stephen P. A.
APPLICANT: Hubbell, Earl A.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Morris, Macdonald S.
APPLICANT: Sheldon, Edward I.
ITILE OF INVENTION: Arrays of Nucleic Acid Probes on TITLE OF INVENTION: Arrays of Nucleic Acid Probes on TITLE OF INVENTION: Biological Chips
NUMBER OF SEQUENCES: 360
CORRESPONDENTE ADRESS:
ADDRESSEE: Townsend and Townsend and Crew LIP
STREET: Two Embarcadero Center, 8th Floor
CTTY: Stan Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,887A
FILING DATE: 16-MAX-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/082,937
FILING DATE: 25-OUT-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/082,937
FILING DATE: 25-UN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, USeeph O.
REFERENCE/DOCKET NUMBER: 018547-004160US
FILECOMMUNICATION UNPORMATION:
TELEPHORE 569-236-240
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
FILES:
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 28, Application US/08441887A ; Patent No. 5837832
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-504-4444
TELEFAX: 215-504-4545
                                                                                                            16:
                                                                                                                                                                                                                                                                                                                                                                                                                     1348 GGGGAAGAAA 1358
                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GAGGAAGAAA 12
                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 95
US-08-441-887A-28/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 94111
                                                                                                                                                                                                                                       ;
US-08-927-165A-16
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                                                                                                                                       Sequence 187, Application US/09281418

Sequence 187, Application US/09281418

Patent No. 6287769

GENERAL INFORMATION:

APPLICANT: Indus. Takakazu

TITLE OF INVENTION: Method of Assaying Microorganisms, Method of Assaying Contaminant

TITLE OF INVENTION: MUMBER: US/09/281,418

CURRENT APPLICATION NUMBER: US/09/281,418

CURRENT APPLICATION WUMBER: US/09/281,418

EARLIER FILING DATE: 1998-03-31

EARLIER FILING DATE: 1999-03-16

NUMBER OF SEQ ID NOS: 216

SEQ ID NOS: 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.2%; Score 9.4; DB 1; Length 12; Best Local Similarity 90.9%; Pred. No. 48; Matches 10; Conservative 0; Mismatches 1; Indels
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US-08-927-165A-16

Sequence 16, Application US/08927165A

Patent No. 6410226

GENERAL INFORMATION:
APPLICANT: Kniec, Eric B

APPLICANT: Romich, William K.
APPLICANT: Smith, Sheryl T.
APPLICANT: Mewcown STREET: 300 Pheasant Run CITY: Newtown STARE: PA

COUNTYY: USA
ZIP: 18940

COMPUTER READABLE FORM:
MEDIUM TYPE: Disketche COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: BeateRO for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/927,165A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: HARBOUTG, DAILE-
REGISTRATION NUMBER: 36156
REFERENCE/DOCKET NUMBER: 7991-010-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1363 TCCACGCATCA 1373
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
CTHER INFORMATION: Primer
US-09-281-418-187
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                          11 AGGAGAAGAA 1
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US-09-281-418-187
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Patent No. 6027920
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GLOTONATCH, Armel
APPLICANT: Purification, Relano
APPLICANT: Purification, Francis
APPLICANT: Renaud, Michel
APPLICANT: Renaud, Michel
ITILE OF INVENTION: System for Protein Expression and
ITILE OF INVENTION: Secretion Especially in Corynebacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.2%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 52; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CLARK, ROBIN
APPLICANT: GUN, SHAW
TITLE OF INVENTION: MEDICAMENTS FOR THE TREATMENT OF
TITLE OF INVENTION: PAPILLOMAVIRUS DISEASES
NUMBER OF SEQUENCES: 10
CORRESPONDENCES: 10
CORRESPONDENCES: ROBINS
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNTIED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,521
FILING DATE: 27-ARR-1995
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,027
FILING DATE: 21-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
REGISTRAATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 2300-0895.11
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION I
                                                                                                                                                                                                            RESULT 97
US-08-430-521-1
; Sequence 1, Application US/08430521
; Patent No. 5925516
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: DNA (genomic) US-08-430-521-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1355 AAAAATATTCC 1365
    1402 TAAAATTGTTA 1412
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Best Local Similarity 90.9
Matches 10; Conservative
                                                    3 TCAAATTGTTA 13
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US-08-508-761B-13
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                                                                                                                                                                      Query Match 7.2%; Score 9.4; DB 1; Length 13; Best Local Similarity 90.9%; Pred, No. 52; Matches 10; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 117, Application US/08441887A;
Sequence 117, Application US/08441887A;
Pacent No. 5837832
GENERAL INPORMATION:
APPLICANT: Chee, Mark
APPLICANT: Cheo, Mark
APPLICANT: Huang, Xiaohua X.
APPLICANT: Huang, Xiaohua X.
APPLICANT: Lipshuz, Peter B.
APPLICANT: Libshuz, Peter B.
APPLICANT: Sheldon, Rdward I.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on TITLE OF INVENTION: Allohogical Chips
NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.2%; Score 9.4; DB 1; Length 13
Best Local Similarity 90.9%; Pred. No. 52;
Matches 10; Conservative 0; Mismatches 1; Indels
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INFORMATION FOR SEQ ID NO: 17
SEQUENCE CHARACTERISTICS:
LEMOTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (probe)
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
US-08-441-887A-28
                                                                                                                                                                                                                                                                                                                                       1463 AAGCAAATAGG 1473
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Sequence 25, Application US/09407549

Petent No. 6303377

GENERAL INFORMATION:
APPLICANT: Bower, Stanley Grant
APPLICANT: Perkins, John B.
APPLICANT: Perkins, John B.
APPLICANT: Perco, Janies G.
TITLE OF INVENTION: SUBTILIS
TITLE OF INVENTION: SUBTILIS
TITLE OF INVENTION: SUBTILIS

NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
CITY: Boston
STRATE: Masachusetts
COUNNEY: U.S.A.
ZIP: 02110-2804
SOFTWARE: WordPerfect (Version 5.1)
CURRENY APPLICATION DATA:
APPLICATION NAME: US/08/676,818
FILING DATE: 08-JUL-1996
CLASSIFICATION NUMBER: 08/29,430
REPRICATION NUMBER: 08/29,430
FILING DATE: May 6, 1994
APPLICATION NUMBER: 08/084,709
FILING DATE: May 6, 1994
APPLICATION NUMBER: 08/084,709
FILING DATE: NUMBER: 29,193
ATYORNEY AGENT INFORMATION:
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 4859/004001
TELLEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION UNMERR: 08/239,430
FILING DATE: May 6, 1994
APPLICATION NUMBER: 08/084,709
FILING DATE: June 25, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFWARE: WORDERFECT (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/407,549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1394 AAAGGAGGTAA 1404
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Matches 10; Conservative
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Fatent No. 6057136
FATENT No. 6057136
FATENT NO. 6057136
FATENT BOWER, Stanley Grant
APPLICANT: Perkins, John B.
APPLICANT: Yocum, R. Rogers
TITLE OF INVENTION: BIOTIN BIOSYNTHESIS IN BACILLUS
TITLE OF INVENTION: SUPTILES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: Ploppy disk
SOFTWARE: Ploppy disk
SOFTWARE: Ploppy disk
SOFTWARE: Ploppy disk
CURRENT APPLICATION DATA:
APPLICATION NUMBER: FR 91/09652
FILING DATE: 29-UTL-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
REPLICATION DATA:
APPLICATION DATA:

    NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium Melassecola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: P58525NA
TELECOMMUNICATION:
TELEPHONE: (202) 639-666
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTER STICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MULECTLE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: COFY

US-08-508-7618-13
                                                                                                                                                          CITY: WE COUNTRY: U.F
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Gaps
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                                                                                                                   FEATURE:
NAMEXKEY: modified_base
LOCATION: 9
LOCATION: /mod_base= OTHER
OTHER INFORMATION:
                                                           OTHER INFORMATION: /mod_base= OTHER OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: April 7, 2004, 07:04:52 Job time : 1 secs
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      NAME/KEY: modified_base
LOCATION: 6
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PCT-US91-03680-08/C
Sequence 108, Application PC/TUS9103680
GENERAL INFORMATION:
APPLICANT: Marteucci, Mark D.
APPLICANT: Krawczyk, Stewar
TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
TITLE OF INVENTION: DUPLEX DNA
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSE: Mortison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Manlo Park
SITHS: California
COUNTRY: USA
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Datentin Release #1.0, Version #1.25
COMPUTER: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION: 435
ATTORNET/AGENT INFORMATION:
MARE: Mutashige, Kate #1.0
REGERENCIOCKET NUMBER: 29,959
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION INFOR
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OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION:
TELECOMMUNICATION INPORMATION:
TELEPRONE (617) 542-5070
TELEX: (617) 542-806
INPORMATION FOR SEQ ID NO: 25:
SEQUENCE CHRACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: DNA
US-09-407-549-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: modified_base
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Best Local Similarity 90.99
Matches 10; Conservative
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US-10-25-017B-110670/c

US-10-25-017B-110670/c

Sequence 110670, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: Detaylations

TITLE OF INVENTION: methylations

FILE REFERENCE: E0/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

SEQ ID NO 110670

LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 10669
LENGTH: 13
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                                                                                              Gaps
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US-10-257-0178-110670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027619
US-10-257-017B-110669
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                          8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 8.4e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 13
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Pred. No. 8.4e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                         Sequence 110669, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.0%;
Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                                                                                                   1434 CAGACATATACA 1445
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                                                                                                    Matches 11; Conservative
                                                                                                                                                                                             2 CAAACATATACA 13
                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                    US-10-257-017B-110669
US-10-257-017B-101130
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APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPERBNCE: E001/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 101129
LENOTH: 13
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US-10-257-017B-101130

US-10-257-017B-101130

SQUENCE 101130 Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FILE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FILE OF INVENTION: Detection of single nucleotide polymorhphisms
FILE OF INVENTION: 300/1033
CURRENT APPLICATION NUMBER: DE 10019173.8
FRICK FILING DATE: 2000-04-07
NUMBER: OF INVENTION: 382046
SEQ ID NOS: 382046
SEQ ID NOS: 382046
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FEATURE:
OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0025162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0025162
US-10-257-017B-101129
                                                                                                                                                                                                        ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0023864
US-10-257-017B-95980
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Pred. No. 8.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                               Query Match
8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
     PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 95980
LENGTH: 13
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Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
SEQ ID NOS: 382046
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US-10-257-017B-95980/c

Sequence 95980, Application US/10257017B

Sequence 95980, Application US/10257017B

SEQUENCE STATE STA
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GENERAL INFORMATION:
APPLICANT: ALexander Olek
APPLICANT: ALexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytos:
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytos:
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytos:
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytos:
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytos:
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2000-10-07
PRIOR PELICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEGO ID NO 95979
LENGTH: 13
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; CTHER INFORMATION: Oligonucleotide for detection of SNP TSC0023002
US-10-257-017B-91972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0023864
US-10-257-017B-95979
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8.0%; Score 10.4; DB 1;

Best Local Similarity 91.7%; Pred. No. 8.4e+02;

Matches 11; Conservative 0; Mismatches 1;
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Pred. No. 8.4e+02;
0; Mismatches 1;
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Best Local Similarity 91.7%;
Matches 11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                        RESULT 443
US-10-257-017B-89812
is Sequence 89812, Application US/10257017B
is Sequence 89812
GENERAL 1872-17-017B
GENERAL 1872-17-015
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION WIMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10-07
FRIGHT APPLICATION NUMBER: US/10-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
SEQ ID NOS: 382046
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE FERENCE: E01/1193/Wo
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 91971
LENGTH: 13
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US-10-257-017B-91971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022510 US-10-257-017B-89812
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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91.7%; Pred. No. 8.4e+02;
tive 0; Mismatches 1;
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US-10-257-017B-91972
; Sequence 91972, Application US/10257017B
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US-10-257-017B-91971/c
; Sequence 91971, Application US/10257017B
; GENERAL INFORMATION:
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                      1434 CAGACATATACA 1445
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Best Local Similarity 91.7
Matches 11, Conservative
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                                                                                             13 CATACATATACA 2
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US100-07
PRIOR FILING DATE: 2000-04-07
RIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 89811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosir
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 2012-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 81586
LENGTH: 13
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                                                  FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0020645
US-10-257-017B-81585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0020645
US-10-257-017B-81586
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                             Length 13
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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8.0%; Score 10.4; DB 1;

Best Local Similarity 91.7%; Pred. No. 8.4e+02;

Matches 11; Conservative 0; Mismatches 1;
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; Sequence 81586, Application US/10257017B
; GENERAL INFORMATION:
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TYPE: DNA ORGANISM: Artificial Sequence
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Sequence 81585, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: MILE Berlin
TITLE OF INVENTION: methylations
FILE REPRENCE: E01/1193/WO
CURRENT PLILIG DATE: 2002-10-07
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 81585
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 79876
LENGTH: 13
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0020278
US-10-257-017B-79875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0020278
US-10-257-017B-79876
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                                                                                                                                                                                                                                                                                                                                                                                                    8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 8.4e+02; tive 0; Mismatches 1; Indels
TITLE OF INVENTION: methylations
FILE REFERENCE: BOL/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 79875
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 11; Conservative
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US-10-257-017B-79876
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RESULT 438
US-10-257-017B-79875/C
; Sequence 79875, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosi
                      US-10-257-017B-77735

Sequence 77735, Application US/10257017B

Sequence 77735, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPRENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: D8 10019173.8
FRIOR REPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Watt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: BO1/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 77736
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0019794
US-10-257-0178-77735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0019794 US-10-257-017B-77736
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Pred. No. 8.4e+02;
0; Mismatches 1;
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; Sequence 77736, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7<sup>3</sup>
Matches 11; Conservative
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Best Local Similarity 91.7
Matches 11; Conservative
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Sequence 75919, Application US/10257017B

Sequence 75919, Application:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Peepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: BO1/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
FRICR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 75919
LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: MITTED THE BELIN
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNP8] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-04-07
NUMBER OF SOG ID NOS: 382046
SEQ ID NO 75920
LENGTH: 13
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  Score 10.4; DB 1; Length 13;
Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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Pred. No. 8.4e+02;
0; Mismatches 1;
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ORGANISM: Artificial Sequence
       8.0%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Query Match
Best Local Similarity 91.73
Matches 11, Conservative
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Best Local Similarity
Matches 11; Conserv
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US-10-257-017B-75919
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TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosir TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosir TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: 2010-10-7
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 75287
LENGTH: 13
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GRNERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: Methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 75288
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US-10-257-017B-64544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0019324 US-10-257-017B-75287
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                      Score 10.4; DB 1;
Pred. No. 8.4e+02;
0; Mismatches 1;
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
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                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.0%;
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                          PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 64544
LENGTH: 13
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US-10-257-017B-75288/c
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US-10-257-017B-75287
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
LENGTH: 13
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US-10-257-017B-62608
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Pred. No. 8.4e+02;
0; Mismatches 1;
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PRIOR APPLICATION NUMBER: DE 10019173.8
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
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Best Local Similarity 91.7%;
Matches 11; Conservative
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US-10-257-017B-64543
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US-10-257-017B-62607

Sequence 62607, Application US/10257017B

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi;
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi;
TITLE OF INVENTION: DATE: 2002-10-07

FRICE REFERENCE: 2001-1193/WO

CURRENT PILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 62607
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015803
US-10-257-017B-58982
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Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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US-10-257-017B-62608/c
Sequence 62608, Application US/10257017B
; GENERAL INFORMATION:
                                                                                                                               US-10-257-017B-58982/c
; Sequence 58982, Application US/10257017B
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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1349 GGGAAGAAAAT 1360
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Best Local Similarity 91.7'
Matches 11; Conservative
                                           1 GGGAAAAAAT 12
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 58981
LENGTH: 13
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0015803
US-10-257-017B-58981
                   FEATURE:
, OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0015625
US-10-257-017B-58211
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US-10-257-017B-58212
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8.0%; Score 10.4; DB 1; Length 13;

Best Local Similarity 91.7%; Pred. No. 8.4e+02;

Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                              13;
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8.0%; Score 10.4; DB 1; Length
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 11; Conserv
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-10-257-017B-58212
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GENERAL INFORMATION:
Sequence 56678, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Petection of single nucleotide polymorhphisms [SNPs] and cytosir
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosir
TITLE OF INVENTION: Methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 108/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1133/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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US-10-257-017B-56678
                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015363 US-10-257-017B-56677
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 56677
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
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LENGTH: 13
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Sequence 56677, Application US/10257017B
Sequence 56677, Application US/10257017B
Sequence 56677, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
                                            Sequence 56443, Application US/10257017B

Sequence 56443, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANTON: methylations
FILE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
FRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
FRIOR FILING DATE: 2000-04-07
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosing
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
SEQ ID NOS: 382046
SEQ ID NO 56444
LENGTH: 13
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US-10-257-017B-56444
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US-10-257-017B-56443
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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US-10-257-017B-56444
Sequence 56444, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
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                                               US-10-257-017B-56443/c
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US-10-227-017B-54077/C

US-10-227-017B-54077/C

Sequence 54077, Application US/10257017B

Sequence 54077, Application US/10257017B

Sequence 54077, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: methylations

TITLE OP INVENTION: methylations

FILE REFERENCE: B01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

PRIOR FILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

WUMBER OF SEQ ID NOS: 382046

SEQ ID NO 54077
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TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 2010-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 54078
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                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0014866
US-10-257-017B-54078
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    Score 10.4; DB 1; Length 13;
Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
       8.0%;
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                                                                                                1442 TACATGGAAGAT 1453
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Best Local Similarity 91.7'
Matches 11; Conservative
  Query Match
Best Local Similarity 91.7'
Matches 11; Conservative
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US-10-257-017B-54078
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Sequence 52751, Application US/10257017B
Sequence 52751, Application US/10257017B
Sequence 52751, Application US/10257017B
Sequence 52751, Application US/10257017B
Sequence 52751, Applications
APPLICANT Alexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/MO
CURRENT APPLICANTON NUMBER: US/10/257,017B
CURRENT APPLICANTON NUMBER: US/10/257,017B
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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US-10-257-017B-52752/c

US-10-257-017B-52752/c

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Cristian Plepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REPERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 52752
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US-10-257-017B-52752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0014606 US-10-257-017B-52751
                                                                                                                                        ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0013987 US-10-257-017B-49464
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 49464
LENGTH: 13
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Best Local Similarity
Matches 11; Conserva
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LENGTH: 13
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Page 98

APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin:
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1133/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 382046
SEQ ID NO 48922
LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Alexander Diepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 108/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
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US-10-257-017B-48922
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US-10-257-017B-49463
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91.7%; Pred. No. 8.4e+02;
tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%
Matches 11; Conservative
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Sequence 48921, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 48921

LENGTH: 13
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US-10-257-017B-48808/C
Sequence 48808, Application US/10257017B
SEQUENCE 48808, Application US/10257017B
SEQUENCE 48808
SEQUENCE 48808
SEQUENCE 1NVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine FILE REFERENCE: 2002/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 48808
LENGTH: 13
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US-10-257-017B-48808
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Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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US-10-257-017B-48922/c
; Sequence 48922, Application US/10257017B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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|AAGATTGTTAAT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 11; Conserval
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US-10-257-017B-48921
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Sequence 44422/c
| Sequence 44422/c
| Sequence 44422, Application US/10257017B
| Sequence 44422, Application US/10257017B
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Piepenbrock
| TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
| TITLE OF INVENTION: methylations
| TITLE OF INVENTION: methylations
| FILE REFERENCE: E01/1193/WO
| CURRENT APPLICATION NUMBER: US/10/257, 017B
| CURRENT APPLICATION NUMBER: DE 10019173.8
| PRIOR APPLICATION NUMBER: DE 10019173.8
| PRIOR FILING DATE: 2000-04-07
| NUMBER OF SEQ ID NOS: 382046
| SEQ ID NO 44422
| LENGTH: 13
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Sequence 48807, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 48807
LENGTH: 13
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        ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0013036 US-10-257-017B-44421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0013036 US-10-257-0178-44422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0013866 US-10-257-017B-48807
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                                                                                                       Length 13;
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                                                                                                                                                             Indels
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
                                                                                                       Score 10.4; DB 1;
Pred. No. 8.4e+02;
0; Mismatches 1;
                                                                                                       8.0%;
ilarity 91.7%;
Conservative
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ORGANISM: Artificial Sequence
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                                                                                               Query Match
Best Local Similarity
Matches 11; Conserv
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US-10-257-017B-48807
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Murt Berlin
APPLICANT: Murt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 42370
LENGTH: 13
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US-10-257-017B-44421

US-10-257-017B-44421

Sequence 44421.

Sequence 44421.

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Peopenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

PRIOR FILING DATE: 2000-04-07

NUMBER: OF SEQ ID NOS: 382046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0012640 US-10-257-017B-42370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 10.4; DB 1; Length 13;
Pred. No. 8.4e+02;
0; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07
                                            PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 42369
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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LENGTH: 13
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Sequence 42367, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Curistian Piepenbrock
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: 10010173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 42367
LENGTH: 13
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; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Defection of single nucleotide polymorhphisms [SNPs] and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 405
US-10-257-017B-42368
US-10-257-017B-42368
US-10-257-017B-42368
Squence 42368 Application US/10257017B
GGENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REPERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: D8 10019173.8
PRIOR FILING DATE: 2002-10-07
PRIOR PRILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SSQ ID NO 42368
LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0012640 US-10-257-017B-42367
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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         US-10-257-017B-42367/c
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILLE REFERENCE 101/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR PELLING DATE: 2002-10-07
PRIOR FILLING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
LENOTH: 13
TYPE-
                                                                                                                                                                                                                      Sequence 4115, Application US/10257017B

Sequence 4115, Application US/10257017B

SERNEAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Estlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 100/21973.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 41115
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US-10-257-017B-41115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0012387
US-10-257-017B-41116
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                             1; Indels
       Pred. No. 8.4e+02;
0; Mismatches 1
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    91.78;
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                                                                             1352 AAGAAAAATATT 1363
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       Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                          13 AAAAAAAATATT 2
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Matches 11; Conserva
                                                                                                                                                                                                RESULT 402
US-10-257-017B-41115
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RESULT 404

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Sequence 41013, Application US/10257017B
Sequence 41013, Application US/10257017B
Sequence 41013, Application US/10257017B
Sequence 41013, Application US/10257017B
Sequence 41013, Applications
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER: 0700-04-07
NUMBER:
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US-10-257-017B-41014, Application US/10257017B
Sequence 41014, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: WUNEMION: Detection of single mucleotide polymorhphisms (SNPs) and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUNBER: US/10/257,017B
CURRENT APPLICATION WUNBER: DE 10019173.8
PRIOR APPLICATION WUNBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
WUMBER OF SEQ ID NOS: 382046
SEQ ID NO 41014
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                                                                                                                          FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0012339 US-10-257-017B-40810
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0012376
US-10-257-017B-41014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0012376 US-10-257-017B-41013
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Pred. No. 8.4e+02;
0; Mismatches 1;
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Pred. No. 8.4e+02;
0; Mismatches 1;
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SEQ ID NO 40810
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.74
Matches 11, Conservative
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Best Local Similarity 91.77
Matches 11; Conservative
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US-10-257-017B-41013
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 40809
LENGTH: 13
                       TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine ritle OF INVENTION: methylations FILE REFERENCE: E01/193/WO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT APPLICATION NUMBER: US/10/257,017B PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 39576 LENGTH: 13
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TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
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US-10-257-017B-40809
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0012093
US-10-257-017B-39576
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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Pred. No. 8.4e+02;
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US-10-257-017B-40810/c
; Sequence 40810, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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      Kurt Berlin
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US-10-257-017B-40809
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Matches
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RESULT 395
US-10-257-017B-36072/C
Sequence 36072, Application US/10257017B
Sequence 36072, Application US/10257017B
Sequence 36072, Application US/10257017B
Sequence 36072, Application Sequence 36072, Application Sequence 36072, Applicant Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Defection of single mucleotide polymorhphisms [SNPs] and cytosin TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR PRICE APPLICATION NUMBER: DE 10019173.8
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS 6072
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REPERBNCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: D8 10019173.8
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
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Pred. No. 8.4e+02;
0; Mismatches 1;
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8.0%; Score 10.4; DB 1;

Best Local Similarity 91.7%; Pred. No. 8.4e+02;

Matches 11; Conservative 0; Mismatches 1;
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Sequence 39576, Application US/10257017B

GENERAL INFORMATION:

APPLICANY: Alexander Olek

APPLICANY: Christian Piepenbrock
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APPLICANT: Alexander Olek
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Best Local Similarity 91.7%;
Matches 11; Conservative
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  1 TAAAATTGTTTA 12
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US-10-257-017B-39575
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nuclectide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENT aPPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 100/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 36071
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
LENGTH: 13
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US-10-257-017B-36071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0010636
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0010636
US-10-257-017B-33447
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                                                                         Length 13
                                                                     Score 10.4; DB 1;
Pred. No. 8.4e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                    RESULT 393
US-10-257-017B-33448/c
; Sequence 33448, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Alexander olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                         8.0%;
91.7%;
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ORGANISM: Artificial Seguence
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                                                                            Query Match
Best Local Similarity 91.74
Matches 11; Conservative
                                                                                                                                                                                                                 1 GAGGTAAGATTG 12
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Sequence 32992, Application US/10257017B
Sequence 32992, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPB] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 32992
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 3447
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                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0010460
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 10.4; DB 1;
Pred. No. 8.4e+02;
0; Mismatches 1;
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 32991
LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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US-10-257-017B-32992/c
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                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                FEATURE:
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: With Barlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
CURRENT APPLICATION NUMBER: 105/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 32554
LENGTH: 13
                                                                                                                                                                        TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations TITLE OF INVENTION: methylations FILE REFERENCE: E01/1193/WO CURRENT FILIS REFERENCE: E01/1193/WO CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: US/10/257,017B PRIOR FILING DATE: 2000-04-07 PRIOR FILING DATE: 2000-04-07 SPIOR FILING DAT
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNDs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
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US-10-257-017B-32553
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US-10-257-017B-32554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 10.4; DB 1; Length 13;
Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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   Sequence 32553, Application US/10257017B
GENERAL INFORMATION:
                                                                                                            Christian Piepenbrock
Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                           APPLICANT: Alexander Olek
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Best Local Similarity
Matches 11; Conserva
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APPLICANT:
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US-01-2570-17B-27836/C

15 Sequence 27836, Application US/10257017B

16 Sequence 27836, Application US/10257017B

17 GENERAL INFORMATION:

2 APPLICANT: Alexander Olek

3 APPLICANT: Christian Piepenbrock

3 APPLICANT: Christian Piepenbrock

3 APPLICANT: Christian Piepenbrock

4 APPLICANT: Christian Piepenbrock

5 TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin:

7 TITLE OF INVENTION: methylations

7 TITLE OF SOURTH APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

5 SEQ ID NO 27836

1 LENGTH: 13
                                                                                                                                                                                                                                                          APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: 2002-10-07
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 27835
ILENGTH: 13
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  Indels
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Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
  1;
  Mismatches
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ORGANISM: Artificial Sequence
FEATURE:
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                                                     1435 AGACATATACAT 1446
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     11; Conservative
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Matches 11, Conserva
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     Matches
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US-10-257-017B-27572
JUS-10-257-017B-27572, Application US/10257017B
Sequence 27572, Application US/10257017B
Sequence 27572, Application US/10257017B
Sequence 27572, Application US/10257017B
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/11931/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 27572
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2751, Application US/10257017B
Sequence 2751, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 27571
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US-10-257-017B-27572
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                                                                                FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0004976
US-10-257-017B-23470
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                                                                                                                                                                                      Length 13;
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Pred. No. 8.4e+02;
0; Mismatches 1;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
        LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity
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US-10-257-017B-27571/c
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CENULT 382
USE 10-257-017B-23469/c
| Sequence 22469, Application US/10257017B
| Sequence 22469, Application US/10257017B
| GENERAL INFORMATION:
| APPLICANT: Hazander Olek
| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Piepenbrock
| TITLE OF INVENTION: Detection of Single nucleotide polymorhphisms [SNPS] and cytosi
| TITLE OF INVENTION: methylations
| FILE REFERENCE: B01/1193/NO
| CURRENT APPLICATION NUMBER: US/10/257,017B
| CURRENT PILING DATE: 2002-10-07
| PRIOR APPLICATION NUMBER: DE 10019173.8
| PRIOR FILING DATE: 2000-04-07
| NUMBER OF SEQ ID NOS: 382046
| SEQ ID NO 23469
| LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 23470
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi TITLE OF INVENTION: methylations FILE REFERRICE: B01/1193/WO CURRENT APPLICATION NUMBER: 0210/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR RILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NOS: 382046 SEQ ID NOS: 1382046
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US-10-257-017B-20186
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Best Local Similarity 91.77
Matches 11; Conservative
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US-10-257-017B-20185/c
US-10-257-017B-20185/c
Sequence 20185, Application US/10257017B
Sequence 20185, Application US/10257017B
Sequence 20185, Application Of Sequence 20185, Application Of Sequence 20185, Applications Theorems of Sequence 20185
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of Single nucleotide polymorhphisms [SNPs] and cytosine;
TITLE OF INVENTION: Detection of Single nucleotide polymorhphisms [SNPs] and cytosine;
FILE REFERENCE: E01/1193/W0
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 20185
LENGTH: 13
                                                                                                                                                                                               APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 10019173.8
PRIOR RILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 20130
LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0004129 US-10-257-017B-20130
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Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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91.7%; Pred. No. 8.4e+02;
tive 0; Mismatches 1; Indels
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US-10-257-017B-20186
Sequence 20186, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
                                                                                       US-10-257-017B-20130/c; Sequence 20130, Application US/10257017B; GENERAL INFORMATION: APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Matches 11; Conservative
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Sequence 15939, Application US/10257017B
Sequence 15939, Application US/10257017B
Sequence 15939, Application US/10257017B
SEQUENCE 15939, Application US/10257017B
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNP9] and cytosin TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 15938
LENGTH: 13
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Arexander Olek
APPLICANT: Enristian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosir
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-64-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 20129
LENGTH: 13
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US-10-257-017B-20129
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US-10-257-017B-15938
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                                           Score 10.4; DB 1;
Pred. No. 8.4e+02;
0; Mismatches 1;
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Pred. No. 8.4e+02;
0; Mismatches 1;
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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Best Local Similarity 91.7%;
Matches 11; Conservative
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                                             Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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US-10-257-017B-15938
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    US-10-257-017B-15937
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APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WC
CURRENT FILING DATE: 2002-10-07
PRIOR REPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 13622
LENGTH: 13
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Petection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT APPLICATION WUMBER: DE 10019173.8
FRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-10-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 15937
LENGTH: 13
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US-10-257-017B-13622
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US-10-257-017B-13621
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PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
UNDRER OF SEQ ID NOS: 382046
SEQ ID NO 13621
LENGTH: 13
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ORGANISM: Artificial Sequence
                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 11, Conserv
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US-10-257-017B-15937/c
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 11541
LENGTH: 13
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Sequence 1154.2.

Sequence 1154.2.

APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosi
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/193/MO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 11542
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Sequence 13621, Application US/10257017B

Sequence 13621, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REPERENCE: B01/1193/WO
FURB REPERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07
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US-10-257-017B-11541
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OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002802
US-10-257-0178-11542
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Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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Best Local Similarity 91.7%;
Matches 11; Conservative
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     APPLICANT: Alexander Olek
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: E002-10-07
PRIOR PILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 10539
LENGTH: 13
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
FILE REPERENCE: E01/1037/W0
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 10540
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US-10-257-017B-10539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0002658 US-10-257-017B-10540
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Pred. No. 8.4e+02;
0; Mismatches 1;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
1402 TAAAATTGTTAA 1413
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Best Local Similarity 91.79
Matches 11, Conservative
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US-10-257-017B-11541/c
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US-10-257-017B-10539
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Sequence 10320, Application US/10257017B
Sequence 10320, Application US/10257017B
Sequence 10320, Application US/10257017B
Sequence 10320, Application US/10257017B
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REFERENCE: 801/1193/W0
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 10320
LENGTH: 13
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Sequence 10319, Application US/10257017B

Sequence 10319, Application US/10257017B

Sequence 10319, Application US/10257017B

GENERAL INPORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO

CURRENT PAPLICATION WUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 10319

LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002624
US-10-257-017B-10319
                                                                   ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002071
US-10-257-017B-6924
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                                                                                                                                               Length 13
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.46+02;
Matches 11; Conservative 0; Mismatches 1;
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Pred, No. 8.4e+02;
0; Mismatches 1;
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 91.7%;
Matches 11; Conservative
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US-10-257-017B-10320/c
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Sequence 6924, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Mit Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 6924
LENGTH: 13
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US-10-257-017B-6923
US-10-257-017B-6923
GENERAL INPORMATION:
APPLICANT: Alexander Olek
APPLICANT: Cristian Plepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT FILING DATE: 2002-10-07
FILE REPERENCE: E01/1193/WO
CURRENT FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 6923
LENGTH: 13
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CHER INFORMATION: Oligonuclectide for detection of SNP TSC0001395
US-10-257-017B-3648
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US-10-257-017B-6923
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                                                                                                                                                                                                                                                                                                                                                                    Score 10.4; DB 1; Length 13;
Pred. No. 8.4e+02;
0; Mismatches 1; Indels
; TITLE OF INVENTION: methylations; FILE REFERENCE: E01/1193/WO CURRENT APPLICATION NUMBER: WO/10/257,017B; CURRENT FILING DATE: 2002-10-07; PRIOR APPLICATION NUMBER: DE 10019173.8; PRIOR FILING DATE: 2000-04-07; NUMBER OF SEQ ID NOS: 382046; SEQ ID NOS: 382046; LENGTH: 13
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Sequence 3647, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/193/%0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
                                  SEGUREAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
TITLE OF INVENTION (WABER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 3646
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Sequence 3648, Application US/10257017B

Sequence 3648, Application US/10257017B

GENERALI INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001395
US-10-257-017B-3647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
// OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001395
US-10-257-017B-3646
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Pred. No. 8.4e+02;
0; Mismatches 1;
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ORGANISM: Artificial Sequence
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91.7%;
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Best Local Similarity 91.7
Matches 11; Conservative
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     RESULT 363
US-10-257-017B-3646/c
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 3645
LENGTH: 13
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Sequence 3642, Application US/10257017B

Sequence 3642, Application US/10257017B

Sequence 3642, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Murt Berlin
APPLICANT: Murt Berlin
FILER REFERENCE: E01/1193/WO
FILER REFERENCE: E01/1193/WO
FILER REFERENCE: E01/1193/WO
FILER REPRENCE: E01/1193/WO
FILER REPRENCE: E01/1193/WO
FILER REPRENCE: E00/1193/WO
FILER REPRENCE: 2000-04-07
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 3642

LENGTH: 13
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US-10-257-017B-3645
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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Pred. No. 8.4e+02;
0; Mismatches 1; Indels
  Score 10.4; DB 1; Length 13; Pred. No. 8.4e+02; 0; Mismatches 1; Indels
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Query Match
Best Local Similarity 91.7'
Matches 11; Conservative
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12 AAAAAAATATT 1
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APPLICANT: Alexander Olek
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Wit Berlin
APPLICANT: Wit Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT APPLICATION WUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
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US-10-257-017B-3641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001237
US-10-257-0178-3262
                                                                                                                                                                                ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001237 US-10-257-017B-3261
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                      Score 10.4; DB 1;
Pred. No. 8.4e+02;
0; Mismatches 1;
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; Sequence 3641, Application US/10257017B
; GENERAL INFORMATION:
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; Sequence 3262, Application US/10257017B
; GENERAL INFORMATION:
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
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                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 3261
LENGTH: 13
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Sequence 3251, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/193/W0
CURRENT PAPPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PRING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 1276
                                                                         TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations TITLE OF INVENTION: methylations FILE REFERENCE: E01/1193/WO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT APPLICATION NUMBER: US/10/257,017B PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07
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Pred. No. 8.4e+02;
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US-10-257-017B-1276/c
i. Sequence 1276, Application US/10257017B
; GENERAL INFORMATION:
                             Christian Piepenbrock
Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.0%;
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ORGANISM: Artificial Sequence
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SEQ ID NC 1275
LENGTH: 13
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Best Local Similarity 91.7
Matches 11; Conservative
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        APPLICANT: Alexander Olek
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Matches 11; Conserv
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Sequence 381455, Application US/10257017B
Sequence 381455, Application US/10257017B
Sequence 381455, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 381455
LENGTH: 12
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US-10-257-017B-381597, Application US/10257017B

Sequence 381597, Application US/10257017B

Sequence 381597, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Murt Barlin
FILE REFERENCE: E01/1193/WO

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT PILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 381597

LENGTH: 12
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; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0064373
US-10-257-017B-381455
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US-10-257-017B-381597
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Pred. No. 9.2e+02;
0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 1
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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US-10-257-017B-1275
; Sequence 1275, Application US/10257017B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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1355 AAAAATATTCCA 1366
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                                              12 AAAAATATTCA 1
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| Sequence 380141, Application US/10257017B
| Sequence 380141, Application US/10257017B
| GENERAL INFORMATION:
| APPLICANT: Alexander Olek
| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Widgel uncleotide polymorhphisms [SNPs] and cytosine | TITLE OF INVENTION: methylations |
| TITLE OF INVENTION: methylations | FILE REFERENCE: 2002-10-07 |
| FILE REFERENCE: 2002-10-07 |
| PRIOR APPLICATION NUMBER: US 10019173.8 |
| PRIOR FILING DATE: 2000-04-07 |
| NUMBER: OF SEQ ID NOS: 382046 |
| SEQ ID NO 380141 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 379867
LENGTH: 12
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FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0063658
US-10-257-0178-380141
                                              ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0008405
US-10-257-017B-379142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0009746 US-10-257-017B-379867
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                               Length 12;
                                                                                                                                                                                Indels
                                                                                                                            Score 10.4; DB 1;
Pred. No. 9.2e+02;
                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 379867, Application US/10257017B; GENERAL INFORMATION: APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
                                                                                                                         Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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US-10-257-017B-379867/c
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosin
FILE REPERBROCE: BO1/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DS 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
LENGTH: 12.
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US-10-257-017B-377842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Oligonuclectide primer for the detection of SNP TSC0061943 US-10-257-0178-376709
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Pred. No. 9.2e+02;
0; Mismatches 1;
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Pred. No. 9.2e+02;
0; Mismatches 1;
FILE REFERENCE: E01/1193/WO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 376709 LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-257-017B-377842/c
; Sequence 377842, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
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Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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US-10-257-017B-379142
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GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nuclectide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
                                                                                                                                                                                                                            APPLICANT: Christian Pipenbrock
APPLICANT: Christian Pipenbrock
APPLICANT: Kurt Berlin
TITLE OF INVANTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVANTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 37323
LENGTH: 12
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                                                                                                  Sequence 373223, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
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Best Local Similarity 91.75
Matches 11; Conservative
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                          RESULT 347
US-10-257-017B-373223/c
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US-10-257-017B-371972/c

Sequence 371972, Application US/10257017B

Sequence 371972, Application US/10257017B

SEQUENCE INFORMATION:
APPLICANT: ALExander Olek

APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TILE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosi
TILE OF INVENTION: methylations
TILE OF INVENTION: methylations
TILE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 371972

LENGTH: 12
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Diepenbrock
APPLICANT: Wit Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
SEQ ID NOS: 382046
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US-10-257-017B-373070
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US-10-257-017B-371972
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Score 10.4; DB 1; Length 12;
Pred. No. 9.2e+02;
0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1;
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  Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                        1352 AAGAAAAATATT 1363
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Matches 11; Conserv
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Sequence 371943, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REPERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257, 017B

CURRENT PILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 371943

LENGTH: 12
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TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 370403
LENGTH: 12
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                                                                                                                                                ; OTHER INFORMATION: Oligonuclectide primer for the detection of SNP TSC0057051
US-10-257-017B-368493
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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US-10-257-017B-370403
; Sequence 370403, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; appLICANT: Kurt Berlin
. appLICANT: """"" Detection of single nu
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ORGANISM: Artificial Sequence
     NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 368493
LENGTH: 12
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                                                                                  TYPE: DNA
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Sequence 366931 Application US/10257017B

Sequence 366931 Application US/10257017B

SEQUENCEAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosir
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 366931
FENTILE OF SECOLOGIA OF THE SECO
                               APPLICANT: Kurt Berlin
TITLE OF INVENTION:
TITLE OF INVENTION: Detection of single nuclectide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REPERENCE: 801/1193/WO
CURRENT APPLICATION NUMBER: 108/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
SEQ ID NOS: 382046
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GENUERCAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
TITLE APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10-257,017B
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US-10-257-017B-365010
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1;
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PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
Christian Piepenbrock
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ORGANISM: Artificial Sequence
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US-10-257-017B-368493/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-257-017B-366931/c
APPLICANT:
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                                                                                                       APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPERBNCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR PELLORING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 363916
LEBWIT: 12
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SEQUENCE 364757, Application US/10257, 017B

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: DETECTION OF SINGLE SOURCE SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0054129 US-10-257-017B-363916
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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US-10-257-017B-365010
; Sequence 365010, Application US/10257017B
; APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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    Best Local Similarity
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US-10-257-017B-364757
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US-10-257-017B-362270,
US-10-257-017B-362270,
Sequence 362270, Application US/10257017B
Sequence 362270, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Mart Berlin
APPLICANT: Mover Enj. 100-1193/WO
CURRENT APPLICATION NUMBER: US 100-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
SEQ.ID NOS: 382046
SEQ.ID NO 362270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi TITLE OF INVENTION: methylations FILE OF INVENTION: methylations FILE REFERENCE: E01/1193/WO CURRENT APPLICATION WUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-0.7 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER: OF SEQ ID NOS: 382046 SEQ ID NOS: 382046 SEQ ID NOS: 382046
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, OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0053756
US-10-257-017B-363295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0053115
US-10-257-017B-362270
                  , OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0052937 US-10-257-017B-361893
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Pred. No. 9.2e+02;
0; Mismatches 1; Indels
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                                                                                          8.0%; Score 10.4; DB 1;
ilarity 91.7%; Pred. No. 9.2e+02;
Conservative 0; Mismatches 1;
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1;
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US-10-257-017B-363295/c
US-10-257-017B-363295, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
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                                                                                                                                                                                              1406 ATTGTTAATGAT 1417
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Best Local Similarity 91.74
Matches 11; Conservative
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Best Local Similarity
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SEQUENCE 361893, Application US/10257017B

SEQUENCE 361893, Application US/10257017B

SEQUENCE 361893, Application US/10257017B

SEQUENCE APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian of single nucleotide polymorhphisms [SNPs] and cytosing
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT PILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 361893

LENGTH: 12
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US-10-257-017B-361641
US-10-257-017B-361641
SQUEDICE 301641 Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
CURRENT FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 361641
                                                                                                                                                                                                                                             ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010489
US-10-257-017B-361414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Oligonuclectide primer for the detection of SNP TSC0052741 US-10-257-017B-361641
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                     Query Match 8.0%; Score 10.4; DB 1; Length 12; Best Local Similarity 91.7%; Pred. No. 9.2e+02; Matches 11; Conservative 0; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 361414
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                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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Sequence 358739, Application US/10257017B

SEQUENCE 358739, Application US/10257017B

SEQUENCE 358739, Application US/10257017B

SEQUENCE 358739, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Wart Berlin

TITLE OF INVENTION: UNGHER: US/10/257,017B

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR FILING DATE: 2002-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 35879

BENCH ILENGTH: 12

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US-10-257-017B-360773/C
US-10-257-017B-360773, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin:
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR PRILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 360773
LENGTH: 12
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GENERAL INFORMATION:
APPLICANT: APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0052285
US-10-257-017B-360773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0051274 US-10-257-0178-358739
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Pred. No. 9.2e+02;
0; Mismatches 1; Indels
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Matches 11; Conservative
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US-10-257-017B-361414
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Sequence 358612, Application US/10257017B
GENERAL INFORMATION:
Sequence 358612, Application of Sequence 358612, Application of Sequence 358612, Application of Sequence 358612, Applicant Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 358612
LENGTH: 12
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Sequence 358602, Application US/10257017B

Sequence 358602, Application US/10257017B

Sequence 358602, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek

APPLICANT: Kurt Berlin

APPLICANT: Kurt Berlin

APPLICANT: Murt Berlin

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 358602

LENGTH: 12
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US-10-257-017B-358602
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  Pred. No. 9.2e+02;
); Mismatches 1; Indels
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91.78;
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                                                                          1407 TIGITAATGATG 1418
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Matches 11; Conservative
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  Best Local Similarity 91.7
Matches 11; Conservative
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US-10-257-017B-358612
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RESULT 331

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US-10-257-017B-355488

Sequence 355488. Application US/10257017B

Sequence 355488. Application US/10257017B

Sequence 355488. Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: With Barlin
APLICANT: WINEMION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT APPLICATION WUMBER: US/10-07
PRIOR APPLICATION WUMBER: DE 10019173.8
PRIOR APPLICATION WUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 355488
LENGTH: 12
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: US/10/257,017B
PRIOR PAPLICATION NUMBER: De 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
LENGTH: 12
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/ OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0049665

US-10-257-017B-355488
                                                                                                                           ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0007996 US-10-257-017B-352586
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US-10-257-017B-354801
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Pred. No. 9.2e+02;
0; Mismatches 1;
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Pred. No. 9.2e+02;
0; Mismatches 1;
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ORGANISM: Artificial Sequence
                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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       SEQ ID NO 352586
LENGTH: 12
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 352584
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US-10-257-017B-352586

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REPRENCE: E01/193/Mo

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: US 1000-10-07

PRIOR FILING DATE: 2002-10-07

WUMBER OF SEQ ID NOS: 382046
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/A193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: D10019173.8
PRIOR APPLICATION NUMBER: D2 1002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
LENGTH: 12
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US-10-257-017B-352584
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US-10-257-017B-351735
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                8.0%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 9.2e+02; ive 0; Mismatches 1; Indels
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ORGANISM: Artificial Sequence
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Matches 11, Conservative
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Mirr Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 349432
LENGTH: 12
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosir
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
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US-10-257-017B-349432
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Pred. No. 9.2e+02;
0; Mismatches 1;
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APPLICANT: Alexander olek
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; Sequence 351735, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
                                                                                                          US-10-257-017B-349432
; Sequence 349432, Application US/10257017B
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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        1 AATAATCCACGC 12
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                        RESULT 320
US-10-12P-347791
US-10-257-011B-347791
US-10-257-012B-347791
Sequence 347791, Application US/10257017B
Sequence 347791, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 347791
LENGTH: 12
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US-10-257-017B-348435

US-10-257-017B-348435

Sequence 348435, Application US/10257017B

Sequence 348435, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Mark Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPRENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: D8 10019173.8

PRIOR APPLICATION NUMBER: D8 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NOS: 382046
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP ISC0043725 US-10-257-017B-344833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Oligonuclectide primer for the detection of SNP TSC0045257
US-10-257-017B-347791
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                                                                             Query Match

8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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US-10-257-017B-344833/C
US-10-257-017B-344833/C
Sequence 344833, Application US/10257017B
Sequence 344833, Application US/10257017B
Sequence 344833, Application US/10257017B
Sequence 344833, Application US/10257017B
Sequence 344833, Application US/10257,017B
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFRENCE: B01/1193/MO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 1001-173.8
PRIOR FILING DATE: 2000-44-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: uS/10/257,017B
CURRENT APPLICATION WUMBER: DE 10019173.8
PRIOR APPLICATION WUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 344120
LENGTH: 12
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US-10-257-017B-343889
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US-10-257-0178-344120
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Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1;
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ilarity 91.7%; Pred. No. 9.2e+02;
Conservative 0; Mismatches 1;
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
WIMBER OF SEQ ID NOS: 382046
SEQ ID NO 343889
LENGTH: 12
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
Matches 11; Conserv
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US-10-257-017B-344120/c
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                                                                                                                                                          TYPE: DNA
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; Sequence 343856, Application US/10257017B
; GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILLE OF INVENTION: methylations
FILLE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILLING DATE: 2002-10-07
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR FILLING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 343856
LENGTH: 12
                              APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILER REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-64-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 343662
LENGTH: 12
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Sequence 343889. Application US/10257017B
Sequence 343889. Application US/10257017B
Sequence 343889. Application US/10257017B
Sequence 343889. Application Sequence 343889. Applicant: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin Petection of single nucleotide polymorhphisms (SNPs) and cytosine
TITLE OF INVENTION: methylations
FILE REPRENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
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US-10-257-017B-343662
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Pred. No. 9.2e+02;
0; Mismatches 1; Indels
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Pred. No. 9.2e+02;
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          Sequence 343662, Application US/10257017B
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity
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Sequence 343317, Application US/10257017B
| Sequence 343317, Application US/10257017B
| GENERAL INFORMATION: APPLICANT: Alexander Olek
| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Poetection of Single nucleotide polymorhphisms [SNPs] and cytosin TITLE OF INVENTION: methylations
| TITLE OF INVENTION: methylations | FILE REFERENCE: E01/1193/WO | CURRENT APPLICATION NUMBER: US/10/257,017B
| CURRENT FILING DATE: 2000-04-07 | PRIOR APPLICATION NUMBER: DE 10019173.8 |
| PRIOR APPLICATION NUMBER: DE 10019173.8 |
| PRIOR APPLICATION NUMBER: DE 2001-04-07 |
| NUMBER FOI SEQ ID NOS: 382046 |
| SEQ ID NO 343317 |
| LENGTH: 12
                                                                                                                                                                                                                                                                     APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 340058
LENGTH: 12
TYPE: DAR
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US-10-257-017B-343317
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US-10-257-017B-340058
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Indels
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1;
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Pred. No. 9.2e+02;
0; Mismatches 1;
0; Mismatches
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; Sequence 340058, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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                                             1399 AGGTAAATTGT 1410
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11; Conservative
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Best Local Similarity
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US-10-257-017B-343662/c
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Defection of single nucleotide polymorhphisms [SNPs] and cytosing
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WHRER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 339866
LENGTH: 12
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nuclectide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 339929
LENGTH: 12
                                                              FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP ISC0040769
US-10-257-017B-338974
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US-10-257-017B-339929
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Pred. No. 9.2e+02;
0; Mismatches 1; Indels
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                                                                                                                                                          Score 10.4; DB 1; Length 12; Pred. No. 9.2e+02; 0; Mismatches 1; Indels
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Pred. No. 9.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 339866, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 339929, Application US/10257017B GENERAL INFORMATION:
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91.7%;
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91.7%;
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ORGANISM: Artificial Sequence
                TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity
Matches 11; Conserv
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Best Local Similarity
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US-10-257-017B-339929
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LENGIH: 12
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Sequence 338255, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 338525
LENGTH: 12
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNP8] and cytosi TITLE OF INVENTION: methylations FILE REFERENCE: E01/1193/WO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR APPLICATION NUMBER: DE 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NOS: 382046 LENGTH: 12
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GENERAL INFORMATION:
APPLICANT: Alexander Oil
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR PLING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 338974
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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ORGANISM: Artificial Sequence
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Matches 11; Conserv
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US-10-257-017B-338525
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                                                                                          Sequence 335461, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Petection of Single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION whore: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 335461
LENGTH: 12
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 336216
LENGTH: 12
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US-10-257-017B-335461
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Pred. No. 9.2e+02;
0; Mismatches 1; Indels
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US-10-257-017B-336856/c
; Sequence 338856, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 336216, Application US/10257017B; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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RESULT 304

10s-10-257-017B-332453

10s-10-257-017B-332453

10s-10-257-017B-332453

10s-10-257-017B-332453

10s-10-257-017B-32453

10s-10-257-017B-32453

10s-10-257-017B-32453

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10s-10-257-017B-32453

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Sequence 333917, Application US/10257017B

Sequence 333917, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Petection of single nucleotide polymorhphisms [SNPs] and cytosin TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 333917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0037828 US-10-257-0178-333917
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                                                        Score 10.4; DB 1; Length 12;
Pred. No. 9.2e+02;
0; Mismatches 1; Indels
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91.7%; Pred. No. 9.2e+02;
tive 0; Mismatches 1;
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ORGANISM: Artificial Sequence
                                                                                                                                                1403 AAAATTGTTAAT 1414
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Best Local Similarity 91.73
Matches 11, Conservative
                                                                                                Matches 11, Conservative
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Best Local Similarity
           US-10-257-017B-331329
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PROR FILING DATE: 2000-04-07
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US-10-257-0178-311329
US-10-257-0178-311329
Sequence 331329, Application US/10257017B
Sequence 331329, Application US/10257017B
Sequence 331329, Application US/10257017B
Sequence 331329
CENTEAL INFORMATION: Detection of single nucleotide polymorhphisms (SNPB) and cytosine TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPB) and cytosine FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 331329
LENGTH: 12
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; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0034804
US-10-257-017B-329173
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0036121
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Pred. No. 9.2e+02;
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APPLICANT: Alexander Olek
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 329173
LENGTH: 12
                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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SEQ ID NO 329460
LENGTH: 12
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Curt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
FURRENT APPLICATION NUMBER: 2010/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 328759
LENGTH: 12
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Sequence 328791, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 328791
LENGTH: 12
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
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US-10-257-017B-328759
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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Pred. No. 9.2e+02;
0; Mismatches 1;
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Best Local Similarity 91.7%;
Matches 11; Conservative (
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US-10-257-017B-328791
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                                                                                                                                                                 Sequence 327259, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 100/21973.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 327259
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Sequence 328388, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Abrander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: D10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 328388
LENGTH: 12
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US-10-257-017B-327259
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Pred. No. 9.2e+02;
0; Mismatches 1; Indels
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US-10-257-017B-328759/c
; Sequence 328759, Application US/10257017B
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Best Local Similarity 91.7%;
Matches 11; Conservative
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ORGANISM: Artificial Sequence
1404 AAATTGTTAATG 1415
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Best Local Similarity 91.7'
Matches 11, Conservative
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Sequence 327216, Application US/10257017B
Sequence 327216, Application US/10257017B
Sequence 327216, Application US/10257017B
SEQUENCE INFORMATION:
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosin TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosin TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 327216
LENGTH: 12
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Sequence 326640, Application US/10257017B
Sequence 326640, Application US/10257017B
Sequence 326640, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosir
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT APPLICATION WUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 326640
                                                         FEATURE:

OTHER INFORMATION: Oligonuclectide primer for the detection of SNP TSC0031811

US-10-257-017B-324120
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US-10-257-017B-326640
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                                                                                                                                                                       Length 12;
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Pred. No. 9.2e+02;
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1;
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Pred. No. 9.2e+02;
0; Mismatches 1;
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             TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                      1396 AGGAGGTAAAAT 1407
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                                                                                                                                                                                                                                                                                                                   12 AGGGGGTAAAT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR RILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
SEQ ID NO 323737
LENGTH: 12
LENGTH: 12
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US-10-257-017B-324120/c
Sequence 324120, Application US/10257017B
Sequence 324120, Application US/10257017B
Sequence 324120, Application US/10257017B
Sequence 324120, APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: D10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 324120
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                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0030321
US-10-257-017B-321550
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TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WINBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
FRIOR APPLICATION NUMBER: DE 10019173.8
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 321550
LENGTH: 12
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US-10-257-017B-323737/c
; Sequence 323737, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
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Matches 11; Conserv
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Matches
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Sequence 319342, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Petection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 319342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-257-017B-320378
Sequence 320378, Application US/10257017B
Sequence 320378, Application US/10257017B
Sequence 320378, Application US/10257017B
Sequence 320378, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257, 017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 320378
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Sequence 321550, Application US/10257017B

Sequence 321550, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0029171

US-10-257-017B-319342
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Pred. No. 9.2e+02;
0; Mismatches 1; Indels
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91.7%; Pred. No. 9.2e+02;
tive 0; Mismatches 1;
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Best Local Similarity 91.7°
Matches 11, Conservative
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                   Sequence 318205, Application US/10257017B
; Sequence 318205, Application US/10257017B
; Sequence 318205, Application US/10257017B
; GENERAL INFORMATION:
   APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
   TITLE OF INVENTION: methylations
   TITLE OF INVENTION: methylations
   TITLE OF INVENTION: methylations
   FILE REPERENCE: E01/1193/WO
   CURRENT APPLICATION NUMBER: US/10/257,017B
   CURRENT PILING DATE: 2002-10-07
   PRIOR FILING DATE: 2000-04-07
   NUMBER OF SEQ ID NOS: 382046
   SEQ ID NO 318205

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US-10-257-017B-318749
Sequence 318749, Application US/10257017B
Sequence 318749, Application US/10257017B
Sequence 318749, Application US/10257017B
Sequence 318749, Applications:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FILE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 318749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0028516 US-10-257-017B-318205
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0
Query Match
8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                      1; Indels
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                     1350 GGAAGAAAAATA 1361
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                                                                                                                                                      12 GGGAGAAAATA 1
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US-10-257-017B-317026
US-10-257-017B-317026
Sequence 317026, Application US/10257017B
Sequence 317026, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVERTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVERTION methylations
FILE REFERENCE: E01/1193/WO
FILE REPERENCE: E01/1193/WO
CURRENT PILING DATE: 2002-10-07
FRIOR PILING DATE: 2000-04-07
FRIOR PILING DATE: 2000-04-07
SEQ ID NO 317026
BENGUEL OF SEQ ID NOS: 382046
BENGUEL OF SEQ ID NOS: 382046
BENGUEL OF SEQ ID NOS: 382046
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Sequence 317789, Application US/10257017B
Sequence 317789, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: ALexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Murt Berlin
APPLICANT: Murt Berlin
APPLICANT: WINTER US 10/257,017B
FILE REFERENCE: E01/1193/WO
TITLE OF INVENTION: methylations
FILE REFERENCE: 2002-10-07
FILE REFERENCE: 2002-10-07
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 31789
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7 OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027768

US-10-257-017B-317026
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                                                                                                                                                                                                                                       ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027026
US-10-257-017B-315661
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8.0%; Score 10.4; DB 1;

Best Local Similarity 91.7%; Pred. No. 9.2e+02;

Matches 11; Conservative 0; Mismatches 1;
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Pred. No. 9.2e+02;
0; Mismatches 1;
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Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 315661
LENGTH: 12
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       APPLICANT: Christian Piegenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FITE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT PILIOR DATE: 2002-10-07
PRIOR PILIOR DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
ENGREE OF SEQ ID NOS: 382046
SEQ ID NO 313947
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US-10-257-017B-314004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026044 US-10-257-017B-313947
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Pred. No. 9.2e+02;
0; Mismatches 1;
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; Sequence 315661, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Plepenbrock
; APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER; DE 10019173.8
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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US-10-257-017B-313944/c

Sequence 313944, Application US/10257017B

Sequence 313944, Application US/10257017B

SEGUENCEAL INFORMATION:
APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 313944
                                                                                                                                     US-10-257-017B-313626
US-10-257-017B-313626
US-10-257-017B-313626
Sequence 313626, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin Piepenbrock
APPLICANT: Kurt Berlin Weibylations
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
FILE REPERENCE: D10/1193/WO
CURRENT PILING DATE: 2000-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 313626
LENGTH: 12
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US-10-257-017B-313626
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Pred. No. 9.2e+02;
0; Mismatches 1;
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91.7%; Pred. No. 9.2e+02;
7ative 0; Mismatches 1;
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US-10-257-017B-313947/c
Sequence 313947, Application US/10257017B
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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1356 AAAATATTCCAC 1367
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                                               1 AAAATATTCTAC 12
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Best Local Similarity
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GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Rurt Berlin
APPLICANT: Rurt Berlin
APPLICANT: Rurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICANTON NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 313597
LIBNGTH: 12
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APPLICANT: Kurt Berlin
TTLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: LD: 10-07
PRIOR APPLICATION NUMBER: DE: 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 315521
LENGTH: 12
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US-10-257-017B-313597
                         FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0023938
US-10-257-017B-310357
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                                                                                                                                                                         1; Indels
                                                                                                                      Length
                                                                                                                    Score 10.4; DB 1;
Pred. No. 9.2e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
  ORGANISM: Artificial Sequence
                                                                                                                      Query Match 8.0%;
Best Local Similarity 91.7%;
Matches 11; Conservative
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US-10-257-017B-312521/c
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US-10-257-017B-313597
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APPLICANT: Alexander Olek
Sequence 310184, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPS] and cytosin TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-077
PRICR FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 310184
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Sequence 310357, Application US/10257017B
Sequence 310357, Application US/10257017B
Sequence 310357, Application US/10257017B
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: Methylations
FILER REFERENCE: E01/1193/NO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 310357
LENGTH: 12
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US-10-257-017B-310184
                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0023317 US-10-257-017B-309005
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                       Score 10.4; DB 1; Length 12;
Pred. No. 9.2e+02;
0; Mismatches 1; Indels
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR PELICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 309005
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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US-10-257-017B-310357/c
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR RILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 308016
LENGTH: 12
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
                                                      Sequence 307911, Application US/10257017B
Sequence 307911, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Plepenbrock
APPLICANT: Wart Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 307971
LENGTH: 12
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US-10-257-017B-307971
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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Pred. No. 9.2e+02;
0; Mismatches 1; Indels
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US-10-257-017B-308016/c
; Sequence 308016, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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US-10-257-017B-309005/c
                        RESULT 274
US-10-257-017B-307971
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Sequence 306904, Application US/10257017B
Sequence 306904, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 306904
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: uS/10/257,017B
CURRENT FILING DATE: 2000-10-07
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 307336
LENGTH: 12
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US-10-257-017B-307736
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
Score 10.4; DB 1; Length 12;
Pred. No. 9.2e+02;
0; Mismatches 1; Indels
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APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
  Query Match 8.0%;
Best Local Similarity 91.7%;
Matches 11; Conservative
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US-10-257-017B-307736/c
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US-10-257-017B-306886/C

US-10-257-017B-306886 Application US/10257017B

SEQUENCE 3.06886 Application US/10257017B

GENERAL INPORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: methylations

FILE REPERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT PILING TATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 306649
LENGTH: 12
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; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022228
US-10-257-017B-306886
                                                                                TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
FRATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021890
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US-10-257-017B-306649
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Pred. No. 9.2e+02;
0; Mismatches 1; Indels
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US-10-257-017B-306649/c
; Sequence 306649, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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ORGANISM: Artificial Sequence
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SEQ ID NO 306886
LENGTH: 12
  NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 306244
LENGTH: 12
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APPLICANT: CLISTIAN Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin;
TITLE OF INVENTION: methylations;
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 304813
LENGH: 12
TYPE: ....
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GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Defection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 305909
LENGTH: 12
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APPLICANT: Alexander Olek
APPLICANT: Alexander Diepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosir
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 108/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-10-07
PRIOR FILING DATE: 2000-04-07
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, OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021696
US-10-257-017B-305909
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US-10-257-017B-304813
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Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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US-10-257-017B-306244
; Sequence 306244, Application US/10257017B
; GENERAL INFORMATION:
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin Of Single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 105/10.07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 301245
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019422 US-10-257-017B-301245
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Pred. No. 9.2e+02;
0; Mismatches 1;
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US-10-257-017B-304813/c
; Sequence 304813, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
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Sequence 301245, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
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1 Similarity 91.7%;
11; Conservative (
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Matches 11; Conservative
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Best Local Similarity
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Sequence 298907, Application US/10257017B
Sequence 298907, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILLING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 298907
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi.
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 2010/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 298531
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018143
US-10-257-0178-298531
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP ISC0018036
US-10-257-017B-298340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.0%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 9.2e+02;
                                                                                          Length 12;
                                                                                                                                              Indels
                                                                                          Score 10.4; DB 1;
Pred. No. 9.2e+02;
0; Mismatches 1;
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Sequence 298531, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
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                                                                                               Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity 91.79
Matches 11; Conservative
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Best Local Similarity 91.74
Matches 11; Conservative
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US-10-257-017B-298907/c
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: BOL/1193/WO
CURRENT APPLICATION NUMBER: 2010-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 298340
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US-10-237-017B-296515
US-10-237-017B-296515
Sequence 226515, Application US/10257017B
Sequence 226515, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR RILING DATE: 2000-04-07
SPRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 296515
LENGTH: 12
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US-10-257-017B-296515
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                                                                                                                                                                                                                                                                                                                           Score 10.4; DB 1; Length 12;
Pred. No. 9.2e+02;
0; Mismatches 1; Indels
  CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 296443
LENGTH: 12
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Best Local Similarity 91.7%;
Matches 11; Conservative
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Plepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 293279
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US-10-127-017B-293307/C
US-10-257-017B-293307/Application US/10257017B
Sequence 293307, Application US/10257017B
Sequence 293307, Application US/10257017B
Sequence 293307, Application Sequence 2021
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin: TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin: TITLE OF INVENTION: MUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2002-10-07
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS 293307
LENGTH: 12
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Defection of single nucleotide polymorhphisms [SNPs] and cytosir
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0015566 US-10-257-0178-293307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0015564 US-10-257-017B-293279
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Pred. No. 9.2e+02;
0; Mismatches 1; Indel8
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; Sequence 296443, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                                 ; Sequence 293279, Application US/10257017B ; GENERAL INFORMATION:
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Best Local Similarity 91.7
Matches 11; Conservative
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Matches 11; Conservative
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Sequence 20236, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: D10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 292736
LENGTH: 12
                                                                                                                                                                                                                                                        Sequence 290754, Application US/10257017B
Sequence 290754, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: WHERE: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-64-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 290754
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US-10-257-017B-292736
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Pred. No. 9.2e+02;
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Pred. No. 9.2e+02;
0; Mismatches 1;
                                                 0; Mismatches
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1. Similarity 91.7%;
11; Conservative
                            91.7%;
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                                                 11; Conservative
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Matches 11; Conserv
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Best Local Similarity
                       Best Local Similarity
Matches 11; Conserv
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US-10-257-017B-290754
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RESULT 258

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Sequence 289070, Application US/10257017B
Sequence 289070, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 288664, Application US/10257017B
Sequence 288664, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNP9] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 288604
LENGTH: 12
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, OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0013593
US-10-257-017B-288604
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                                                                                                                                                                             ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0012671
US-10-257-017B-286325
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Pred. No. 9.2e+02;
0; Mismatches 1;
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1;
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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US-10-257-017B-289070/c
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          SEQ ID NO 286325
                                                                                                                                                        FEATURE:
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Sequence 6087 Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kutt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: WHERE: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 100-210-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 286087
LENGTH: 12
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US-10-257-017B-286325
US-10-257-017B-286325, Application US/10257017B
Sequence 286325, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander 0lek
APPLICANT: Curistian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE REPRENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERBORS: E01/1193/WO
CURRENT PAPLICATION NUMBER: US/10/257,017B
CURRENT PAPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
SEQ ID NO 285127
LENGTH: 12
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US-10-257-017B-286087
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US-10-257-017B-285127
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Pred. No. 9.2e+02;
0; Mismatches 1; Indels
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Matches 11, Conservative
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Sequence 284231, Application US/10257017B
APPLICANT: Rart Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Deception of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 284231
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Oligonuclectide primer for the detection of SNP TSC0011889
US-10-257-017B-284590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0011734 US-10-257-0178-284231
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1;
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APPLICANT: Alexander Olek; APPLICANT: Christian Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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1 AAATTGATAATG 12
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
SEQ ID NO 2820 ID NOS: 382046
SEQ ID NO 283401
LENGTH: 12
                                                                                                                                                                                                                                                  RESULT 247
US-10-257-017B-282776
US-10-257-017B-282776
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPRENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: D10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 282776
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US-10-257-017B-283401
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; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0009854
US-10-257-017B-281507
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                                                          Score 10.4; DB 1; Length 12;
Pred. No. 9.2e+02;
0; Mismatches 1; Indels
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Pred. No. 9.2e+02;
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APPLICANT: Alexander Olek
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity 91.7%;
Matches 11; Conservative
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US-10-257-017B-283401
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Sequence 281507, Application US/10257017B
Sequence 281507, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-0.7
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 281507
LENGTH: 12
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: uS/10/257,017B
CURRENT FILING DATE: 2000-04-07
RRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
                                                                                                                                                                                                                                     ) OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0005468 US-10-257-0178-278001
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8.0%; Score 10.4; DB 1;

Best Local Similarity 91.7%; Pred. No. 9.2e+02;

Matches 11; Conservative 0; Mismatches 1;
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Pred. No. 9.2e+02;
0; Mismatches 1;
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
PRIOR APPLICATION NUMBER: 2002-10-07
PRIOR PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 278001
LENGTH: 12
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Best Local Similarity 91.7%;
Matches 11; Conservative
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US-10-257-017B-280021/c
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Defection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: BOL/1193/WO
CURRENT APPLICATION NUMBER: 2012-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 276034
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
                                                           DEBUGGAT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OP INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OP INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 275611
LENGTH: 12
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US-10-257-017B-276034
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Pred. No. 9.2e+02;
0; Mismatches 1; Indels
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US-10-257-017B-276034
; Sequence 276034, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                       Sequence 275611, Application US/10257017B GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 11; Conserva
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Sequence 23367, Application US/10257017B
Sequence 23367, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: 10210-07
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 273667
LENGTH: 12
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Sequence 274418 Application US/10257017B
Sequence 274418 Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Murt Berlin
APPLICANT: Usur Berlin
FILE REFERENCE: E01/1193/WO
FILE REFERENCE: E01/1193/WO
FILE REFERENCE: E01/1193/WO
FILE REFERENCE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 274418
LENGTH: 12
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ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003540
US-10-257-017B-274418
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US-10-257-017B-273667
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1; Indels
Mismatches
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ORGANISM: Artificial Sequence
                                              1401 GTAAAATTGTTA 1412
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Matches 11; Conservative
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                                                                                             12 GTAAAATTGGTA 1
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US-10-257-017B-275611/c
                                                                                                                                                                                             US-10-257-017B-273667
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US-10-257-0178-273275/c

Sequence 273275, Application US/10257017B

Sequence 273275, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Curistian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPS] and cytosine

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1195/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 273275

LENGTH: 12
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Sequence 273627, Application US/10257017B

Sequence 273627, Application US/10257017B

GENERALI INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 273627
                                                                     ; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003013
US-10-257-017B-273012
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US-10-257-017B-273627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003123
US-10-257-017B-273275
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8.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.2e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                     Length 12;
                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                   Score 10.4; DB 1;
Pred. No. 9.2e+02;
0; Mismatches 1;
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91.7%;
                       TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                   Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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1 ATAAAATATTC 12
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Best Local Similarity
LENGIH: 12
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TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPS] and cytosi TITLE OF INVENTION: methylations FILE REPERBINCE: E01/1193/WO CURRENT APPLICATION NUMBER: US/10/257,0178
CURRENT APPLICATION NUMBER: US/10/257,0178
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO SEQ 15 NOS: 382046
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Sequence 272719, Application US/10257017B

Sequence 272719, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Wart Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION UNMBER: US/10/257,017B
CURRENT FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 272719
LENGTH: 12
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Sequence 273012, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Abstander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Defection of single nucleotide polymorhphisms [SNP8] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
SEQ ID NOS: 382046
SEQ ID NO 273012
                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP ISC0001782
US-10-257-017B-269495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Oligonuclectide primer for the detection of SNP ISC0002915
US-10-257-017B-272719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.0%; Score 10.4; DB 1; Length 12; Best Local Similarity 91.7%; Pred. No. 9.2e+02; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.0%; Score 10.4; DB 1; Length 12; Best Local Similarity 91.7%; Pred. No. 9.2e+02; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                    Sequence 267832, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/MO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-10-07
PRACOR PRICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 267832
LENGTH: 12
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US-10-257-017B-269017/C

S SEQUENCE 269017, Application US/10257017B

S SEQUENCE 269017, Application US/10257017B

S SEQUENCE 269017, Application US/10257017B

S PEDICANT: Alexander Olek

APPLICANT: Kurt Berlian Piepenbrock

APPLICANT: Kurt Berlian Piepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

FILE REFERENCE: E01/1193/40

CURRENT APPLICATION NUMBER: US/10/257,017B

PRIOR FILING DATE: 2000-04-07

NUMBER: OF SEQ ID NOS: 382046

SEQ ID NO 269017
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US-10-257-017B-267832
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US-10-257-017B-269017
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US-10-257-U17B-269495
Sequence 269495, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
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RESULT 231
US-10-257-017B-79623/C
Sequence 79623, Application US/10257017B
Sequence 79623, Application US/10257017B
Sequence 79623, Application US/10257017B
Sequence 79623, Application US/10257017B
Sequence 79623, Application Sequence 79623, Applicant Applicant Applicant Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE OF INVENTION: methylations
FILE REPRENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257, 017B
CURRENT APPLICATION NUMBER: D10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 79623
LENGTH: 13
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Sequence 79524, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Detection of single nucleotide polymorhphisms [SNPs] and cytosin TITLE OF INVENTION: methylations
FILE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT FILING DATE: 2000-10-07
FRICH PAPPLICATION NUMBER: 10019173.8
FRICH APPLICATION NUMBER: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 79524
LENGTH: 13
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US-10-257-017B-79623
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US-10-257-017B-79624
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                                                Score 10.6; DB 1; Length 13;
Pred. No. 7.5e+02;
1; Mismatches 0; Indels
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Pred. No. 7.5e+02;
1; Mismatches 0;
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ORGANISM: Artificial Sequence
                                                      8.2%;
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Best Local Similarity 90.9
Matches 10; Conservative
                                                Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                 1 RAAATATTCCA 11
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       US-10-257-017B-66308
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 66307
LENGTH: 13
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Sequence 66308, Application US/10257017B
Sequence 66308, Application US/10257017B
Sequence 66308, Application US/10257017B
Sequence 66308, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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                                                                                                                                                                                    ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0013366
US-10-257-017B-46142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0017421 US-10-257-017B-66307
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8.2%; Score 10.6; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 7.5e+02;
Matches 10; Conservative 1; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 46142
LENGTH: 13
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                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 90.9
Matches 10; Conservative
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LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 2010-10-7
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 46138
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Kutt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT APPLICATION WUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 46141
LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/Wo
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DAIE: 2002-10-07
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                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0013366 US-10-257-017B-46138
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8.2%; Score 10.6; DB 1;
Best Local Similarity 90.9%; Pred. No. 7.5e+02;
Matches 10; Conservative 1; Mismatches 0;
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Best Local Similarity 90.9
Matches 10; Conservative
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US-10-257-017B-46137/C

US-10-257-017B-46137/C

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Cristian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 46137
                                                                                                                                                                                                                                          Sequence 302875, Application US/60545213
Sequence 302875, Application US/60545213
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William Martin
TITLE OF INVENTION: Target Genes
TILE REFERENCE: AM101083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 302875
LENGTH: 25
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US-10-257-017B-46137
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              Length 13;
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              Score 11; DB 1; Le
Pred. No. 5.9e+02;
8.5%; bcc.
100.0%; Pred. No. ...
0; Mismatches
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US-10-257-017B-46138
; Sequence 46138, Application US/10257017B
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ORGANISM: Artificial Sequence
    Query Match
Best Local Similarity 100.'
Matches 11, Conservative
                                                                                                   1451 GATGGGTTGAT 1461
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Best Local Similarity 90.9
Matches 10; Conservative
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12 GATGGGTTGAT 2
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; ORGANISM: probe
US-60-545-213-302875
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US-60-545-213-302875
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Sequence 259837, Application US/10257017B
Sequence 259837, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Rurt Berlin
TITLE OF INVENTION: Defection of single nucleotide polymorhphisms [SNPs] and cytosin:
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 25987
FIRE APPLICATION NUMBER: DE 10019173.8
FRIOR FILING DATE: 2002-10-07
FRIOR FILING DATE: 2005-10-07
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US-1018-259838, Application US/10257017B
Sequence 259838, Application US/10257017B
Sequence 259838, Application US/10257017B
Sequence 259838, Application Sequence 259838, Applicant: Hexander Olek
APPLICANT: Christian Plepenbrock
APPLICANT: Christian Petection of single nucleotide polymorhphisms (SNPs) and cytosir
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 259838
LENGTH: 13
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| FEATURE:
| CTHER INFORMATION: Oligonuclectide for detection of SNP TSC0063098
US-10-257-017B-259838
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                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0060726
US-10-257-017B-248478
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100.0%; Pred. No. 5.9e+02;
ive 0; Mismatches 0; Indels
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Pred, No. 5.9e+02;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 84.6%;
Matches 11; Conservative
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NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 248478
LENGTH: 13
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Best Local Similarity 100.
Matches 11; Conservative
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICANTON NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
SEQ ID NO 248477
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE ON INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
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TITLE OF INVENTION: methylations
CURRENT PRILICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
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US-10-257-017B-236360
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US-10-257-017B-248477
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84.6%; Pred. No. 5.9e+02;
Live 1; Mismatches 1; Indels
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US-10-257-017B-248478/c
'Sequence 248478, Application US/10257017B
; GENERAL INFORMATION:
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Best Local Similarity 84.6'
Matches 11; Conservative
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Best Local Similarity
Matches 11; Conserv
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
FURENT APPLICATION WUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 234266
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US-10-257-017B-236359/c
Sequence 236359, Application US/10257017B
Sequence 236359, Application US/10257017B
SEQUENCE 236359, Application US/10257017B
SEQUENCE STATEMENT Christian Piepenbrock
APPLICANT: Kurt Berlin Piepenbrock
APPLICANT: Kurt Berlin methylations
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: Detection Of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE REPERENCE: E01/1133/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 236359
LENGTH: 13
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Pred. No. 5.9e+02;
0; Mismatches 0; Indels
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                                                                                                                                                                         US-10-257-017B-234266/c

Sequence 234266, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek
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8.5%; Soc
Best Local Similarity 100.0%; P:
Matches 11; Conservative 0;
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              1396 AGGAGGTAAAA 1406
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US-10-257-017B-236360
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Sequence 221992, Application US/10257017B
Sequence 221992, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Plepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 221992
IENGTH: 13
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/Wo
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 234265
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                                                   ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0054021
US-10-257-017B-221991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0054021
US-10-257-017B-221992
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OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0004687

US-10-257-017B-234265
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                                                                                                                                   Query Match 8.5%; Score 11; DB 1; Length 13; Best Local Similarity 84.6%; Pred. No. 5.9e+02; Matches 11; Conservative 1; Mismatches 1; Indels
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-257-017B-234265
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US-10-257-017B-221991

Sequence 221991, Application US/10257017B

Sequence 221991, Application US/10257017B

Sequence 221991, Application US/10257017B

Sequence 221991, Application US/10257017B

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: Detection of single mucleotide polymorhphisms [SNPs] and cytosir

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/MO

CURRENT APPLICATION NUMBER: US/10/257,017B

PRIOR PELICATION NUMBER: US 1000-10-07

PRIOR FILING DATE: 2000-10-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 221991

LENGTH: 13

TYPE: DNA
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APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosir
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: D8 10019173.8
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 220306
LENGTH: 13.
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US-10-257-017B-220305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0008997
US-10-257-017B-220306
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           FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 220305
LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
Matches 11, Conserva
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RESULT 210
3.6210-227-0178-219253/c
Sequence 219253, Application US/10257017B
Sequence 219253, Application US/10257017B
Sequence 219253, Application US/10257017B
Sequence 219253, Application Sequence 2105.
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Wirt Berlin
APPLICANT: WIRTHOR BETSER E01/1193/WO
FILE REFERENCE: E01/1193/WO
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 219253
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US-10-257-017B-220305
; Sequence 220305, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: methylations
; TITLE OF INVENTION: methylations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FILE REPERENCE: BOL/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
CURRENT FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0053312 US-10-257-017B-219253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0053312
US-10-257-017B-219254
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US-10-257-017B-219254
; Sequence 219254, Application US/10257017B
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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LENGTH: 13
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US-10-257-017B-217505/C
US-10-217505, Application US/10257017B
Sequence 217505, Application US/10257017B
Sequence 217505, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Christian Plepenbrock
APPLICANT: Christian Plepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 105/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 217505
LENGTH: 13
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Sequence 217506, Application US/10257017B

Sequence 217506, Application US/10257017B

GENERALI INFORMATION:
APPLICANT: Alexander Colek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Mure Berlin
APPLICANT: Mure Berlin
FILE REFERENCE: E01/1193/WO
FILE REFERENCE: E01/1193/WO
FILE REFERENCE: E01/1193/WO
FILE REPERENCE: 2002-10-07
PRIOR APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 217506
LENGTH: 13
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US-10-257-017B-217505
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US-10-257-0178-217506
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              Query Match 8.5%; Score 11; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 5.9e+02; Matches 11; Conservative 0; Mismatches 0; Indels
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84.6%; Pred. No. 5.9e+02;
tive 1; Mismatches 1;
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ORGANISM: Artificial Sequence
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                                                                                                                                                     1355 AAAAATATTCC 1365
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Best Local Similarity
Matches 11; Conservat
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1133/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 217297
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APPLICANT: Christian Piepenbrock
TITLE OF INVENTION:
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                                                                                                                                                            FEATURE:

OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0052604

US-10-257-0178-216280
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US-10-257-017B-217297
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US-10-257-017B-217298
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100.0%; Pred. No. 5.9e+02;
ive 0; Mismatches 0; Indels
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; Sequence 217297, Application US/10257017B
; GENERAL INFORMATION:
                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 382046
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Matches 11; Conservative
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                             SEQ ID NO 216280
LENGTH: 13
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LENGTH: 13
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APPLICANT: Kurr Berlin
TITLE OF INVENTION: Detection of single nuclectide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 212474
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: D8 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 216279
LENGTH: 13
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US-10-257-017B-216280/c
is Sequence 216280 Application US/10257017B
sequence 216280 Application US/10257017B
sequence 216280 Application
is Sequence 216280 Application
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosir
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.B
PRIOR FILING DATE: 2000-04-07
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US-10-257-017B-212474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0052604
US-10-257-017B-216279
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100.0%; Pred. No. 5.9e+02;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 5.9e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 216279, Application US/10257017B GENERAL INFORMATION:
       Christian Piepenbrock
                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 11; Conservative
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Matches 11; Conservative
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US-10-257-017B-212473/C

US-10-257-017B-212473/C

Sequence 212473, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

SEQ ID NO 212473

LENGTH: 13

LENGTH: 13
                                                                                                                                                                                                                          APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 212188
LENGTH: 13
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009958
US-10-257-017B-212188
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                                                                                                  RESULT 201
US-10-257-017B-21218B/C
; Sequence 21218B, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander 01ek
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; APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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1 TTTTAATGATGAY 13
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US-10-257-017B-212474
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: womber: us/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 208744
LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNP8] and cytosi
TITLE OF INVENTION: methylations
FILLE NEPERENCE: E01/1193/WO
CURRENT FILLING DATE: 2002-10-07
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 212187
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                                   ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0050985 US-10-257-017B-208743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0050985 US-10-257-017B-208744
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US-10-257-017B-212187
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8.5%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                                                              8.5%; Score 11; DB 1; Le
100.0%; Pred. No. 5.9e+02;
tive 0; Mismatches 0;
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; Sequence 208744, Application US/10257017B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11; Conservative
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             FEATURE:
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US-10-257-0178-208743/c

Sequence 208743, Application US/10257017B

Sequence 208743, Application US/10257017B

Sequence 208743, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Cur Berlin

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REPERBYCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: US/10/257,017B

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 208743

LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin Perfection of single mucleotide polymorhphisms [SNPs] and cytosine
ITILE OF INVENTION: Detection of single mucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 201212
LENGTH: 13
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US-10-257-017B-201211
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US-10-257-017B-201212
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8.5%; Score 11; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 11; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 201211
LENGTH: 13
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                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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Sequence 184485, Application US/10257017B

GREEAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVERTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVERTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 184485
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APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 184486
LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosir
FILLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0045528 US-10-257-017B-184485
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8.5%; Score 11; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 11; Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 196
US-10-257-017B-201211/c
; Sequence 201211, Application US/10257017B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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US-10-257-0178-178652
US-10-257-0178-178652
Sequence 178652, Application US/10257017B
Sequence 178652, Application US/10257017B
Sequence 178652, Application Sequence 178652, Application Sequence 178652, Application Sequence 178652, Applicant Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 178652
                                                                                                                                                                                                                                                                                                                                APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: 2010/257,017B
CURRENT APPLICATION WUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 178651
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US-10-257-017B-178651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0044255
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  84.6%; Pred. No. 5.9e+02;
iive 1; Mismatches 1; Indels
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100.0%; Pred. No. 5.9e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                       Sequence 178651, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                              1450 AGATGGGTTGATC 1462
Best Local Similarity 84.6'
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1357 AAATATTCCAC 1367
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                                                                                                                           13 AGATGGGTTTATY 1
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Matches 11; Conserv
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Page 49

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RESULT 191

US-10-257-017B-174982/C

Sequence 174982, Application US/10257017B

Sequence 174982, Application US/10257017B

Sequence 174982, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REFERENCE: BO1/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

PRIOR FILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

WUMBER OF SEQ ID NOS: 382046

SEQ ID NO 174982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 174981, Application US/10257017B
Sequence 174981, Application US/10257017B
GENERAL INFORMATION: Application US/10257017B
GENERAL INFORMATION: APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 174981
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                                   TYPE: DNA
CRANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Oligonucleotide for detection of SNP TSC0043329
US-10-257-0178-174150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:

COTHER INFORMATION: Oligonucleotide for detection of SNP TSC0043499
US-10-257-017B-174981
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US-10-257-017B-174982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 13;
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Best Local Similarity 84.6%; Pred. No. 5.9e+02;
Matches 11; Conservative 1; Mismatches 1;
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ORGANISM: Artificial Sequence
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                  SEQ ID NO 174150
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FITLE OF INVENTION: METAPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 171856
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Mut Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/Wo
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 174149
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US-10-255-0178-174150
Sequence 174150.

APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 10019173.8
FRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0042837 US-10-257-017B-171856
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100.0%; Pred. No. 5.9e+02;
ive 0; Mismatches 0; Indels
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84.6%; Pred. No. 5.9e+02;
tive 1; Mismatches 1; Indels
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US-10-257-017B-174149/c
; Sequence 174149, Application US/10257017B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 171678
LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosir
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 11855
LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042792
US-10-257-017B-171678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042837
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8.5%; Score 11; DB 1; L4
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 11; Conservative 0; Mismatches 0;
                                                                                                                             ; Sequence 171678, Application US/10257017B; GENERAL INFORMATION: APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 186
US-10-257-017B-171855
Sequence 171855, Application US/10257017B
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 187
US-10-257-017B-171856/c
; Sequence 171856, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 11; Conservative
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       12 TCCACGCATCA 2
                                                                                                     10-257-017B-17167B
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APPLICANT: Christian Plepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNP8] and cytosine
TITLE OF INVENTION: methylations
FILE REPERBNCE: BOJ/1193/WO
CURRENT REPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 171677
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APPLICANT: Christian Plepenbrock
APPLICANT: Christian Plepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0040212 US-10-257-017B-159743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040212
US-10-257-017B-159744
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US-10-257-017B-171677
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8.5%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                      Query Match 8.5%; Score 11; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 5.9e+02; Matches 11; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 5.9e+02;
cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                               RESULT 183
US-10-257-017B-159744/c
; Sequence 159744, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11; Conservative
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12 GAGGTAAAATT 2
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RESULT 181
US-quence 155618, Application US/10257017B
i Sequence 155618, Application US/10257017B
i GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
ITILE OF INVENTION: methylations
ITILE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 199618
LENGTH: 13
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US-10-257-017B-159743
Sequence 159743, Application US/10257017B
Sequence 159743, Application US/10257017B
Sequence 159743, Application US/10257017B
Sequence 159743, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Petection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: Methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 159743
LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040184 US-10-257-017B-159618
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8.5%; Score 11; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 5.9e+02;
Matches 11; Conservative 1; Mismatches 1; Indels
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CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
WIMBER OF SEQ ID NOS: 382046
SEQ ID NO 159617
LENGTH: 13
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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Matches 11; Conserv
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Sequence 159616, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
THORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT PELLION DATE: 2002-10-07
FRIOR FILING DATE: 2002-10-07
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 159616
LENGTH: 13
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US-10-257-017B-159617/c
; Sequence 159617, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Christian Piepenbrock
; APPLICANT: Nurt Berlin
; TITLE OF INVENTION: methylations
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
                                        APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Cristian Piepenbrock
APPLICANT: Cristian Piepenbrock
APPLICANT: Cristian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FILE REFERENCE: E01/1133/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR RILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 159615
LENGTH: 13
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US-10-257-017B-159615
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US-10-257-017B-159616
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Pred. No. 5.9e+02;
1; Mismatches 1; Indels
Sequence 159615, Application US/10257017B
GENERAL INFORMATION:
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Best Local Similarity 84.6%
Matches 11; Conservative
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Best Local Similarity
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US-10-257-017B-159616
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APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: methylations

TITLE 
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Sequence 156087, Application US/10257017B
GENERAL INFORMATION:
Sequence 156087, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: 10019173.8
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 156087
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Gaps
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US-10-257-017B-156088
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8.5%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels
Indels
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0; Mismatches
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Best Local Similarity 100.0
Matches 11; Conservative
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                                                        1404 AAATTGTTAAT 1414
11; Conservative
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US-10-257-017B-159615/c
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: muchylations
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR PAPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 151881
LENGTH: 13
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APPLICANT: Christian Pipenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 151882
LENGTH: 13
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                                                                                 FEATURE:
COTHER INFORMATION: Oligonuclectide for detection of SNP TSC0037898
US-10-257-0178-150146
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CTHER INFORMATION: Oligonucleotide for detection of SNP TSC0038376
US-10-257-017B-151881
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US-10-257-0178-151882
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Pred. No. 5.9e+02;
1; Mismatches 1; Indels
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US-10-257-017B-151882/c
Sequence 151882, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
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Best Local Similarity 84.6%;
Matches 11; Conservative 1
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ORGANISM: Artificial Sequence
                                                    ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
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US-10-257-017B-151881
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GENERAL INFORMATION:
FULL OF INVENTION:
FILLE REFERENCE:
FOR THILE OF INVENTION:
GURRENT APPLICATION NUMBER:
CURRENT FILLING DATE:
2002-10-07
FRIOR FILING DATE:
2002-10-07
FRIOR FILING DATE:
2002-04-07
NUMBER OF SEQ ID NOS:
382046
SEQ ID NO 150145
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi TITLE OF INVENTION: methylations FILE REFERENCE: Bol/1193/WO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NOS: 382046 LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Dispenbrock
APPLICANT: Kutt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PLING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 150146
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US-10-257-017B-145424
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8.5%; Score 11; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 11; Conservative 0; Mismatches 0;
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APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                             IS-10-257-017B-144840
Sequence 144840, Application US/10257017B
Sequence 144840, Application US/10257017B
Sequence 144840, Application US/10257017B
Sequence 144840, Application US/10257017B
SEQUENCANT: Alexander Olek
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPS] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 144840
LENGTH: 13
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Sequence 14542. Application US/10257017B

Sequence 145423. Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Plepenbrock

APPLICANT: Christian Plepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPB] and cytosine

TITLE OF INVENTION: methylations

FILE REPERBRICE: E01/1193/W0

CURRENT APPLICATION WUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 145423
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US-10-257-017B-144840
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Curistian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
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Kurt Berlin
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 11; Conserva
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US-10-257-017B-143212
US-10-257-017B-143212
US-10-257-017B-143212
Sequence 143212, Application US/10257017B
Sequence 143212, Application Sequence
Sequence 143212, Application:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1133/WO
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 143212
LENGTH: 13
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Sequence 144839, Application US/10257017B

Sequence 144839

Sequence 144839, Application US/10257017B

Sequence 144839, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin:

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 144839

LENGTH: 13
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0036426
US-10-257-017B-144839
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US-10-257-017B-143212
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84.6%; Pred. No. 5.9e+02;
Live 1; Mismatches 1; Indels
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84.6%; Pred. No. 5.9e+02;
tive 1; Mismatches 1;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.6'
Matches 11; Conservative
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                                                   Query Match 8.5
Best Local Similarity 84.6
Matches 11; Conservative
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       US-10-257-017B-143211
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Sequence 139296, Application US/10257017B

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 139296
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPB] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 143211
LENGTH: 13
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                                                                                                                                                                            FRATURE:
, OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0034884
US-10-257-017B-139295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Oligonuclectide for detection of SNP ISC0034884
US-10-257-017B-139296
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100.0%; Pred. No. 5.9e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                         8.5%; Score 11; DB 1; Length 13; 100.0%; Pred. No. 5.9e+02; ative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 139295
LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity
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US-10-257-017B-143211/c
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Page 43

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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 138227
LENGTH: 13
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Sequence 138.28, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Curt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
FILLE OF INVENTION: methylations
FILLE OF INVENTION: methylations
FILLE OF INVENTION: D1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILLING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 138228
LENGTH: 13
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US-10-257-017B-138227
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8.5%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels
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8.5%; Score 11; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 11; Conservative 0; Mismatches 0;
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; Sequence 139295, Application US/10257017B
; GENERAL INFORMATION:
APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPRENCE: BOL/1193/MO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 137534
TENGTH: 13
                                                                                                                                                               Sequence 137533, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEG OF NOW 137533
LENGTH: 13
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Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 11; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
1402 TAAATTGTTAAT 1414
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                               13 TAAAATTGTTTAY 1
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Matches 11, Conservative
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US-10-257-017B-138227
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US-10-257-017B-134328/c
| Sequence 134328, Application US/10257017B
| Sequence 134328, Application US/10257017B
| GENERAL INFORMATION:
| APPLICANT: Alexander Olek
| APPLICANT: Christian Piepenbrock
| TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosii
| TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosii
| TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosii
| TITLE OF INVENTION: DATE: 2002-10-07
| PRIOR APPLICATION NUMBER: DE 10019173.8
| PRIOR FILING DATE: 2000-04-07
| NUMBER: OF SEQ ID NOS: 382046
| SEQ ID NO 134328
| LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin TITLE OF INVENTION: Detection of Single nucleotide polymorhphisms (SNPs] and cytosin TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/W0
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR PILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 14327
LENGTH: 13
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US-10-257-017B-134328
                                                                                   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Oligonucleotide for detection of SNP ISC0033481
US-10-257-017B-134327
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                                                                                                                                                                         Length 13;
                                                                                                                                                                                                                          Indels
                                                                                                                                                                 Query Match 8.5%; Score 11; DB 1; Les
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 134327, Application US/10257017B GENERAL INFORMATION:
APPLICANT: Alexander Olek
     TYPE: DNA OKGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                US-10-257-017B-134020
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILLING DATE: 2002-10-07
PRIOR PILLING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 156
US-10-127-134019/C
US-10-127-134019/C
US-10-127-134019 Application US/10257017B
i GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REPRENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 134019
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                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0030317 US-10-257-017B-121398
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100.0%; Pred. No. 5.9e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            8.5%; Score 11; DB 1; Length 13;
100.0%; Pred. No. 5.9e+02;
tive 0; Mismatches 0; Indels
; TITLE OF INVENTION: methylations; FILE REFERENCE: E01/1193/WO CURRENT APPLICATION NUMBER: 0270-10-07; PRIOR APPLICATION NUMBER: DE 10019173.8; PRIOR FILING DATE: 2000-04-07; NUMBER OF SEQ ID NOS: 382046; SEQ ID NO 121398
                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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SEQ ID NO 134020
LENGTH: 13
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Best Local Similarity
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0;
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR SEQ ID NOS: 382046
; SEQ ID NO 119736
LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OP INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OP INVENTION: Detection of Single nucleotide polymorhphisms [SNPs] and cytosi
FILE REPERBNG: BO1/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 121397
LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029876
US-10-257-017B-119736
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100.0%; Pred. No. 5.9e+02;
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Pred. No. 5.9e+02;
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Best Local Similarity 84.6%;
Matches 11; Conservative
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US-10-257-017B-121398/c
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                                                                                                                                                                                                                                                                             Sequence 96950, Application US/10257017B
Sequence 96950, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Petection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 96950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 119735, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR PILING DATE: 2000-04-07
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US-10-257-017B-96950
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Pred. No. 5.9e+02;
1; Mismatches 1; Indels
                                   Score 11; DB 1; Length 13; Pred. No. 5.9e+02;
                                                                                 1; Mismatches
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ORGANISM: Artificial Sequence
                                     Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
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Best Local Similarity 84.6%;
Matches 11; Conservative
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SEQ ID NO 119735
LENGTH: 13
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RAAAAAATATT 13
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es 11; Conserva
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US-10-257-017B-96950
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Best Local S:
Matches 11
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US-10-257-017B-96949/C
US-10-257-017B-96949/C
Sequence 96949, Application US/10257017B
Sequence 96949, Application US/10257017B
Sequence 96949, Application Sequence 96949, Sequence 96949, Sequence 96949, Sequence 96949, Sequence 96949, Sequence 96949
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosir
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 96949
LENGTH: 13
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Sequence 88596, Application US/10257017B

Sequence 88596, Application US/10257017B

Sequence 88596, Application US/10257017B

Sequence 88596, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1033/W0

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 88596
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- OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022266
US-10-257-017B-8B596
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024053
US-10-257-017B-96949
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                                                                                                                                                                                                                                                                       8.5%; Score 11; DB 1; Length 13; 100.0%; Pred. No. 5.9e+02; tive 0; Mismatches 0; Indels
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                                                                                                         TYPB: DNA ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 88595
LENGTH: 13
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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; Sequence 85204, Application US/10257017B
; GENERAL INFORMATION:
APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR PRIOR PILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
; SEQ ID NO 85204
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Sequence 88595, Application US/10257017B
Sequence 88595, Application US/10257017B
Sequence 88595, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Mark Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION VUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
                                                                 TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations FILE REFERENCE: E01/1193/WO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER: OF SEQ ID NOS: 382046 SEQ ID NO 85203 LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0021429 US-10-257-017B-85203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0021429
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100.0%; Pred. No. 5.9e+02;
iive 0; Mismatches 0; Indels
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                            Christian Piepenbrock
Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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        APPLICANT: Alexander Olek
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hes 11; Conserv
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                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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US-10-257-017B-82280/c
; Sequence 82280, Application US/10257017B
; Sequence 82280, Application US/10257017B
; GENERAL INFORMATION:
    APPLICANT: Alexander Olek
; APPLICANT: Kart Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
; TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 82280
LENGTH:: 13
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT PAPLICATION NUMBER: uS/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 82279
LENGTH: 13
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US-10-257-017B-82280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0020783

US-L0-257-017B-82279
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Pred. No. 5.9e+02;
0; Mismatches 0; Indels
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US-10-257-017B-85203
'Sequence 85203, Application US/10257017B
'GENERAL INFORMATION:
                                                                                                                                                                                                                                    Sequence 82279, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 11; Conservative
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1353 AGAAAAATATT 1363
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                                                               12 AGAAAAATATT 2
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US-10-127-04315
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US-10-126-0416
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OP INVENTION: methylations
FILE REPERENCE: 801/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PRILICATION DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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                             FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0014737
US-10-257-017B-53384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0016972
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                                                                                                                                                                    Query Match 8.5%; Score 11; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 5.9e+02; Matches 11; Conservative 0; Mismatches 0; Indels
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; Sequence 64316, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
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Matches 11; Conservative
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LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TILL Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPE] and cytosin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR SEQ ID NOS: 382046
SEQ ID NO 53384
LENGTH: 13
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Sequence 53383, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Potection of single nucleotide polymorhphisms (SNPs) and cytosir
TITLE OF INVENTION: methylations
FILE REFRENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT APPLICATION WUMBER: DE 10019173.8
PRIOR APPLICATION WUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-10-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
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US-10-257-017B-39540
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US-10-257-017B-53383
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8.5%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                            Query Match 8.5%; Score 11; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 5.9e+02; Matches 11; Conservative 0; Mismatches 0; Indels
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 39540
LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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Sequence 30756, Application US/10257017B

SEQUENCE 30756, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Giristian Piepenbrock

APPLICANT: Giristian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILER REPERENCE: E01/1193/W0

CURRENT APPLICATION NUMBER: US/10/257,017B

FILER REPERENCE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

SEQ ID NO 30756

LENGTH: 13
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US-10-257-017B-39539

US-10-257-017B-39539

i GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Cristian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

FILE REFERENCE: Boll/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NOS: 382046
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, OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0012088
US-10-257-017B-39539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009454 US-10-257-017B-30756
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100.0%; Pred. No. 5.9e+02;
tive 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity
Matches 11; Conserv
                                    US-10-257-017B-30756
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US-10-257-017B-27546

US-10-257-017B-27546

Sequence 27546, Application US/10257017B

Sequence 27546, Application US/10257017B

Sequence 27546, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REFERENCE: B01/1193/MO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 27546

LENGTH: 13
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Sequence 30755, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Detection of single nuclectide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR PRILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 30755
LENGTH: 13
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OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0009454
US-10-257-017B-30755
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Query Match 8.5%; Score 11; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 5.9e+02; Matches 11; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 5.9e+02;
ive 0; Mismatches 0; IndelB
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 11; Conserva
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US-10-257-017B-30755/c
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 27545
LENGTH: 13
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US-10-257-017B-26414
Sequence 26414, Application US/10257017B
Sequence 26414, Application US/10257017B
Sequence 26414, Application US/10257017B
Sequence 26414, Application US/10257017B
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Murt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FILE REFERENCE: E01/1133/W0
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 26414

LENGTH: 13
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US-10-257-017B-27545
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US-10-257-017B-26414
                                                                                                                                                         OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0006957
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84.6%; Pred. No. 5.9e+02;
tive 1; Mismatches 1; Indels
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; Sequence 27545, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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       NUMBER OF SEQ ID NOS: 382046
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Matches 11; Conservative
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                                 SEQ ID NO 26413
LENGTH: 13
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Page 36

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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 16456
                APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nuclectide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPRENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosir
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
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                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003586
US-10-257-017B-16455
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APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-257-017B-16456
; Sequence 16456, Application US/10257017B
; GENERAL INFORMATION:
Christian Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 11; Conservative
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US-10-257-017B-26413/c
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Murt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-10-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 13340
                                                                                                                         IS-10-257-017B-13339/c
Sequence 13339, Application US/10257017B
SEGUENCE 13339, Application US/10257017B
SEQUENCE 13339, Application US/10257017B
SEQUENCE 13339, Application US/10257017B
SEPERANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: DETECTION UNBER: US/10/257,017B
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 13339
LENGTH: 13
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COTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003085 US-10-257-017B-13340
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Best Local Similarity 84.6%; Pred. No. 5.9e+02;
Matches 11; Conservative 1; Mismatches 1;
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US-10-257-017B-16455/c
'Sequence 16455, Application US/10257017B
'GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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TAAAATTGTTA 1
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR RILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 11445
LENGTH: 13
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Sequence 11446, Application US/10257017B
Sequence 11446, Application US/10257017B
Sequence 11446, Application US/10257017B
Sequence 11446, Application
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: MUNENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 11446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002795
US-10-257-017B-11445
                           ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0000021
US-10-257-017B-78
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                                                                                                               Length 13;
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100.0%; Pred. No. 5.9e+02;
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8.5%; Score 11; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 11; Conservative 0; Mismatches 0;
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; Sequence 11445, Application US/10257017B
; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 11; Conservative
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US-10-257-017B-11446/c
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Abrander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Polection of Single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
FILE REFERENCE: E01/1193/WO
FILE REFERENCE: E01/1193/WO
FILE REPERENCE: 2002-10-07
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR APPLICATION NUMBER: DE 2000-04-07
NUMBER OF SEQ ID NOS: 382046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nuclectide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 77
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US-10-257-0178-77
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8.5%; Score 11; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 11; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 10/376,770
PRIOR FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 628
SOFTWARE: PASLSEQ for Windows Version 4.0
SEQ ID NO 549
LENGTH: 12
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                         OTHER INFORMATION: Primer
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US-10-257-017B-78/c
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Sequence 381382, Application US/10257017B

Sequence 381382, Application US/10257017B

Sequence 381382, Application:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin Diepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION whater: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
CURRENT PILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 381382
TENGRAL 10 381382
                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0062669 US-10-257-017B-378197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Oligonuclectide primer for the detection of SNP TSC0064322 US-10-257-017B-381382
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GENERAL INFORMATION:
GENERAL INFORMATION:
JAPPLICANT: Dhallan, Ravinder S.
TITLE OF INVENTION: METHODS FOR DETECTION OF GENETIC
TITLE OF INVENTION: DISORDERS
TITLE REFERENCE: 54331200420
CURRENT APPLICATION NUMBER: US/10/661,165
CURRENT APPLICATION NUMBER: DCT/US03/06198
PRIOR PILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 60/378,354
PRIOR APPLICATION NUMBER: US 60/378,354
PRIOR APPLICATION NUMBER: US 0/093,618
PRIOR APPLICATION NUMBER: US 0/093,618
PRIOR PILING DATE: 2002-03-11
PRIOR PILING DATE: 2002-03-01
PRIOR PLING DATE: 2002-03-01
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100.0%; Pred. No. 6.4e+02;
tive 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 378197
LENGTH: 12
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Matches 11; Conservative
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US-10-257-017B-381382/c
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US-10-257-017B-378196, Application US/10257017B
Sequence 378196, Application US/10257017B
Sequence 378196, Application US/10257017B
Sequence 378196, Application:
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
SCURRENT APPLICATION WHERE: 2002-10-07
FILE REFERENCE: E01/1193/WO
SCURRENT FILING DATE: 2002-10-07
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 378196
SEQ ID NO 378196
                                                                                                               APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 100/210-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
SPRIOR PILING DATE: 2000-04-07
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APPLICANT: Alexander Olek
APPLICANT: Christian Fiepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0054493
US-10-257-017B-364483
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            US-10-257-017B-364483/c
; Sequence 364483, Application US/10257017B
; GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-257-017B-378197/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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Sequence 357907, Application US/10257017B
Sequence 357907, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Plepenbrock
APPLICANT: Christian Plepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
FILE REFERENCE: Bol/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 357907
LENGTH: 12
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FILE REPRENCE: 801/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-0.7
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 360594
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Oligonuclectide primer for the detection of SNP TSC0004855
US-10-257-017B-357907
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100.0%; Pred. No. 6.4e+02;
ive 0; Mismatches 0; Indels
                          Indels
100.0%; Pred. No. 6.4e+02; ative 0; Mismatches 0;
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Sequence 360594, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 11, Conservative
                                                                           1355 AAAAATATTCC 1365
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Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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US-10-257-017B-357907/c
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APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 347793
LENGTH: 12
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US-10-257-017B-353427/c
is Sequence 353427, Application US/10257017B
is Sequence 353427, Application US/10257017B
is GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Diepenbrock
APPLICANT: Christian Diepenbrock
APPLICANT: Christian Diepenbrock
APPLICANT: Muxt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
FERNING 353427
                                                TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043880
US-10-257-017B-345115
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US-10-257-017B-347793
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
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ORGANISM: Artificial Sequence
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1 AAGAAAATAT 11
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US-10-257-017B-347793
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     SEQ ID NO 345115
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RESULT 119

8.5%; Score 11; DB 1; Length 12;

Query Match

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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/#0
CURRENT APPLICATION NUMBER: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
SEQ ID NOS: 382046
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US-10-257-017B-345115

Sequence 345115, Application US/10257017B

Sequence 345115, Application US/10257017B

Sequence 345115

APPLICANT: Alexander Olek

APPLICANT: Alexander Olek

APPLICANT: Alexander Olek

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNP8] and cytosir

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNP8] and cytosir

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNP8] and cytosir

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNP8] and cytosir

TITLE OF INVENTION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: US 100/257,017B

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Oligonuclectide primer for the detection of SNP TSC0038581 US-10-257-017B-335063
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100.0%; Pred. No. 6.4e+02;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 6.4e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity
Matches 11; Conserva
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                                                                                                                                                                                                       Sequence 315231/C
| Sequence 315231/Application US/10257017B
| Sequence 31521, Application US/10257017B
| GENERAL INFORMATION:
| APPLICANT: Alexander Olek
| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Poetection of single nucleotide polymorhphisms [SNPS] and cytosine | TITLE OF INVENTION: methylations | TITLE OF INVENTION: methylations | FILE REFERENCE: E01/1193/WO | CURRENT APPLICATION NUMBER: US/10/257,017B | CURRENT APPLICATION NUMBER: DE 10019173.8 | PRIOR PILING DATE: 2002-10-07 | PRIOR FILING DATE: 2000-04-07 | NUMBER OF SEQ ID NOS: 382046 | SEQ ID NO 315231 | LENGTH: 12
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR RAPPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 334734
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP ISC0038375
US-10-257-017B-334734
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100.0%; Pred. No. 6.4e+02;
tive 0; Mismatches 0; Indels
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Pred. No. 6.4e+02;
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8.5%; Score 11; DB
Best Local Similarity 100.0%; Pred. No. 6.4
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US-10-257-017B-335063
; Sequence 335063, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: ALEXANder Olek
; APPLICANT: Christian Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 334734, Application US/10257017B; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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                                                                                                                                  12 AAGAAAAATAT 2
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Best Local Similarity
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RESULT 109

US-10-257-017B-288484/c

i Sequence 288484, Application US/10257017B

i GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/NO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-64-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 288484
                                                                                                                                                                                                                                                                                                                                                                   US-10-257-017B-285252

Sequence 285252, Application US/10257017B

Sequence 285252, Application US/10257017B

GENERAL INPORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 108710/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS 285252
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  . OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0011450 US-10-257-017B-283665
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                                                                                   8.5%; Score 11; DB 1; Length 12;
100.0%; Pred. No. 6.4e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Oligonukleotid-Primer US-10-257-017B-285252
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                 Best Local Similarity 100.
Matches 11; Conservative
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                                                                                            Query Match
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Sequence 283-65, Application US/10257017B

Sequence 283-65, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: More Beaction of single nucleotide polymorhphisms (SNPs) and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: E01/1937-W0
CURRENT FILING DATE: 2002-10-07
PRIOR PAPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046

SEQ ID NOS: 382046
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APPLICANT: Christian Pippenbrock
APPLICANT: Christian Pippenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 282391
LENGTH: 12
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                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010466 US-10-257-017B-282132
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US-10-257-017B-282391/c
; Sequence 282391, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 282132
LENGTH: 12
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ORGANISM: Artificial Sequence
                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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Sequence 282131, Application US/10257017B
| Sequence 282131, Application US/10257017B
| Sequence 282131, Application US/10257017B
| GENERAL INFORMATION:
| APPLICANT: Abrander Olek
| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Defection of single nucleotide polymorhphisms (SNPs) and cytosir | TITLE OF INVENTION: methylations | TITLE OF INVENTION: methylations | FILE REFERENCE: E01/1193/WO | CURRENT APPLICATION NUMBER: US/10/257,017B | CURRENT APPLICATION NUMBER: DE 10019173.8 | PRIOR APPLICATION NUMBER: DE 10019173.8 | PRIOR FILING DATE: 2000-04-07 | NUMBER OF SEQ ID NOS: 382046 | SEQ ID NOS 282131 | SED ID NOS: 2822131 | SED ID NOS: 282313 | SED ID NOS: 2822131 | SED ID NOS: 282231 | SED ID NOS: 2822131 | SED ID NOS
                             GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Mure Early
TITLE OF INVENTION: methylations
FILE REPERRANCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 279373
LENGTH: 12
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosir
FILLE OF INVENTION: methylations
FILLE OF INVENTION: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Oligonuclectide primer for the detection of SNP TSC0007280 US-10-257-017B-279373
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8.5%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels
Sequence 279373, Application US/10257017B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 11; Conservative
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US-10-257-017B-282132
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US-10-257-017B-268599, Application US/10257017B

Squence 268599, Application US/10257017B

SGUENCEAL INPORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Murt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
SEQ ID NOS: 382046
SEQ ID NO 268599
INDEATH: 12
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Sequence 276339, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Abrander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: D100/257,017B
PRIOR FILING DATE: 2002-10-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 276339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0001245
US-10-257-017B-268599
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Best Local Similarity
Matches 11; Conserv
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US-10-257-017B-279373
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
SEQ ID NOS: 382046
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 227050
LENGTH: 13
                                                                                                                       ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0057828 US-10-257-017B-237048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0057828
US-10-257-017B-237049
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US-10-257-017B-237050
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8.8%; Score 11.4; DB 1;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1;
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8.8%; Score 11.4; DB 1;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1;
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Pred. No. 4.6e+02;
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; Sequence 237049, Application US/10257017B
; GENERAL INFORMATION:
APPLICANT: Alexander Olek
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; Sequence 237050, Application US/10257017B
; GENERAL INFORMATION:
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92.3%;
                                      TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
           LENGTH: 13
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US-10-257-017B-237047
is Sequence 237047, Application US/10257017B
is GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
CURRENT FILING DATE: 2002-10-07
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 237047
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US-10-257-017B-237048/C

US-10-257-017B-237048, Application US/10257017B

Sequence 237048, Application US/10257017B

Sequence 237048, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Kurt Berlin

TITLE OF INVENTION: methylations

TITLE OF INVENTION WIMBER: US 1002-10-07

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

SEQ ID NO 237048
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine FITLE OF INVENTION: methylations FITLE OF INVENTION: methylations FILLE SEPERATOR (1193/WO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILLING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 SEQ ID NOS: 382046 SEQ ID NOS: 382046 SEQ ID NOS: 382046
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US-10-257-017B-237020
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ORGANISM: Artificial Sequence
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Sequence 231560, Application US/10257017B
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Sequence 231560, Application Application Of Sequence 231560, Application Sequence 231560
TITLE OF INVENTION: methylations TITLE OF INVENTION: methylations FILE REFERENCE: E01/1193/WO CURRENT Application NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/277,017B
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 231560
LENGTH: 13
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Sequence 237019, Application US/10257017B
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Detection of single nucleotide polymorhphisms [SNPs] and cytosir
ITILE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosir
ITILE OF INVENTION: Methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT APPLICATION WUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 237019
LENTING: APPLICATION WIMBER: DE 10019173.8
LENTING: MUMBER OF SEQ ID NOS: 382046
SEQ ID NO 237019
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US-10-257-017B-237019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0056462
US-10-257-017B-231560
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8.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.8%; Score 11.4; DB 1; Length 13; Best Local Similarity 92.3%; Pred. No. 4.6e+02; Matches 12; Conservative 0; Mismatches 1; Indels
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US-10-257-017B-237020
US-10-257-017B-237020, Application US/10257017B
; Sequence 237020, Application US/10257017B
; SAPPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
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ORGANISM: Artificial Sequence
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 231559
LENGTH: 13
                                                                                                                                                                                                                                                                                                               Sequence 223956 Application US/10257017B
Sequence 223956 Application US/10257017B
SEQUENCE INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-10-07
PRIOR FILING DATE: 2000-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 223956
LENGTH: 13
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llarity 92.3%; Pred. No. 4.6e+02;
Conservative 0; Mismatches 1; Indels
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                                          Query Match

8.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels
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Best Local Similarity
Matches 12; Conserv
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US-10-257-017B-231559
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US-10-257-017B-223955
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Sequence 221380/c

195-10-257-017B-221380/c

Sequence 221380 Application US/10257017B

Sequence 221380 Application US/10257017B

Sequence 221380 Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Oligonucleotide for detection of SNP ISC0053879 US-10-257-017B-221380
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US-10-257-017B-221379
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8.8%; Score 11.4; DB 1;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1;
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US-10-257-017B-223955/C
i Sequence 223955, Application US/10257017B
i GENERAL INFORMATION:
   APPLICANT: Alexander Olek
i APPLICANT: Kurt Berlin Piepenbrock
i APPLICANT: Kurt Berlin Detection of single nucle,
ITLE OF INVENTION: Detection of single nucle,
ITLE OF INVENTION: methylations
FILE REPERBACE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
i RIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
i NUMBER OF SEQ 1D NOS: 382046
i SEQ 1D NO 223955
i LENGTH: 13
                                                                                                                                             PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 221379
LENGTH: 13
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 92.31
Matches 12; Conservative
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### schultz91

Lalcant: Caristian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REPRENCE: E01/1193/WO

CURRENT PILING DATE: 2002-10-07

PRIOR PELING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 216235

LENGTH: 13

TYPE
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APPLICANT: Alexander Olek

APPLICANT: Kurt Berlin

APPLICANT: Wurt Berlin

APPLICANT: Wurt Berlin

APPLICANT: Wurt Berlin

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APPLICANT: Berlin

APPLICANT: Berlin

APPLICANT: NOW MURBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 216236

LENGTH: 13
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Sequence 221379, Application US/10257017B
Sequence 221379, Application US/10257017B
Sequence 221379, Application S
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
FILE REFERENCE: E01/1193/W0
CURRENT APPLICANTON NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
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8.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels
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Best Local Similarity
Matches 12; Conserva
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Sequence 216234, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TILLS OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin: TILLS OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT PAPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 216234
                                                                                                                           US-10-257-017B-216233
US-10-257-017B-216233
US-10-257-017B-216233
US-10-257-017B-216233
Sequence 216233. Application US/10257017B
Sequence 216234. Application:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
FRIGH APPLICATION NUMBER: DE 10019173.8
PRIGH APPLICATION DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 216233
LANGTH. 10 201223
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CONTINUE INFORMATION: Oligonucleotide for detection of SNP TSC0052586

US-10-257-017B-216233
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8.8%; Score 11.4; DB 1;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1;
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             1356 AAAATATTCCACG 1368
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                                                            1 ACAATATTCCACG 13
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Best Local Similarity
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US-10-257-017B-216234/c
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US-10-257-017B-216235
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 189806
LENGTH: 13
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APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
RRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
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US-10-257-017B-189806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046704 US-10-257-017B-189805
                                                         ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0043213
US-10-257-017B-173478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.8%; Score 11.4; DB 1; Length 13; 92.3%; Pred. No. 4.6e+02;
                                                                                                                                           Length 13;
                                                                                                                                                                                             1; Indels
                                                                                                                                      Query Match

8.8%; Score 11.4; DB 1;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1;
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                          US-10-257-017B-189805/c; Sequence 189805, Application US/10257017B; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 92.3
Matches 12; Conservative
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1 AAATACTCCACG 13
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US-10-257-017B-189806
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Sequence 173478, Application US/10257017B
Sequence 173478, Application US/10257017B
Sequence 173478, Application US/10257017B
SEQUENCE 173478, Application of Sequence 173478
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of Single nucleotide polymorhphisms (SNPS) and cytosi
TITLE OF INVENTION: methylations
FILE OF INVENTION: methylations
FILE OF INVENTION: methylations
FILE OF INVENTION: Detection of Single nucleotide polymorhphisms (SNPS) and cytosi
FILE OF INVENTION: DETECTION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-04-07
RECORDER OF SEQ ID NOS: 382046
SEQ ID NO 173478
LENGTH: 13
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US-10-257-0178-173477/C

US-10-257-0178-173477/C

Sequence 173477, Application US/10257017B

Sequence 173477, Application US/10257017B

Sequence 173477, Application US/10257017B

Sequence 173477, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: methylations

FILE REFRENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 173477
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0043213
US-10-257-017B-173477
                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042981
US-10-257-017B-172420
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92.3%; Pred. No. 4.6e+02;
tive 0; Mismatches 1; Indels
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Pred. No. 4.6e+02;
0; Mismatches 1;
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 172420
LENGTH: 13
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Matches 12; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
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                                                           US-10-257-017B-171584/C
Sequence 171584, Application US/10257017B
Sequence 171586
Sequ
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PLING DATE: 2000-04-07
NUMBER OF SEC ID NOS: 382046
SEC ID NO 172419
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; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
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US-10-257-017B-171584
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; Sequence 172419, Application US/10257017B
; GENERAL INFORMATION:
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US-10-257-017B-172420/c
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Best Local S
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APPLICANT: Christian Piepenbrock
APPLICANT: Curistian Piepenbrock
APPLICANT: Curistian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosir
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 11583
LENGTH: 13
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US-10-257-017B-161090, Application US/10257017B
SQUENCE 161090, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Murt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosir
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 161090
LENTING APPLICATION NOS: 382046
SEQ ID NO 161090
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US-10-257-017B-171583
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    8.8%; Score 11.4; DB 1; Length 13; 92.3%; Pred. No. 4.6e+02; ive 0; Mismatches 1; Indels
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8.8%; Score 11.4; DB 1;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1;
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8.8%; Score 11.4; DB 1;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1;
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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                                                                                          1403 AAAATTGTTAATG 1415
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          9.89
Best Local Similarity 92.33
Matches 12; Conservative
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Sequence 161089, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 161089
LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009515 US-10-257-017B-154796
                                                                                                                                 ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009515
US-10-257-017B-154795
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Pred. No. 4.6e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                          Length 13
                                                                                                                                                                                                                                                1; Indels
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8.8%; Score 11.4; DB 1;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 154796, Application US/10257017B GENERAL INFORMATION:
APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                           1352 AAGAAAAATATTC 1364
      2000-04-07
PRIOR FILING DATE: 2000-04-0' NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 154795 LENGTH: 13
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Best Local Similarity
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US-10-257-017B-161089
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: BO1/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 154357
LENTH: 13
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Sequence 154358, Application US/10257017B
Sequence 154358, Application US/10257017B
Sequence 154358, Application US/10257017B
Sequence 154358, Application Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Diepenbrock
APPLICANT: NurBerlin methylations
TITLE OF INVENTION: methylations
FILLS OF INVENTION: methylations
FILLS OF INVENTION: methylations
FILLS OF INVENTION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILLING DATE: 2000-04-07
RATOR FILLING DATE: 2000-04-07
RATOR FILLING DATE: 2000-04-07
SEQ ID NO 154358
LENGTH: 13
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CURRENT APPLICATION NUMBER: 2002-10-07
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US-10-257-017B-154357
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Pred. No. 4.6e+02;
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
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Best Local Similarity 92.3%;
Matches 12; Conservative
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US-10-257-017B-151702/ Application US/10257017B
Sequence 151702, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Abrander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Detection of single nucleotide polymorhphisms [SNP8] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNP8] and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 151702
LENGTH: 13
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 151701
LENGTH: 13
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US-10-257-017B-151702
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8.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels
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Pred. No. 4.6e+02;
0; Mismatches 1; Indels
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US-10-257-017B-154357
; Sequence 154357, Application US/10257017B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    ; Sequence 151701, Application US/10257017B; GENERAL INFORMATION: , APPLICANT: Alexander Olek
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Local Similarity 92.3%;
hes 12; Conservative (
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ORGANISM: Artificial Sequence
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US-10-257-017B-151701
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Sequence 150141, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Curistian Piepenbrock
APPLICANTON: methylations
FILE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 150141
LENGTH: 13
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                        FEATURE:
CTHER INFORMATION: Oligonucleotide for detection of SNP TSC0036706
US-10-257-0178-145724
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8.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels
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8.8%; Score 11.4; DB 1;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1;
                                                                                                                            Score 11.4; DB 1;
Pred. No. 4.6e+02;
0; Mismatches 1;
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ORGANISM: Artificial Sequence
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                                                                                                                               Query Match
Best Local Similarity 92.3%;
Matches 12; Conservative
ORGANISM: Artificial Sequence
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US-10-257-017B-150141/c
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENITON: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENITON: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO S: 382046
SEQ ID NO 145724
TYPE: DNA
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US-10-257-017B-145723
US-10-257-017B-145723
US-10-257-017B-145723
Sequence 145723, Application US/10257017B
Sequence 145723, Application US/10257017B
Sequence 145723, Application Sequence 10-18
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Detection of single nucleotide polymorhphisms (SNPB) and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPB) and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-10-07
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 145723
LENGTH: 13
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US-10-257-017B-145723
                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Oligonuclectide for detection of SNP TSC0034809 US-10-257-017B-138954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.8%; Score 11.4; DB 1; Length 13; ilarity 92.3%; Pred. No. 4.6e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Length 13;
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Pred. No. 4.6e+02;
0; Mismatches 1;
     FILE REFERENCE: E01/1193/WO CURRENT APPLICATION NUMBER: U5/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 138954
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; Sequence 145724, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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11 Similarity 92.3%;
12; Conservative (
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Best Local Similarity
Matches 12; Conservat
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tes 12; Conserv
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Best Local Si
Matches 12,
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RESULT 62

US-10-257-017B-137724/c

Sequence 137724, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 137724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 138953
LENGTH: 13
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) Sequence 138954, Application US/10257017B
; Sequence 138954, Application US/10257017B
; GENERAL INFORMATION:
) APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
; TITLE OF INVENTION: methylations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0034809
US-10-257-017B-138953
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US-10-257-017B-138953
; Sequence 138953, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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Matches 12, Conserv
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Sequence 137723, Application US/10257017B
Sequence 137723, Application Sequence
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 13723
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Sequence 137374, Application US/10257017B

Sequence 137374, Application US/10257017B

Sequence 137374, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10.07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER: OF SEQ ID NOS: 382046

SEQ ID NO 137374
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US-10-257-0178-137723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0034317
US-10-257-017B-137374
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        8.8%; Score 11.4; DB 1; Length 13; 92.3%; Pred. No. 4.6e+02; Live 0; Mismatches 1; Indels
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8.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels
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ORGANISM: Artificial Sequence
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                                                                                                                1396 AGGAGGTAAAATT 1408
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          Query Match
Best Local Similarity 92.3
Matches 12; Conservative
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hes 12; Conserv
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US-10-257-017B-137723
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US-10-257-017B-136992

US-10-257-017B-136992

Sequence 136992, Application US/10257017B

Sequence 136992, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosir

TITLE OF INVENTION: methylations

TILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR PILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 136992

LENGTR: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REFERENCE: BO1/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 137373
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ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0034317
US-10-257-017B-137373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0034234
US-10-257-0178-136992
                                                                                                                                                                    ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0034234
US-10-257-017B-136991
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8.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels
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8.8%; Score 11.4; DB 1;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1;
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
SEQ ID NO 136991
LENGTH: 13
TYPE: DNA
CREANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 1002-10-07
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
        APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 99881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Berling
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/MO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 99882
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US-10-257-017B-99882
                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0024826
US-10-257-017B-998B1
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8.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels
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US-10-257-017B-998B2/c
; Sequence 998B2, Application US/10257017B
; GENERAL INFORMATION:
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US-10-257-017B-136991/c
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Sequence 97197, Application US/10257017B
GEQUENCE 97197, Application US/10257017B
GEQUENCE 97197, Application US/10257017B
GEQUENCE 97197, Application US/10257017B
GEQUENCE 97197, Application Of Single US/10257017B
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of Single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: Detection of Single nucleotide polymorhphisms [SNPs] and cytosi
FILE OF INVENTION: Detection of Single nucleotide polymorhphisms [SNPs] and cytosi
FILE OF INVENTION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 97197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-257-017B-97198/C
Sequence 97198 Application US/10257017B
Sequence 97198 Application US/10257017B
Sequence 97198 Application US/10257017B
Sequence 97198 Application US/10257017B
GENERAL INROADION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT RILING DATE: 2002-10-07
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
SEQ ID NO 97198
SEQ ID NO 97198
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US-10-257-0178-97197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024108 US-10-257-017B-97198
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8.8%; Score 11.4; DB 1;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1;
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ORGANISM: Artificial Sequence
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RESULT 53
US-10-257-017B-97197
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US-10-257-017B-85504/c
US-10-257-017B-85504/c
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
FILE OF INVENTION: MUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER: CF SEQ ID NOS: 382046
SEQ ID NO 85504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: BO1/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 85503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0021486 US-10-257-017B-85503
  ; FEATURE:
; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0021078
US-10-257-017B-83730
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                                                                                                           Query Match 8.8%; Score 11.4; DB 1; Length 13; Best Local Similarity 92.3%; Pred. No. 4.6e+02; Matches 12; Conservative 0; Mismatches 1; Indels
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8.8%; Score 11.4; DB 1;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1;
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; Sequence 85503, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: Alexander Olek

1403 AAAATTGTTAATG 1415

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US-10-257-017B-83730/c
Sequence 83730, Application US/10257017B
Sequence 83730, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Petection of single nucleotide polymorhphisms [SNPs] and cytosin TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 83730
LENGTH: 13
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Unertion of single nucleotide polymorhphisms [SNP8] and cytosin
TITLE OF INVENTION: Unerhylations
FILER REFERENCE: E01/1193/W
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 83729
LENGTH: 13
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US-10-257-017B-83729
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US-10-257-017B-66954
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8.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels
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8.8%; Score 11.4; DB 1;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1;
     CURRENT APPLICATION NUMBER: US/10/257,017B
                          CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 66954
LENGTH: 13
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                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-257-017B-83729
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 66953
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10-10-25-017B-66954/C
18-10-25-017B-66954, Application US/10257017B
18-10-25-01-20-25
2 GENERAL INFORMATION:
2 APPLICANT: Abelican Piepenbrock
3 APPLICANT: Kurt Berlin
4 APPLICANT: Kurt Berlin
5 TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
6 TITLE OF INVENTION: methylations
7 TITLE OF INVENTION: methylations
7 FILE REFERENCE: E01/1193/WO
US-10-257-0i7B-64670/c

Sequence 64670, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Defection of single nucleotide polymorhphisms [SNP8] and cytosine

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: DS 1001-0-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 64670
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US-10-257-017B-66953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0017054
US-10-257-017B-64670
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8.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels
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ORGANISM: Artificial Sequence
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US-10-257-017B-66953
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Best Local
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US-10-257-017B-64669
US-10-257-017B-64669
Sequence 64669 Application US/10257017B
Sequence 64669 Application US/10257017B
Sequence 64669 Application US/2025017B
Sequence 64669
Sequence 64669 Application US/20257017B
APPLICANT: Alexander Olek
APPLICANT: Kurt Barlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: DETECTION UNMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 64669
LENGTH: 13
                                                                                                                                                                                                                        US-10-257-017B-64464/c

Sequence 64464 Application US/10257017B

Sequence 64464 Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Murt Barlin
APLICANT: Murt Barlin
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 64464
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US-10-257-017B-64464
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US-10-257-017B-64669
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92.3%; Pred. No. 4.6e+02;
tive 0; Mismatches 1;
Best Local Similarity 92.3%; Pred. No. 4.6e+02; Matches 12; Conservative 0; Mismatches 1;
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8.8%; Score 11.4; DB 1;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1;
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Rut Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: D10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 64463
LENGTH: 13
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US-10-257-017B-63940/C
Sequence 63940, Application US/10257017B
Sequence 63940, Application US/10257017B
Sequence 63940, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 63940
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US-10-257-017B-63940
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US-10-257-017B-64463
                                                                                                                            ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016878
US-10-257-017B-63939
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8.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                     8.8%; Score 11.4; DB 1; Length 13; 92.3%; Pred. No. 4.6e+02; tive 0; Mismatches 1; Indels
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ORGANISM: Artificial Sequence
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                                                   TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 92.34
Matches 12; Conservative
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  SEQ ID NO 63939
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RESULT 46

8.8%; Score 11.4; DB 1; Length 13;

Query Match

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TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin; TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin; TITLE OF INVENTION: methylations; FILE REFERENCE: BOL/1193/WO; CURRENT APPLICATION NUMBER: US/10/257,017B; CURRENT FILING DATE: 2002-10-07; PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR PRILING DATE: 2000-04-07; NUMBER OF SEQ ID NOS: 382046 SEQ ID NOS: 382046 SEQ ID NOS: 5939 LENGTH: 13
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US-10-257-017B-59940/C

US-10-257-017B-59940/C

Sequence 59940, Application US/10257017B

Sequence 59940, Application US/10257017B

Sequence 59940, Application Sequence 59940, Application Sequence 59940, Application Plepenbrock

APPLICANT: Christian Plepenbrock

APPLICANT: Christian Plepenbrock

APPLICANT: Christian Plepenbrock

APPLICANT: Christian Plepenbrock

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NOS: 382046
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Sequence (2) 339, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
FRIOR FILING DATE: 2000-044
FRIOR FILING DATE: 2000-046
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US-10-257-017B-59940
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Pred. No. 4.6e+02;
0; Mismatches 1;
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Best Local Similarity 92.3%;
Matches 12; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
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US-10-257-017B-63939
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Mathylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
SPRIOR FILING DATE: 1000-04-07
SPRIOR FILING DATE: 2000-04-07
SPRIOR FILING DATE: 1000-04-07
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SPRIOR FILING DATE: 1000-04-07
                                                                                                                                                                                                                                                                      Sequence 56899, Application US/10257017B
Sequence 56899, Application US/10257017B
SEQUENCE 56899, Application US/10257017B
SEQUENCE 56899, Application US/10257017B
SEQUENCE CARTISTIAN PROPRIED OF SINGLE BENTIAL PROPRIED OF INVENTION: methylations
TITLE OF INVENTION WIMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015400 US-10-257-017B-56899
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Pred. No. 4.6e+02;
0; Mismatches 1;
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US-10-257-017B-59939
; Sequence 59939, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 38
US-10-257-017B-56900/c
US-10-257-017B-56900, Application US/10257017B
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 92.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-257-017B-56899
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US-10-257-017B-46250/c

Sequence 46250, Application US/10257017B

Sequence 46250, Application US/10257017B

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Wint Berlin
APPLICANT: Wint Berlin
APPLICANT: Wint Berlin
APPLICANT: WINTON: methylations
FILE REFERENCE: E01/1193/WO
GURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 46250
LENGTH: 13
                                                                                                                                                                                                                                                                                                                    Sequence 46249, Application US/10257017B
Sequence 46249, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Plepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REPERENCE: 801/1193/W0
CURRENT PILING DATE: 2002-10-07
FRIDE APPLICATION NUMBER: US/10/257,017B
CURRENT APLICATION NUMBER: D8 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 46249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0013388 US-10-257-017B-46249
OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0013109
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Pred. No. 4.6e+02;
0; Mismatches 1; Indels
                                                                     Length 13,
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                                                                     Score 11.4; DB 1;
Pred. No. 4.6e+02;
0; Mismatches 1;
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92.3%;
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                                                                     Query Match
Best Local Similarity 92.3%;
Matches 12; Conservative
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Best Local Similarity 92.33
Matches 12; Conservative
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       ; US-10-257-017B-44790
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 44789
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kut Berlin
APPLICANT: Kut Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: 2010-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
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US-10-257-017B-44789
                                                                                                                                                                                                 ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0011826
US-10-257-017B-38156
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                                                                                                                                                                                                                                                                                                                                                 1; Indels
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                                                                                                                                                                                                                                                                                                Score 11.4; DB 1;
Pred. No. 4.6e+02;
0; Mismatches 1;
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; Sequence 44790, Application US/10257017B
; GENERAL INFORMATION:
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
WIMBER OF SEQ ID NOS: 382046
SEQ ID NO 38156
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 33
US-10-257-017B-44789
; Sequence 44789, Application US/10257017B
; GRNERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 92.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1394 AAAGGAGGTAAAA 1406
                                                                                                                                                                                                                                                                                                                                                                                               1361 ATTCCACGCATCA 1373
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                                                                                                                                                                                              FEATURE
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US-10-23-017B-38155/C

US-10-257-017B-38155/C

US-10-257-017B-38155/C

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Mir Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosir:
TITLE OF INVENTION: Detection of Single nucleotide polymorhphisms (SNPs) and cytosir:
TITLE OF INVENTION: Methylations
FILE REFERENCE: Boil 11937 WO
CURRENT APPLICATION NUMBER: D80/1097 NO
FRIOR APPLICATION NUMBER: D10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 38155
LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosir
TITLE OF INVENTION: methylations
FILLE REPERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
                                                                                          APPLICANT: Christian Vienness vien Applicant: Christian Piepenbrock APPLICANT: Christian Piepenbrock APPLICANT: Christian Piepenbrock APPLICANT: Kurt Berlin TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosin TITLE OF INVENTION: methylations FILE REPERENCE: B01/1193/WO CURRENT APPLICATION NUMBER: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NOS: 382046 SEQ ID NOS: 382046
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US-10-257-017B-38155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046671 US-10-257-017B-189700
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8.8%; Score 11.4; DB 1;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 0; Mismatches 1;
Sequence 189700, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
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Matches 11; Conservative
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US-10-257-017B-189699/C
Sequence 189699, Application US/10257017B
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Sequence 189699, Application US/10257017B
SEQUENCE CHISTIAN STATE OF TAXABLE OF TA
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICANTON NUMBER: US 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 245004
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US-10-257-017B-189699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Oligonuclectide for detection of SNP ISC0059825
US-10-257-017B-245004
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; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 12; Conservative
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US-10-257-017B-189700
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Sequence 245003, Application US/10257017B
Sequence 245003, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: With Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-10-07
PRIOR PELICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 245003
LENGTH: 13
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Sequence 173476, Application US/10257017B

Sequence 173476, Application US/10257017B

Sequence 173476, Application US/10257017B

Sequence 173476, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Plepenbrock

APPLICANT: Kurt Berlin

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10.07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 173476

LENGTH: 13
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US-10-257-017B-173476
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US-10-257-017B-245003
                                                                                                                       ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0043213
US-10-257-017B-173475
                                                                                                                                                                                                       DB 1; Length 13; 3.2e+02;
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100.0%; Pred. No. 3.2e+02;
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ORGANISM: Artificial Sequence
                                          TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
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US-10-257-017B-245003
                                                                                                FEATURE:
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Sequence 158576, Application US/10257017B
Sequence 158576, Application US/10257017B
Sequence 158576, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Murt Berlin
FILE REFERENCE: E01/1193/WO
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 158576
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Sequence 173475, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Curistian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 173475
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations FILE REFERENCE: E01/1193/WO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: D1019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER of SEQ ID NOS: 382046 SEQ ID NO 158575 LENGTH: 13
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US-10-257-0178-158576
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100.0%; Pred. No. 3.2e+02;
ive 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 12; Conservative
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US-10-257-017B-173475/c
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Sequence 142019, Application US/10257017B
Sequence 142019, Application US/10257017B
Sequence 142019, Application US/10257017B
SEQUENCE 11 INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin TITLE OF INVENTION: methylations
FILE REFERENCE: BOJ/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 142019
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosin
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/W0
CURRENT APPLICATION NUMBER: 104/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 142020
LENGTH: 13
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US-10-257-017B-142020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0035574 US-10-257-017B-142019
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9.2%; Score 12; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels
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9.2%; Score 12; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 0;
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 142020, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
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US-10-257-017B-142020/c
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US-10-287-017B-122876/c

US-10-287-017B-122876, Application US/10257017B

Sequence 122876, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Curistian Piepenbrock
FILE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: De 10019173.8
PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 122876
LENGTH: 13
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US-10-2875, Application US/10257017B
Sequence 122875, Application US/10257017B
Sequence 122875, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Curistian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 122875
LENGTH: 13
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US-10-257-017B-122876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0030713
US-10-257-017B-122875
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                                          9.2%; Score 12; DB 1; Length 13; 100.0%; Pred. No. 3.2e+02; ive 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                               12; Conservative
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                                               Query Match
Best Local Similarity
Matches 12; Conserv
US-10-257-017B-95978
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Sequence 95978 Application US/10257017B

Sequence 95978 Application US/10257017B

Sequence 95978 Application US/10257017B

Sequence 95978 Application US/10257017B

Sequence 95978 Application US/10257,017B

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

APPLICANT: Mitt Berlin

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/W0

CURRENT APPLICATION NUMBER: US/10-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

NUMBER: OF SEQ ID NOS: 382046

SEQ ID NO 95978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 95977, Application US/10257017B
Sequence 95977, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Murk Barlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosi
FILE REPERBROE: 801/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2000-04-07
PRIOR PELICATION NUMBER: DE 10019173.8
PRIOR PELICATION NUMBER: DE 10019173.8
PRIOR PELICATION NUMBER: DE 10019173.8
PRIOR PELICATION 095977
LENGTH: 13
                                                                                                                                                                                                                                            ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0058409
US-10-257-017B-370810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Oligonucleotide for detection of SNP ISC0023864
US-10-257-017B-95977
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PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 370810
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Sequence 358611. Application US/10257017B
Sequence 358611. Application Sequence
APPLICANT: Alexander Olek
APPLICANT: Christian Plepenbrock
APPLICANT: Christian Plepenbrock
APPLICANT: Kurt Berlin Plepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 358611
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine;
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
                                         APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Barlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: 801/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 275206
LENGTH: 12
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US-10-257-0178-275206
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9.2%; Score 12; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 12; Conservative 0; Mismatches 0;
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                         GENERAL INFORMATION:
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US-10-257-017B-358611
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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Sequence 377046, Application US/10257017B

Sequence 377046, Application US/10257017B

Sequence 4 Devander Olek

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kutt Berlin

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REFERENCE: B01/1193/MO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

LENGTH: 13
                                                                                                                                                                                             APPLICANT: Alexander Olek
APPLICANT: Christian Plepenbrock
APPLICANT: Christian Plepenbrock
APPLICANT: Christian Plepenbrock
APPLICANT: Christian Plepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 237045
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US-10-257-017B-237046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Oligonucleotide for detection of SNP ISC0057828 US-10-257-017B-237045
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10.0%; Score 13; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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         1356 AAATATTCCACG 1368
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Best Local Similarity 100.0
Matches 13; Conservative
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                                                         1 AAAATATTCCACG 13
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US-10-257-017B-275206/c
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US-10-257-017B-237046/c
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 173480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Christian Pipenbrock
APPLICANT: Christian Pipenbrock
APPLICANT: Christian Pipenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 108/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 173479
LENGTH: 13
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US-10-257-017B-173480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0043213
US-10-257-017B-173479
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                                                                                                                                                                                        2; Indels
                                                                                                                                      Score 13.8; DB 1;
Pred. No. 72;
                                                                                                                                                                                        0; Mismatches
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US-10-257-017B-173480
Sequence 173480, Application US/10257017B
; GENERAL INFORMATION:
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; Sequence 173479, Application US/10257017B
; GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                             1385 CTTCTGATCAAAGGAGG 1401
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ORGANISM: Artificial Sequence
                                                                                                                                           10.6%;
88.2%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 13; Conservative
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; SEQ ID NO 149
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
PCT-US03-32805-149
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Best Local Similarity
Matches 15; Conserv
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Gaps

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APPLICANT: Wyeth
APPLICANT: Wartinez, Robert
APPLICANT: Martinez, Robert
APPLICANT: Bugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
FILLE OF INVENTION: CANCERS
FILLE AM10927 (031896-002000)
CURRENT APPLICATION NUMBER: PCT/USO4/00035
PRIOR REPERENCE: AM1092 DATE: 2004-01-06
PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
PRIOR FILLING DATE: 2003-01-06
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
TITLE OF INVENTION: CANCERS
FILE REPERBENCE: AM1002927 (031996-002000)
CURRENT APPLICATION NUMBER: PCT/US04/00035
CURRENT FILING DATE: 2004-01-06
FRIOR FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
SSQ ID NOS: 54873
SSQ ID NO 28417
LENGTH: 21
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Sequence 149, Application PC/TUS0332805

GENERAL INFORMATION:

APPLICANT: deCODE genetics ehf.

APPLICANT: Glicher, Jeffrey R.

APPLICANT: Glicher, Jeffrey R.

APPLICANT: Glicher, Jeffrey R.

TITLE OF INVENTION: Infarction

TITLE OF INVENTION: LInfarction

TITLE OF INVENTION: Linfarction

CURRENT APPLICATION NUMBER: PCT/US03/32805

CURRENT FILING DATE: 2003-10-16

PRIOR APPLICATION NUMBER: 60419,432

PRIOR FILING DATE: 2002-10-17

NUMBER OF SEQ ID NOS: 535

SOFTWARE: FRAESEQ for Windows Version 4.0
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Pred. No. 35;
5; Mismatches
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88.9%; Pred No. 35;
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 28418
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61.1%;
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Best Local Similarity 61.1
Matches 11; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: homo sapiens
PCT-USO4-00035-28417
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PCT-US04-00035-28418
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                                                                                                                                                                             APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
TITLE OF INVENTION: CANCERS
FILE REPERENCE: AM100927 (031896-002000)
CURRENT APPLICATION NUMBER: PCT/US04/00035
CURRENT FILING DATE: 2004-01-06
PRIOR PILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
SOFTWARE: Patentin version 3.2
SEQ ID NO 28414
LENGTH: 21
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Pred. No. 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28415, Application PC/TUS0400035 GENERAL INFORMATION:
                                                                                 Sequence 28414, Application PC/TUS0400035 GENERAL INFORMATION:
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61.1%;
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Brown, Eugene
Liu, Wei
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Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
COGANISM: homo sapiens
PCT-US04-00035-28414
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Best Local Similarity
Matches 16; Conserv
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ORGANISM: RNAİ
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Sequence 10180.

Sequence 10180.

Sequence 10180.

APPLICANT: Wyeth

APPLICANT: Brown, Eugene

APPLICANT: Liu, Wei

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATIN

TITLE OF INVENTION: CANCERS

TITLE OF INVENTION: CANCERS

TITLE OF INVENTION: CANCERS

CURRENT PELICATION NUMBER: US/10/770,726

CURRENT FILING DATE: 2004-02-04

NUMBER OF SEQ ID NOS: 48640
                                                                                                                                                                                                                                                                                                               APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Warinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
TITLE OF INVENTION: CANCERS
TITLE OF INVENTION: CANCERS
CURRENT APPLICATION NUMBER: PCT/USO4/00035
CURRENT APPLICATION NUMBER: DF PROPERTION FILING DATE: 2004-01-06
PRIOR FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
SOFTWARE: Patentin version 3.2
SEQ ID NO 39723
LENGTH: 21
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                                                                                                           3; Indels
                                                                         DB 1;
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             ; OTHER INFORMATION: Antisense Oligonucleotide PCT-US04-02003-307
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                                                                       Score 15.2; I
Pred. No. 29;
0; Mismatches
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SEQ ID NO 10180
LENGTH: 21
                                                                       11.7%;
85.0%;
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Best Local Similarity 85.03
Matches 17; Conservative
                                                                     Query Match
Best Local Similarity 85.0
Matches 17; Conservative
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Best Local Similarity
Matches 12; Conserv
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US-10-770-726-10180
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US-10-770-726-10180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
ORGANISM: RNAi
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FEATURE:
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GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: UG1896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
IENGTH: 25
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228870,
232897,
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Sequence 232897,
Sequence 232898,
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Sequence 234088,
Sequence 235997,
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APPLICANT: Sanjay Bhanot
APPLICANT: Sanjay Bhanot
APPLICANT: Sanjay Bhanot
APPLICANT: Gargueline Wyatt
APPLICANT: Susan M. Freier
APPLICANT: Bact P. Monia
APPLICANT: Robert M. Butler
APPLICANT: Robert M. Butler
APPLICANT: Robert M. Dobie
TILLE OF INVENTION: ANTIENSE MODULATION OF PTP1B EXPRESSION
TILLE REFERENCE: BIOLOGOLWO.4
CURRENT APPLICATION NUMBER: PCT/US04/02003
CURRENT FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 415
IENGTH: 20
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US-10-257-017B-223703

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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 0202-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 112260
LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OP INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: 100/10/13.8
PRIOR APPLICATION NUMBER: DE 100/19173.8
PRIOR FILING DATE: 2000-04-07
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations FILE REFERENCE: E01/1193/WO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT APPLICATION NUMBER: US/10/257,017B PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 112259 LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0028043 US-10-257-017B-112260
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91.7%; Pred. No. 8.4e+02;
tive 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 112260, Application US/10257017B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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SEQ ID NO 114029
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                                                                                 US-10-257-017B-110758/c
Sequence 110758/c
Sequence 110758, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Abrander Olek
APPLICANT: Christian Piepembrock
APPLICANT: Christian Piepembrock
APPLICANT: Christian Potection of single mucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR PRIOR PILING DATE: 2002-01-077
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 110758
LENGTH: 13
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US-10-257-017B-110757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0027637
US-10-257-017B-110758
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Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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; Sequence 112259, Application US/10257017B
; GENERAL INFORMATION:
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Kurt Berlin
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Best Local Similarity 91.7%;
Matches 11; Conservative (
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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APPLICANT: Christian Pieg
APPLICANT: Kurt Berlin
                                                                            JS-10-257-017B-110757
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GENERAL INFORMATION:
Sequence 115349, Application US/10257017B
Sequence 115349, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNP8] and cytosine;
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 115349
                                                                                                                                                                    US-10-257-017B-115144/c
US-10-257-017B-115144/c
US-10-257-017B-115144/c
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Cure Berlin
TITLE OF INVENTION: methylations
FILE OF INVENTION: Methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 115144
LENGTH: 13
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US-10-257-0178-115349
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
1; Indels
  0; Mismatches
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     11; Conservative
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       Matches
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT PILING DATE: 2010/107
PRIOR APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-04-07
RNIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 115143
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US-10-257-017B-114030, Application US/10257017B

Sequence 114030, Application US/10257017B

Sequence 114030, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

APPLICANT: Mut Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/W0

CURRENT FILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 114030

LENGTH: 13
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; CTHER INFORMATION: Oligonuclectide for detection of SNP TSC0028539 US-10-257-017B-114030
                                                                                        FEATURE:
, OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0028539
US-10-257-017B-114029
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Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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US-10-257-017B-115143
; Sequence 115143, Application US/10257017B
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
                                               TYPE: DNA ORGANISM: Artificial Seguence
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Best Local Similarity
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GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
ITILE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs] and cytosine
ITILE OF INVENTION: methylations
FILE REFERENCE: BOI/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 116833
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Sequence 116834, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REPERBNCE: B0/1/133/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR PEDLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029237
US-10-257-017B-116833
                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029134 US-10-257-017B-116366
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Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
                               PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 116366 LENGTH: 13
           2002-10-07
                                                                                                                                                                                                                                                                                                                                            Query Match 8.0%;
Best Local Similarity 91.7%;
Matches 11; Conservative C
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Seguence
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           CURRENT FILING DATE:
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LENGTH: 13
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Sequence 115350, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin Piepenbrock
APPLICANT: Kurt Berlin Of Single nucleotide polymorhphisms [SNPS] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 115350
LENGTH: 13
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APPLICANT: Kurt Berlin Diepenbrock
APPLICANT: Kurt Berlin Diepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 116365
LENGTH: 13
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Sequence 116366, Application US/10257017B
Sequence 116366, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Rurt Berlin
APPLICANTON: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
ITTLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
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Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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ORGANISM: Artificial Sequence
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Matches 11; Conservative
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Sequence 117057, Application US/10257017B

Sequence 117057, Application US/10257017B

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Mit Berlin
APPLICANT: 
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 117058
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US-10-257-0178-117057
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Pred. No. 8.4e+02;
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US-10-257-017B-119549
; Sequence 119549, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
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Best Local Similarity 91.7%;
Matches 11; Conservative
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   13 AAAGGATGTAAA
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of Single nucleotide polymorhphisms of title REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 117055
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 105/10/257,017B
CURRENT FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 117056
LENGTH: 13
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US-10-257-017B-117056
; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0029237 US-10-257-017B-116834
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                                                                                                              Length 13;
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                                                                                                      Score 10.4; DB 1;
Pred. No. 8.4e+02;
0; Mismatches 1;
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US-10-257-017B-117056/c
; Sequence 117056, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-257-017B-117055
; Sequence 117055, Application US/10257017B
; GENERAL INFORMATION:
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                                                                                                          Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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ORGANISM: Artificial Sequence
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Matches 11; Conserval
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Sequence 122873, Application US/10257017B
Sequence 122873, Application US/10257017B
Sequence 122873, Application US/10257017B
SEQUENCE 122873, Application US/10257017B
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION UNMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
RESOURCE TILING DATE: 2002-10-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 122873
FILENGTH: 13
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0030029
US-10-257-017B-120329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0030029 US-10-257-017B-120330
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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; Sequence 120330, Application US/10257017B
; GENERAL INFORMATION:
APPLICANT: Alexander Olek
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US-10-257-017B-122873
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LENGTH: 13
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LENGTH: 13
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### SCAPILE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations | FILE REFERENCE: E01/1193/WORER: US/10/257,017B | CURRENT FILING DATE: 2002-10-07 | PRIOR APPLICATION NUMBER: DE 10019173.8 | PRIOR PILING DATE: 2000-04-07 | NUMBER OF SEQ ID NOS: 382046 | SEQ ID NO 119549 | LENGHH: 13 | TYPET.
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Sequence 119550, Application US/10257017B

Sequence 119550, Application US/10257017B

Sequence 119550, Application US/10257017B

Sequence 119550, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REFERENCE: B01/1133/W0

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT PILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 119550
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US-10-257-017B-120329
US-10-257-017B-120329
Sequence 120329, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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ORGANISM: Artificial Sequence
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Sequence 122878, Application US/10257017B
Sequence 122878, Application US/10257017B
Sequence 122878, Application US/10257017B
SEQUENCE 122878, Application US/10257017B
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT PAPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 122878
IENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 125127
LENGTH: 13
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
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US-10-257-017B-125127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0030713
US-10-257-017B-122878
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 13;

Best Local Similarity 91.7%; Pred. No. 8.4e+02;

Matches 11; Conservative 0; Mismatches 1; Indels
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; Sequence 125128, Application US/10257017B
; GENERAL INFORMATION:
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; Sequence 125127, Application US/10257017B
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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Sequence 20, 104.18-14401/
Sequence 20, 104.18-14401/
Sequence 20, 104.18-14401/
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kute Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/NO
CURRENT APPLICATION NUMBER: US/10/257,017B
FILE REFERENCE: 2002-10-07
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 122877
LENGTH: 13
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US-10-257-017B-122874/C

US-10-257-017B-122874, Application US/10257017B

Sequence 122874, Application US/10257017B

Sequence 122874, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Curistian Piepenbrock
APPLICANT: Curistian Piepenbrock
TITLE OF INVENTION: methylations
FILE OF INVENTION: methylations
FILE REFERRICE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR PALLING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 122874

LENGTH: 13
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                                       Gaps
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0030713
US-10-257-017B-122874
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US-10-257-017B-122877
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8.0%; Score 10.4; DB 1; Length 13;

Best Local Similarity 91.7%; Pred. No. 8.4e+02;

Matches 11; Conservative 0; Mismatches 1; Indels
           Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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ORGANISM: Artificial Sequence
           Best Local Similarity 91.7%;
Matches 11; Conservative
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ORGANISM: Artificial Sequence
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                                                                                           1403 AAAATTGTTAAT 1414
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                                                                                                                                1 AAAATTATTAAT 12
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RESULT 477

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US-10-257-017B-132023/C
19-10-257-017B-132023, Application US/10257017B
Sequence 133023, Application US/10257017B
Sequence 132023, Application US/10257017B
Sequence 132023, Application US/10257017B
Sequence 132023, Applications
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PLING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 132023
LENGTH: 13
FURNTH: 13
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Sequence 132024, Application US/10257017B

Sequence 132024, Application US/10257017B

Sequence 132024, Application US/10257017B

Sequence 132024, Application US/10257017B

APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Watt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: SO1/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

REACH FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 132024
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                                ) OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0031761
US-10-257-017B-126930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032951
US-10-257-017B-132023
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US-10-257-017B-132024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 8.4e+02; tive 0; Mismatches 1; Indels
                                                                                                                   Length 13;
                                                                                                                                                                    Indels
                                                                                                                Query Match 8.0%; Score 10.4; DB 1; Best Local Similarity 91.7%; Pred. No. 8.4e+02; Matches 11; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%
Matches 11; Conservative
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          ; FEATURE:
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Sequence 126929, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE OF INVENTION: methylations
FILE OF INVENTION: methylations
FILE OF INVENTION: WINDER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-10-07
PRIOR FILING DATE: 2000-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 126929
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
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                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0031262
US-10-257-017B-125128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0031761
US-10-257-017B-126929
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                                                                                                                                                                                                                                                                                                                                              / Match 8.0%; Score 10.4; DB 1; Length 13; Local Similarity 91.7%; Pred. No. 8.4e+02; Nes 11; Conservative 0; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 125128 LENGTH: 13
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; Sequence 126590, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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SEQ ID NO 126930
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-257-017B-126929
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Matches
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US-10-257-017B-137827, Application US/10257017B

Sequence 137827, Application US/10257017B

Sequence 137827, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REPERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07
                      APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 137595
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations TITLE OF INVENTION: methylations FILE REFERENCE: E01/1193/WO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 137596 LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0034394
US-10-257-017B-137596
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
Christian Piepenbrock
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                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                          US-10-257-017B-136835
Sequence 136835, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: BO1/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PLILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 136835
LENTH: 13
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38-10-257-017B-136836/c
Sequence 136836 Application US/10257017B
Sequence 136836 Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/NO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 136836
LENGTH: 13
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US-10-257-017B-136836
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US-10-257-017B-136835
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8.0%; Score 10.4; DB 1; Length
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-257-017B-138473, Application US/10257017B
Sequence 138473, Application US/10257017B
Sequence 138473, Application US/10257017B
Sequence 138473, Application US/10257017B
Sequence 138473, Application US/10257017B
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Must Berlin
FILE REFERENCE: E01/1193/W0
FILE REFERENCE: E01/1193/W0
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR APPLICATION 1005: 382046
SEQ ID NO 138473
LENGTH: 13
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Sequence 138160, Application US/10257017B
Sequence 138160, Application US/10257017B
Sequence 138160, Application US/10257017B
Sequence 138160, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Usur Bertian
APPLICANT: Usur Bertian
APPLICATION WINBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
WUMBER OF SEQ ID NOS: 382046
SEQ ID NO 138160
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Score 10.4; DB 1; Length 13; Pred. No. 8.4e+02;
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Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                         11; Conservative
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  Query Match
Best Local Similarity
Matches 11; Conserv
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 2010-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 137828
LENGTH: 13
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Sequence 138159, Application US/10257017B

Sequence 138159, Application US/10257017B

Sequence 138159, Application US/10257017B

Sequence 138159, Application US/20257017B

APPLICANT: Crisitian Piepenbrock

APPLICANT: Kirt Berlin Piepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPB] and cytosine

TITLE OF INVENTION: mechylations

TITLE OF INVENTION: mechylations

FILE REFERENCE: E01/1193/W

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 138159
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0034582
US-10-257-017B-138159
                                                                                                                                   FEATURE:
) OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0034453
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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Pred. No. 8.4e+02;
0; Mismatches 1;
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                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
  NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 137827
LENGTH: 13
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0034874
US-10-257-017B-139220
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Pred. No. 8.4e+02;
0; Mismatches 1;
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Pred. No. 8.4e+02;
0; Mismatches 1;
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 139220
LENGTH: 13
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7
Matches 11; Conservative
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Best Local Similarity
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                                                                                 APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DS 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
RNDHER OF SEQ ID NOS: 382046
SEQ ID NO 138474
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/27
PRIOR APPLICATION NUMBER: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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US-10-257-017B-139219
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US-10-257-017B-138474
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91.7%; Pred. No. 8.4e+02;
tive 0; Mismatches 1; Indels
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Pred. No. 8.4e+02;
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 139219, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                     Sequence 138474, Application US/10257017B GENERAL INFORMATION:
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Matches 11; Conservative
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US-10-257-017B-139220/c
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                  RESULT 493
US-10-257-017B-138474
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LENGTH: 13
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US-10-257-017B-142022/C
Sequence 142022/ Application US/10257017B
Sequence 142022, Application US/10257017B
Sequence 142022, Application US/10257017B
Sequence 142022, Application US/10257017B
Sequence 142022, Application Sequence 142022
Sequence 142022, Application Sequence 142022
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPS] and cytosine TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
SPRIOR FILING DATE: 2000-04-07
SPRIOR FILING DATE: 2000-04-07
SEQ ID NO 142022
LENGTH: 13
Sequence 14201, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: D8 10019173.8
PRIOR APPLICATION NUMBER: 2000-04-07
RHORE OF SEQ ID NOS: 382046
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Sequence 145569, Application US/10257017B

Sequence 145569, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 145569
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Sequence 145570, Application US/10257017B
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Wart Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
FRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 145570
LENGTH: 13
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Pred. No. 8.4e+02; 
0; Mismatches 1; Indels
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Pred. No. 8.4e+02;
0; Mismatches 1;
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US-10-257-017B-146343
; Sequence 146343, Application US/10257017B
; GENERAL INFORMATION:
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Matches 11; Conservative C
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1447 GGAAGATGGGTT 1458
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                                                                                                                                                US-10-257-017B-145569
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Sequence 144935. Application US/10257017B

GERNRAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
FILE REPERENCE: 2002-10-07
FRICE APPLICATION NUMBER: DE 10019173.8
FRICE APPLICATION NUMBER: DE 10019173.8
FRICE RILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 144935
LENGTH: 13
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US-10-257-017B-144936, Application US/10257017B
Sequence 144936, Application US/10257017B
Sequence 144936, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
FITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FILE REPERENCE: E01/1193/W0
CURRENT FILING DATE: 2002-10-07
FRIOR APPLICATION NUMBER: US/10-257,017B
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 144936
LENGTH: 13
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                  FEATURE:
; CTHER INFORMATION: Oligonucleotide for detection of SNP TSC0035574 US-10-257-017B-142022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Oligonucleotide for detection of SNP ISC0036443 US-10-257-017B-144935
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CTHER INFORMATION: Oligonuclectide for detection of SNP TSC0036443
US-10-257-017B-144936
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Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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                                                                                                                      8.0%; Score 10.4; DB 1; Length 13. 91.7%; Pred. No. 8.4e+02;
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                                                                                                                                                                       0; Mismatches
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Best Local Similarity 91.7%;
Matches 11; Conservative
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ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
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Best Local Similarity 91.74
Matches 11; Conservative
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CTHER INFORMATION: Oligonucleotide for detection of SNP TSC0036932 US-10-257-017B-146463

TYPE: DNA ORGANISM: Artificial Sequence

FEATURE:

PRIOR FILING DATE: 2000-04-07

ID NOS: 382046

NUMBER OF SEQ IC SEQ ID NO 146463 LENGTH: 13

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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: met
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Sequence 146344, Application US/10257017B

Sequence 146344, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT PELLICATION NUMBER: US 100-01-07

PRIOR FULING DATE: 2002-10-07

PRIOR FULING DATE: 2000-04-07
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US-10-257-017B-146343
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US-10-257-017B-146344
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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Sequence 146463, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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LENGTH: 13
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Best Local S:
Matches 11
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PRIOR APPLICATION NUMBER: DE 10019173.8

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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: Bol/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILLING DATE: 2002-10-07
PRIOR FILLING DATE: 2000-04-07
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APPLICANT: Alexander olek
APPLICANT: Alexander olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Mitt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 147957
LENGTH: 13
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Query Match 8.0%; Score 10.4; DB 1; Length 13; Best Local Similarity 91.7%; Pred. No. 8.4e+02; Matches 11; Conservative 0; Mismatches 1; Indel8
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                            Sequence 146464, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-257-017B-147957
; Sequence 147957, Application US/10257017B
; GENERAL INFORMATION:
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SEQ ID NO 146464
LENGTH: 13
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GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
APPLICANT: WINGER: US/10/257,017B
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR PRIOR APPLICATION NUMBER: UE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 148004
LENGTH: 13
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 148005
LENGTH: 13
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; Sequence 148006, Application US/10257017B
; GENERALI NINCORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
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US-10-257-017B-148004
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US-10-257-017B-148005
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Pred. No. 8.4e+02;
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; Sequence 148005, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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US-10-257-017B-147958/C
US-10-257-017B-147958/C
Sequence 147958, Application US/10257017B
Sequence 147958, Application US/10257017B
Sequence 147958, Application Sequence 147958, Applications
APPLICANT: Cristian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPERRINGE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257, 017B
CURRENT FILING DATE: 2000-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 147958
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US-10-257-017B-148003/C
Sequence 148003, Application US/10257017B
Sequence 148003, Application US/10257017B
Sequence 148003, Application US/10257017B
Sequence 148003, Application US/10257017B
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 148003
LENGTH: 13
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0037358
US-10-257-017B-147958
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0037367
US-10-257-017B-148003
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Pred. No. 8.4e+02;
0; Mismatches 1; Indels
  Length 13;
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
ch 8.0%; Score 10.4; DB 1;
1. Similarity 91.7%; Pred. No. 8.4e+02;
11; Conservative 0; Mismatches 1;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative (
                                                                                               1373 ACGAGCGATCGT 1384
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Query Match
Best Local Similarity
Matches 11; Conserv
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US-10-257-017B-149883

Sequence 149883, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION WINBER: US/10/257,017B

CURRENT APPLICATION WINBER: DE 10019173.8

PRIOR APPLICATION WINBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER: OF SEQ ID NOS: 382046

SEQ ID NO 149883

LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 149884
LENGTH: 13
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                                                                                            ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037804 US-10-257-017B-149826
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037822
US-10-257-017B-149884
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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91.7%; Pred. No. 8.4e+02;
tive 0; Mismatches 1; Indels
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Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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; Sequence 149884, Application US/10257017B
; GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                   ORGANISM: Artificial Sequence FEATURE:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 11, Conservative
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Wit Berlin
TITIE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITIE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 149826
LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 149825
LENGTH: 13
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US-10-257-017B-148006
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; TITLE OF INVENTION: methylations; FILE REFRENCE: E01/1193/WO; CURRENT APPLICATION NUMBER: US/10/257,017B; CURRENT FILING DATE: 2002-10-07; PRIOR APPLICATION NUMBER: DE 10019173.8; NUMBER OF SEQ ID NOS: 382046; SEQ ID NO 148006; LENGTH: 13
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; Sequence 149826, Application US/10257017B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
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US-10-257-017B-149825
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TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations FILE REFERENCE: B01/1193/W0 CURRENT APPLICATION NUMBER: US/10/257,0178
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
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Sequence 150204, Application US/10257017B

Sequence 150204, Application US/10257017B

Sequence 150204, Application US/10257017B

Sequence 150204, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: US/10/257,017B

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 150204

LENGTH: 13
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Sequence 150693, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07
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, OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0037911 US-10-257-017B-150203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037911
US-10-257-017B-150204
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
                        APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 150203
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APPLICANT: Alexander Olek
APPLICANT: Christian Pippenbrock
APPLICANT: Christian Christian
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: 105 10019173.8
PRIOR FILING DATE: 2000-04-07
RNDRER OF SEQ ID NOS: 382046
SEQ ID NO 150062
LENGTH: 13
                                                                                                                                                                                                                                                                        APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nuclectide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: 108/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
SEQ ID NOS: 382046
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US-10-257-017B-150061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037873
US-10-257-017B-150062
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91.7%; Pred. No. 8.4e+02;
tive 0; Mismatches 1; Indels
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Pred. No. 8.4e+02;
0; Mismatches 1;
                                                                                                                                                                          US-10-257-017B-150061
; Sequence 150061, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
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US-10-257-017B-150203/c
; Sequence 150203, Application US/10257017B
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Best Local Similarity 91.7%;
Matches 11; Conservative
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                   1397 GGAGGTAAAATT 1408
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                                                                  GCAGGTAGAATT 2
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Best Local Similarity
Matches 11; Conserval
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US-10-257-017B-150062/c
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: BO1/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 151928
LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0038388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0038467
US-10-257-017B-152249
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                                                            Score 10.4; DB 1; Length 13; Pred. No. 8.4e+02;
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                                                                                                                Indels
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Sequence 152249, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of Single nuclee
TITLE OF INVENTION: Detection of Single nuclee
TITLE OF INVENTION: Detection of Single nuclee
TITLE OF INVENTION: Detection of
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR SEQ ID NOS: 382046
SEQ ID NO 152249
LENGTH: 13
                                                                                                                                                                                                                                                                                                                               Sequence 151928, Application US/10257017B GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                    Query Match 8.0%;
Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                                                                                                            1353 AGAAAATATTC 1364
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Best Local Similarity 91.77
Matches 11; Conservative
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US-10-257-017B-151928
       US-10-257-017B-151927
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Curistian Piepenbrock
APPLICANT: Murt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 10019173.B
RICR APPLICATION NUMBER: DE 10019173.B
RICR FILING DATE: 2000-04-07
RNDRER OF SEQ ID NOS: 382046
SEQ ID NO 151927
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Sequence 150694, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosine
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: 12002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 150694
LENGTH: 13
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US-10-257-017B-150693
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US-10-257-017B-150694
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OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0038388
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Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 150693
LENGTH: 13
                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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ORGANISM: Artificial Sequence
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FITLE OF INVENTION: METHYLON: METHYLON: METHYLON: METHYLON: CORRENT APPLICATION NUMBER: US 1002-110-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 153537
LENGTH: 13
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine FITLE OF INVENTION: methylations FITLE OF INVENTION: methylations FILLE SEPRENCE: E01/1193/WO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT APPLICATION NUMBER: US/10/257,017B PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILLING DATE: 2000-04-07 PRIOR FILLING DATE: 2000-04-07 SEQ ID NOS: 382046 SEQ ID NO 152798 LENGTH: 13
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Sequence 153538, Application US/10257017B
Sequence 153538, Application US/10257017B
Sequence 153538, Application US/10257017B
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
APPLICANT: Mark Berlin
APPLICANT: Mark Berlin
APPLICANTON: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
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US-10-257-017B-152798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 10.4; DB 1; Length 13;
Pred. No. 8.4e+02;
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                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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SEQ ID NO 153538
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Matches 11; Conserv
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US-10-257-017B-153537
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                                                         IS-10-257-017B-152250/c
Sequence 152250, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 152250
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 152797
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0038616
US-10-257-017B-152797
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 11; Conservative
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US-10-257-017B-152797
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Sequence 18574, Application US/10257017B

Sequence 18574, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

APPLICANT: Mir Berlin

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

PRIOR PILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 158574

IENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of Single nucleotide polymorhphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT PRILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US/10/257,0178
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 158573
LENGTH: 13
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US-10-257-0178-158573
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Pred. No. 8.4e+02;
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    Mismatches
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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                                               1355 AAAAATATTCCA 1366
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Matches 11; Conservative
  Matches 11; Conservative
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US-10-257-017B-158574/c
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US-10-257-017B-158577
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Knrt Berlin
APPLICANT: Knrt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-04-07
PRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 153906
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER: DE 10019173.8
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 153905
LENGTH: 13
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                                                                                         ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0038815
US-10-257-017B-153538
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US-10-257-017B-153906
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                                                                                                                                                                Score 10.4; DB 1; Length 13; Pred. No. 8.4e+02; 0; Mismatches 1; Indels
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APPLICANT: Alexander Olek
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US-10-257-017B-153906
; Sequence 153906, Application US/10257017B
; GENERAL INFORMATION:
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91.7%;
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Best Local Similarity 91.7%;
Matches 11; Conservative
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                      TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
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US-10-257-017B-153905/c
LENGTH: 13
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Sequence 161201, Application US/10257017B

SEQUENCE 161201, Application US/10257017B

SEQUENCE 161201, Application US/10257017B

SEQUENCE 161201, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Alexander Olek

APPLICANT: Kurt Berlin

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2002-04-07

SRIOR FILING DATE: 2000-04-07

SRIOR FILING DATE: 2000-04-07

SRIOR FILING DATE: 2000-04-07

SRO ID NO 161201

LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Defection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
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OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040462
US-10-257-017B-160677
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Pred. No. 8.4e+02;
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
                          PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 160677 LENGTH: 13
          2002-10-07
                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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SEQ ID NO 160678
LENGTH: 13
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       CURRENT FILING DATE:
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US-10-257-017B-161201/c
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                                                                                                                 TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations FILE REFERENCE: E01/1193/WO CURRENT APPLICATION WUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NOS: 382046
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: 2810/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 158578
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0039915
US-10-257-017B-158577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0039915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 10.4; DB 1; Length 13; Pred. No. 9.4e+02; 0; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/10/257,017B
Sequence 158577, Application US/10257017B GENERAL INFORMATION:
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; Sequence 158578, Application US/10257017B
; GENERAL INFORMATION:
APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
                                                                         APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.0%;
Best Local Similarity 91.7%;
Matches 11; Conservative
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ORGANISM: Artificial Sequence
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                                               APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 TAAAATCGTTAA 2
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Matches 11; Conserv
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RESULT 541

US-10-257-017B-165194/C

Sequence 165194, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Alexander Olek

APPLICANT: Alexander Olek

TITLE OF INVENTION: METHOD OF Single nucleotide polymorhphisms [SNPS] and cytosine

FILE REFERENCE: E01/1193/MO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: US/10/257,017B

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 165194

LENGTH: 13
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Sequence 165707, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 165707
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91.7%; Pred. No. 8.4e+02;
tive 0; Mismatches 1;
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; Sequence 165708, Application US/10257017B
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.74
Matches 11, Conservative
        2 GGAAAATGGGTT 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 161202
LENGTH: 13
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GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 165193
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040584
US-10-257-017B-161202
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040584 US-10-257-017B-161201
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                                                                                 Length 13;
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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                                                                               Query Match 8.0%; Score 10.4; DB 1; Length 1 Best Local Similarity 91.7%; Pred. No. 8.4e+02; Matches 11; Conservative 0; Mismatches 1; Indels
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ORGANISM: Artificial Sequence
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US-10-257-017B-165193
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Sequence 170635, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 100/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEG ID NOS: 382046
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Sequence 170636, Application US/10257017B
Sequence 170636, Application US/10257017B
GENERAL INTORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFRENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
FRIOR APPLICATION NUMBER: US/10/257,017B
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR APPLICATION NUMBER: DE 2002-10-07
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR FILING DATE: 2000-04-07
SEQ ID NO 170636
SEQ ID NO 170636
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                                                                                                                                                 ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042491 US-10-257-017B-170192
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) OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0042571
US-10-257-0178-170635
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US-10-257-017B-170636
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91.7%; Pred. No. 8.4e+02;
cive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                           Indels
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                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.73
Matches 11, Conservative
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           SEQ ID NO 170192
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                                          LENGTH: 13
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                                                                                                                           FEATURE:
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US-10-257-017B-170191/C

US-10-257-017B-170191, Application US/10257017B

Sequence 170191, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

FILE REPERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 170191

LENGTH: 13
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 165708
LENGTH: 13
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Sequence 170192, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DS 100-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: D8 10019173.8
PRIOR SPEINT DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0041557 US-10-257-017B-165708
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Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.0%;
Best Local Similarity 91.7%;
Matches 11; Conservative (
                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 171859
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US-10-257-017B-171860, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE REPERENCE: 201/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PRIOR DATE: 2000-04-07
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
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OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0042837
US-10-257-0178-171860
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8.0%; Score 10.4; DB 1; Length 13;

Best Local Similarity 91.7%; Pred. No. 8.4e+02;

Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 13.

Best Local Similarity 91.7%; Pred. No. 8.48+02;

Matches 11; Conservative 0; Mismatches 1; Indels
        US-10-257-017B-171859/c
; Sequence 171859, Application US/10257017B
; GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-257-017B-172945
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LENGTH: 13
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Sequence 17073.2 Application US/10257017B

SEQUENCE 17073.2 Application US/10257017B

SEQUENCE 17073.2 Application US/10257017B

APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Earlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
FILE REFERENCE: 2002-10-07

PRIOR APPLICATION NUMBER: US 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 170732

LENGTH: 13
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US-10-257-017B-170731/c
US-10-257-017B-170731/c
Sequence 170731, Application US/10257017B
Sequence 170731, Application US/10257017B
SEQUENCE 170731, Application US/10257017B
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE E 2011.193/W0
CURRENT PELING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 170731
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0042589
US-10-257-017B-170731
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US-10-257-017B-170732
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Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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91.7%; Pred. No. 8.4e+02;
tive 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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ORGANISM: Artificial Sequence
                                                                              1441 ATACATGGAAGA 1452
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  Best Local Similarity 91.7
Matches 11, Conservative
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                                                                                                                         12 ATAAATGGAAGA 1
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR PILLING DATE: 2000-04-07
NUMBER OF SED ID NOS: 382046
SEQ ID NO 173474
LENGTH: 13
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Sequence 176213, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: ALExander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REPERBRE: E0/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR PELING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 176213
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       ; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0043213
US-10-257-0178-173473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:

OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0043213
US-10-257-017B-173474
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                                                                                                                  Length 13;
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                                                                                                                                                                  1; Indels
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Pred. No. 8.4e+02;
0; Mismatches 1;
                                                                                                                Score 10.4; DB 1;
Pred. No. 8.4e+02;
0; Mismatches 1;
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                                                                                                        Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity 91.7%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 91./3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 172946, Application US/10257017B
GENERAL INFORMATION: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Plepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
FRIOR APPLICATION NUMBER: 10019173.8
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 172946
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 173473
TYPE: DNA
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0043092 US-10-257-017B-172946
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.46+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 172945
LENGTH: 13
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; Sequence 173473, Application US/10257017B
; GENERAL INFORMATION:
                                                                                                                                                                                                 ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       1352 AAGAAAATATT 1363
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US-10-257-017B-172946/c
                                                                                                                                                                             TYPE: DNA
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,0178
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 180954
LENGTH: 13
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT PRILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 182703
LENGTH: 13
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Sequence 182704, Application US/10257017B
GENERAL INFORMATION:
Sequence 182704, Application US/10257017B
GENERAL INFORMATION:
Sequence 182704, Application of Sequence 182704
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANTION:
Defection of single nucleotide polymorhphisms (SNPs) and cytosine TITLE OF INVENTION:
ELIA REPERENCE: EQ1/1133/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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; Sequence 182703, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
  Christian Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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US-10-257-017B-182704/c
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Sequence 176214, Application US/10257017B
Sequence 176214, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Rurt Berlin
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APPLICANT: With Berlin
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APPLICANT: With Berlin
APPLICANT: With Berlin
APPLICANT: US/10/257,017B
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT APPLICATION WUMBER: DE 10019173.8
FRIOR APPLICATION WUMBER: DE 10019173.8
FRIOR FILING DATE: 2000-04-07
WUMBER OF SEQ ID NOS: 382046
SEQ ID NO 176214
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nuclectide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: us/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 180953
LENGTH: 13
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US-10-257-017B-176214
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Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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US-10-257-017B-180954/c
; Sequence 180954, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 180953, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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1 AGAATTGTTAAT 12
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Matches
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 188264
LENGTH: 13
                                                                                                                                                                                                                                                               Sequence 188263, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1133/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
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US-10-257-017B-188263
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US-10-257-017B-188264
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8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 8.4e+02; tive 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 13;

Best Local Similarity 91.7%; Pred. No. 8.4e+02;

Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
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PRIOR FILING DATE: 2000-04-07
WUMBER OF SEQ ID NOS: 382046
SEQ ID NO 188263
LENGTH: 13
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                      Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                                                                                                                      RESULT 564
US-10-257-017B-188263
     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 182811, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Plepenbrock
APPLICANT: Christian Plepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
RNDHERE OF SEQ ID NOS: 382046
SEQ ID NO 182831
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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                                                                                                                       ; FEATURE:
; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0045152
US-10-257-017B-182704
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                                                                                                                                                                                                                      Length 13;
                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                   Score 10.4; DB 1;
Pred. No. 8.4e+02;
0; Mismatches 1;
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; Sequence 182832, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                                                                                                                                                                                                                   Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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ORGANISM: Artificial Sequence
                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 182704
LENGTH: 13
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Best Local Similarity
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US-10-257-017B-182831
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LENGTH: 13
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Sequence 189802. Application US/10257017B

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian 
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Albeander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: 201/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,0178
CURRENT PILLING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
                            CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 189801 LENGTH: 13
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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SEQ ID NO 190889
FILE REFERENCE: E01/1193/WO
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US-10-257-017B-189802
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   GENERAL INFORMATION:
Sequence 188597, Application US/10257017B
Sequence 188597, Application US/10257017B
GENERAL INFORMATION:
Sequence 188597, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Are series and sequence of sequence truth of sequence truth of inversions of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 188597
LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
FILE REFERENCE: 2002-10-07
PRIOR PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
RNDMER OF SEQ ID NOS: 382046
SEQ ID NO 188598
LENGTH: 13
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Sequence 189801, Application US/10257017B
Sequence 189801, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin Piepenbrock
APPLICANT: Kurt Berlin Single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
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Pred. No. 8.4e+02;
0; Mismatches 1;
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91.7%;
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Best Local Similarity 91.7%;
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Best Local Simi:
Matches 11;
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Sequence 191284, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Curistian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
FILE REFERENCE: 2002-10-07
PRIOR PILING DATE: 2002-04-07
PRIOR FILING DATE: 2000-04-07
SEQ ID NO 191284
LENGTH: 13
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ALL BELLIAN PLEPENDER OF SINGLE INCLEDENCE OF INVENTION: DETECTION of Single nucleotide polymorhphisms [SNPS] and cytosine TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
TITLE OF INVENTION: METHYLATION WINBER: US/10/257,017B
FILE REFERENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 191357
MATHYLE OF INSTALLATION NUMBER: DE 10019173.8
MATHYLE OF INSTALLATION NUMBER: DE 10019173.8
MATHYLE OF SEQ ID NOS: 382046
SEQ ID NO 191357
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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ORGANISM: Artificial Sequence
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1447 GGAAGATGGGTT 1458
                                               2 GGAAGATGGTTT 13
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                                                                                                                      RESULT 573
US-10-257-017B-191284/c
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US-10-257-017B-191357/c
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GENERAL INFORMATION:
Sequence 191283. Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: METHYLATION
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 100-210-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 191283
LENGTH: 13
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US-10-257-017B-190890/C

US-10-257-017B-190890/C

US-10-257-017B-190890/C

Sequence 190890, Application US/10257017B

Sequence 190890, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek

APPLICANT: Curistian Piepenbrock
APPLICANT: Kurt Berlin

TITLE OF INVENTION: methylations
FILE REPRENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: D10019173.B

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 190890
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CTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046952

US-10-257-017B-190890
                       FEATURE:
; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0046952 US-10-257-017B-190889
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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Pred. No. 8.4e+02;
0; Mismatches 1;
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ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Matches 11; Conservative
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Sequence 191895, Application US/10257017B

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: methylations

FILE REFERENCE: E00/1193/WO

CURRENT PILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 191895

LENGTH: 13
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Sequence 191896, Application US/10257017B

Sequence 191896, Application US/10257017B

Sequence 191896, Application US/10257017B

Sequence 191896, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR FILING DATE: 2002-10-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 191896

LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 8.0%; Score 10.4; DB 1; al Similarity 91.7%; Pred. No. 8.4e+02; 11; Conservative 0; Mismatches 1;
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SEQ ID NO 191756
LENGTH: 13
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Best Local Similarity
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Best Local Similarity
Matches 11; Conserv
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US-10-257-017B-191895
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: met
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: 2002-10-07
TITLE OF INVENTION WIMBER: DS 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER: PS SEQ ID NOS: 382046
SEQ ID NOS: 382046
LENGTH: 13
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0047086 US-10-257-0178-191358
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Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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Sequence 191756, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
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US-10-257-017B-191755
; Sequence 191755, Application US/10257017B
; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: DE 10019173.8
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity 91.74
Matches 11; Conservative
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Page 135

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Sequence 196025, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 196025
LENGTH: 13
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Sequence 196026, Application US/10257017B
Sequence 196026, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Much Barlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
FRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 196026
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
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US-10-257-017B-196026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Oligonucleotide for detection of SNP TSC0048226 US-10-257-0178-196025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WOMBER: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
WUMBER OF SEQ ID NOS: 382046
SEQ ID NO 193278
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION WUMBER: 105/10/257,017B
CURRENT APPLICATION WUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 193277
LENGTH: 13
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; OTHER INFORMATION: Oligonucleotide for detection of SNP ISC0047551

US-10-257-017B-193277
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US-10-257-017B-193278
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
ch 8.0%; Score 10.4; DB 1; Length 13; 1. Similarity 91.7%; Pred. No. 8.4e+02; 11; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                Sequence 193277, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                                                                     1446 TGGAAGATGGGT 1457
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Best Local Similarity
                             Best Local Similarity
Matches 11; Conserv
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US-10-257-017B-193277/c
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              Query Match
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 198423
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: 801/1193/WO
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                                                                    ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0005726 US-10-257-017B-197645
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US-10-257-017B-197646
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                                                                                                                                    8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 8.4e+02; ve 0; Mismatches 1; Indels
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CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 197646
                                                                                                                                                                                                                                                                                                                                        RESULT 587
US-10257-017B-197646
Sequence 197646, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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    TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Matches 11; Conservative
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US-10-257-017B-197452, Application US/10257017B

Sequence 197452, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Petection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REPERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: 108/0257,017B

CURRENT APPLICATION NUMBER: D10019173.8

PRIOR APPLICATION NUMBER: D10019173.8

PRIOR FILING DATE: 2002-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 197452

LENGTH: 13
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0048601
US-10-257-017B-197452
                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0048601
US-10-257-017B-197451
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Pred. No. 8.4e+02;
0; Mismatches 1;
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION UNMERS: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 197451
LENGTH: 13
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity
Matches 11; Conserva:
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR PELICATION NUMBER: US/10/257,017B
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 200896
LENGHH: 13
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Sequence 203099, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Arxander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Barlin
APPLICANT: Kurt Barlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: 201/1193/W0
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION WUMBER: B 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 203099
LENGTH: 13
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US-10-257-017B-203100/c

US-10-257-017B-203100, Application US/10257017B

Sequence 203100, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Alexander Olek

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

TITLE OF INVENTION: UNERPRESENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07
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US-10-257-017B-200896
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8.0%; Score 10.4; DB 1; Length 13;

Best Local Similarity 91.7%; Pred. No. 8.4e+02;

Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                         APPLICANT: Christian Piepenbrock
TILE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR PELICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 198424
LENGTH: 13
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 200895
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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; Sequence 200895, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-257-017B-200896
; Sequence 200896, Application US/10257017B
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 11; Conserva
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Sequence 206951, Application US/10257017B

Sequence 206951, Application US/10257017B

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
TITLE OF INVENTION NUMBER: 2010/257,017B
CURRENT PELING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
SRQ ID NO 206951
LENGER OF SEQ ID NOS: 382046
SRQ ID NO 206951
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US-10-257-017B-206952/c
US-10-257-017B-206952, Application US/10257017B
; Sequence 206952, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: methylations
; FILE OF INVENTION: methylations
; FILE REPERBNCE: E01/1193/W0
; CURRENT FILING DATE: 2002-10-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 206952
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                   Length 13;
                                                 Query Match
8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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ORGANISM: Artificial Sequence
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US-10-257-017B-205660
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Sequence 205659, Application US/10257017B

Sequence 205659, Application US/10257017B

Seguence 205659, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 205659

LENGTH: 13
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Sequence 205660, Application US/10257017B

SEQUENCE 205660, Application US/10257017B

SEQUENCE 205660, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Curistian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1191/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

FILE REPERENCE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046
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                                                                                                                                                                                                              ) OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0049882 US-10-257-017B-203100
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US-10-257-017B-205659
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                           Length 13;
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
  PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 203100
LENGTH: 13
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,0178
CURRENT APPLICATION NUMBER: US 10.07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 210186
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nuclectide polymorhphisms [SNPs] and cytosine;
TITLE OF INVENTION: methylations
TITLE REFERENCE: 801/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine FITLE OF INVENTION: methylations FITLE OF INVENTION: methylations FILLE REFERENCE: E01/1193/WO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT PILLING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILLING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 210185 LENGTH: 13
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0051322
US-10-257-017B-210185
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Pred. No. 8.4e+02;
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                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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SEQ ID NO 213077
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Matches 11; Conserv
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                                                                                Sequence 207455, Application US/10257017B
Sequence 207455, Application US/10257017B
GENERAL INPORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 207425
LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Cristian Piepenbrock
APPLICANT: Curistian Piepenbrock
APPLICANT: Curistian Piepenbrock
APPLICANT: Curistian Piepenbrock
TITLE OF INVENTION: methylations
FITLE OF INVENTION: methylations
FITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 207426
LENGTH: 13
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US-10-257-017B-207425
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US-10-257-017B-207426
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; Sequence 210185, Application US/10257017B
; GENERAL INFORMATION:
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Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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APPLICANT: Christian Pieg
APPLICANT: Kurt Berlin
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                                                              RESULT 598
US-10-257-017B-207425
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Sequence 214400, Application US/10257017B

Sequence 214400, Application US/10257017B

SEQUENCE 214400, Application US/10257017B

SEQUENCE 214400, Application US/10257017B

SEQUENCE 214400, Application US/10257,017B

TITLE OF INVENTION: methylations
FILE REFERENCE: SOUL/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

FILE REFERENCE: 2002-10-07

PRIOR FILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 214400

LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Murt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1133/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
FILE REPERENCE: 2000-10-07
PRIOR FILING DATE: 2000-04-07
RNORE OF SEQ ID NOS: 382046
SEQ ID NO 216849
LENGTH: 13
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  Gaps
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0052153
US-10-257-017B-214400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
; CTHER INFORMATION: Oligonucleotide for detection of SNP TSC0052703
US-10-257-017B-216849
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Indels
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
  Mismatches
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ORGANISM: Artificial Sequence
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                                                   1352 AAGAAAATATT 1363
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  Matches 11; Conservative
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                                                                                               1 AAGAATAATAT
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Best Local Similarity
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US-10-257-017B-216850/c
                                                                                                                                                                                                 US-10-257-017B-214400/c
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US-10-257-077B-214399

Sequence 214399, Application US/10257017B

Sequence 214399, Application US/10257017B

Sequence 214399, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Wurt Berlin

TITLE OF INVENTION: methylations
FITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: US/10/257,017B

PRIOR FILING DATE: 2000-04-07

SPRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                         RESULT 603
US-10-257-017B-21307B/c
US-10-257-017B-21307B, Application US/10257017B
Sequence 21307B, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Cristian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 213078
LENGTH: 13
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US-10-257-017B-213078
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CHER INFORMATION: Oligonucleotide for detection of SNP TSC0052153
US-10-257-017B-214399
                                                                          FEATURE:
; FEATURE:
; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0051905
US-10-257-017B-213077
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                                                                                                                                                                        Query Match

8.0%; Score 10.4; DB 1; Length 13;

Best Local Similarity 91.7%; Pred. No. 8.4e+02;

Matches 11; Conservative 0; Mismatches 1; Indels
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Pred. No. 8.4e+02;
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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91.7%;
  LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nuclectide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT PLILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 217383
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APPLICANT: Christian Piepenbrock
APPLICANT: Kutt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING NATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 217384
LENGTH: 13
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US-10-257-017B-217383
                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0052841
US-10-257-017B-217344
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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Pred. No. 8.4e+02;
0; Mismatches 1;
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 610
US-10-257-017B-217383
Sequence 217383, Application US/10257017B
GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 217344
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Best Local Similarity 91.7%;
Matches 11; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-257-017B-217384/c
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-10-07
READER APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 217343
LENGTH: 13
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
                                                                                        APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: BOL/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 1002-10-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
RNDHER OF SEQ ID NOS: 382046
SEQ ID NO 216850
LENGTH: 13
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0052703
US-10-257-017B-216850
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US-10-257-017B-217343
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 13;

Best Local Similarity 91.7%; Pred. No. 8.4e+02;

Matches 11; Conservative 0; Mismatches 1; Indels
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; Sequence 217343, Application US/10257017B
; GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
                      Sequence 216850, Application US/10257017B
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                   APPLICANT: Alexander Olek
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US-10-257-017B-220057

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Sequence 220169, Application US/10257017B
; GEBREAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbröck
; APPLICANT: Christian Piepenbröck
; APPLICANT: Christian Piepenbröck
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: methylations
; TITLE OF INVENTION: methylations
; TITLE OF INVENTION: methylations
; TITLE OF INVENTION NUMBER: 2010/1037,017B
; CURRENT PILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR APPLICATION NUMBER: DE 10019173.8
; SEQ ID NO 220169
; SEQ ID NO 220169
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Sequence 220170, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Plepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
FRICE REPRENCE: 2002-10-07
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 220170
LENGTH: 13
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US-10-257-017B-220170
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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; Sequence 220461, Application US/10257017B
; GENERAL INFORMATION:
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APPLICANT: Christian Pie
  13 TGGGTTGATGAA 2
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                                                                                    RESULT 614
US-10-257-017B-220169
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APPLICANT: Christian Pipenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPB] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION WUMBER: 108/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 220058
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 220057
LENGTH: 13
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0052861
US-10-257-017B-217384
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                                                                              Query Match

8.0%; Score 10.4; DB 1; Length 13;

Best Local Similarity 91.7%; Pred. No. 8.4e+02;

Matches 11; Conservative 0; Mismatches 1; Indels
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US-10-257-017B-220058/c
; Sequence 220059, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 220057, Application US/10257017B GENERAL INFORMATION:
APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.74
Matches 11; Conservative
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Length 13; Indels

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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPS] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 222533
LENGTH: 13
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Sequence 222436, Application US/10257017B
Sequence 222436, Application US/10257017B
Sequence 222436, Application US/10257017B
GENERAL INFORMATION: The Set Information Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR SEQ ID NOS: 382046
SEQ ID NOS: 382046
SEQ ID NO 222436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0054123 US-10-257-017B-222436
                                                                                                                                                                                                                       TYPE: DNA ORDER SEQUENCE CONTROL OF SNP TSC0054123 CHER INFORMATION: Oligonucleotide for detection of SNP TSC0054123 US-10-257-0178-222435
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Pred. No. 8.4e+02;
0; Mismatches 1;
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Best Local Similarity 91.7%;
Matches 11; Conservative
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ORGANISM: Artificial Sequence
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US-10-257-017B-222533
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                                                                                                                                                                                  SEQ ID NO 222435
LENGTH: 13
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### CONDITION | CONDITION | CONDITION | CONDITION |

TITLE OF INVENTION | Detection of single nucleotide polymorhphisms [SNP8] and cytosine | TITLE OF INVENTION | methylations |

TITLE OF INVENTION | methylations |

TITLE OF INVENTION | methylations |

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Sequence 222435, Application US/10257017B
Sequence 222435, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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US-10-257-017B-220462/c
US-10-257-017B-220462 Application US/10257017B
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: MOWHERE: US/10/257,017B
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 220462
SEQ ID NOS: 382046
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred: No. 8.46+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.46+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: WUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 223879
LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Murt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 223368
LENGTH: 13
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US-10-257-017B-223879
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US-10-257-017B-223368
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.46+02;
Matches 11; Conservative 0; Mismatches 1;
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; Sequence 223880, Application US/10257017B
; GENERAL INFORMATION:
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; Sequence 223879, Application US/10257017B
; GENERAL INFORMATION:
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Sequence 223367, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07
PRIOR PPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 223367
LENGTH: 13
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US-10-257-017B-222534/Application US/10257017B
Sequence 222534, Application US/10257017B
Sequence 222534, Application US/10257017B
Sequence 222534, Application US/10257017B
CENTRAL INFORMATION:
APPLICANT: Cristian Piepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US/10/257,017B
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 222534
LENGTH: 13
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US-10-257-017B-223367
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US-10-257-017B-222534
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
     Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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RESULT 623

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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OP INVENTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 228140
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Murt Berlin
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
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US-10-257-0178-228140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055636
US-10-257-017B-228139
             ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055447 US-10-257-017B-227296
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                                                                                              Length 13;
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                                                                                            Score 10.4; DB 1;
Pred. No. 8.4e+02;
0; Mismatches 1;
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; Sequence 228140, Application US/10257017B
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                 Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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SEQ ID NO 228139
LENGTH: 13
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Best Local Similarity 91.74
Matches 11; Conservative
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FEATURE:
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TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE REFERENCE: BO1/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR PAPLICATION NUMBER: DE 10019173.8
PRIOR PAPLICATION NUMBER: DE 10019173.8
PRIOR SEQ ID NOS: 382046
SEQ ID NO 227295
LENGTH: 13
TYPE
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US-10-257-017B-227296, Application US/10257017B
; Sequence 227296, Application US/10257017B
; GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
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TITLE OF INVENTION: Detection of Single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of Single nucleotide polymorhphisms [SNPs] and cytosine
FILE REPREMENTE: 2001/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 227296
LENGTH: 13
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; CTHER INFORMATION: Oligonuclectide for detection of SNP TSC0054529 US-10-257-017B-223880
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US-10-257-017B-227295
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 223880
LENGTH: 13
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ORGANISM: Artificial Sequence
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Sequence 22857, Application US/10257017B
Sequence 22857, Application US/10257017B
GENERAL INFORMATION:
Sequence 22857, Application of Sequence 22857, Applicant of Sequence 22857, Applicant Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of Single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1133/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
TITLE OF INVENTION: WINBER: US/10/257,017B
FILE REFERENCE: E01/1193/WO
FILE REFERENCE: E01/1193/WO
FILE REPERENCE: E01/1
                        APPLICANT: Kurt Berlin Treperior of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations FILE REPERBNCE: BO1/1193/MO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT APPLICATION NUMBER: US 100773.8 PRIOR FILING DATE: 2000-04-07 PRIOR FILING DATE: 2000-04-07 SEQ ID NO 228215 LENGTH: 13
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US-10-257-017B-228216
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    Christian Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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SEO ID NO 228216
LENGTH: 13
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US-10-257-017B-228567
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: 201/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 282012
                                                                                                                                                                                                                                                                                                    APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0004626
US-10-257-017B-228212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0004626 US-10-257-017B-228211
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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US-10-257-017B-228212
Sequence 228212, Application US/10257017B
Sequence 128212, Application US/10257017B
Sequence 228212, Application US/10257017B
Sequence 228212, Application US/10257017B
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US-10-257-017B-228215/c
Sequence 228215, Application US/10257017B
GENERAL INFORMATION:
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; Sequence 228211, Application US/10257017B
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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LENGTH: 13
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US-10-257-017B-234847

Sequence 234847, Application US/10257017B

Sequence 234847, Application US/10257017B

Sequence 234847, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR PLING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 2234847

LENGTH: 13

LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 232256
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  ch 8.0%; Score 10.4; DB 1; Length 13; 1. Similarity 91.7%; Pred. No. 8.4e+02; 11; Conservative 0; Mismatches 1; Indels
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Pred. No. 8.4e+02;
0; Mismatches 1;
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; Sequence 232256, Application US/10257017B
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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al Similarity 91.7%;
11; Conservative
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Query Match
Best Local Similarity
Matches 11; Conserva
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Best Local Similarity
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Sequence 228668 Application US/10257017B
SEQUENCE 228668 Application US/10257017B
SEQUENCE 228668 Application US/10257017B
SEQUENCE 228568 Application US/10257017B
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations FILE REFERENCE: E01/1193/WO CURRENT APPLICATION NUMBER: US/10/257,017B
FILE REFERENCE: E01/1193/WO CURRENT APPLICATION NUMBER: US/10/257,017B
FILE REPERENCE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
SEQ ID NO 228568
LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-7
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR RILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 232255
LENGTH: 13
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                                                                                                                                        ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0055748 US-10-257-017B-228567
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                                                                                                                                                                                                                                   Query Match

8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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; Sequence 232255, Application US/10257017B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                    ORGANISM: Artificial Sequence
FEATURE:
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 228567
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                           1396 AGGAGGTAAAAT 1407
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Gaps

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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0057760 US-10-257-017B-236640

TYPE: DNA ORGANISM: Artificial Sequence

CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 236640 LENGTH: 13

FILE REFERENCE: E01/1193/WO

Query Match 8.0%; Score 10.4; DB 1; Length 13; Best Local Similarity 91.7%; Pred. No. 8.4e+02; Matches 11; Conservative 0; Mismatches 1; Indels

1355 AAAAATATTCCA 1366

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2 AAAAATAATCCA 13

Sequence 239414, Application US/10257017B

GRUERAZ INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Cristian Piepenbrock
APPLICANT: Cristian Piepenbrock
APPLICANT: Murt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/103/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 239414

MENOR APPLICATION NUMBER: DE 10019173.8 APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT EPLING UNTER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 239413
LENGTH: 13 ; 0 Gaps ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0058397 US-10-257-017B-239413 ö 8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 8.4e+02; tive 0; Mismatches 1; Indels Sequence 239413, Application US/10257017B GENERAL INFORMATION: APPLICANT: Alexander Olek TYPE: DNA ORGANISM: Artificial Sequence 1351 GAAGAAAATAT 1362 11; Conservative 1 GAAGAAAAAGAT 12 Query Match Best Local Similarity US-10-257-017B-239414/c US-10-257-017B-239413 Matches à d

US-10-257-017B-236640
Sequence 236640, Application US/10257017B
Sequence 236640, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations

12 AAAAATAATCCA 1

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RESULT 641

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APPLICANT: ALCANAULEL OLDER
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 242609
LENGTH: 13
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GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Rurt Berlin Piepenbrock
APPLICANT: Rurt Berlin Detection of single nucleotide polymorhphisms (SNPs) and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: B1 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 242610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0059184 US-10-257-017B-242610
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8.0%; Score 10.4; DB 1; Length 13,
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
                                                                                                                                                                                ; Sequence 242609, Application US/10257017B; GENERAL INFORMATION: ; APPLICANT: Alexander olek
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; Sequence 245005, Application US/10257017B
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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     1356 AAATATTCCAC 1367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1349 GGGAAGAAAAT 1360
                                                       1 AAAATATTCAAC 12
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                                                                                                                                 RESULT 646
US-10-257-017B-242609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 241817
LENGTH: 13
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Sequence 241818, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 241818
LENGTH: 13
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US-10-257-017B-241817
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) OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0058966
US-10-257-017B-241818
                                            ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0058397
US-10-257-017B-239414
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                                                                                                                         Score 10.4; DB 1; Length 13;
Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.0%; Score 10.4; DB 1; Length 13; Best Local Similarity 91.7%; Pred. No. 8.4e+02; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 241817, Application US/10257017B GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                      Query Match 8.0%;
Best Local Similarity 91.7%;
Matches 11; Conservative
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                             1351 GAAGAAAAATAT 1362
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                                                                                                                                                                                                                                                             13 GAAGAAAAAGAT 2
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US-10-257-017B-241817/c
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Sequence 245466, Application US/10257017B

Sequence 245466, Application US/10257017B

GENERAL INPORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1133/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
FILE REPERENCE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 245486
LENGTH: 13
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 100/07
PRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 245489
LENGTH: 13
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                                                                                                                                                              FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0059938
US-10-257-017B-245485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: Oligonuclectide for detection of SNP TSC0059938 US-10-257-017B-245486
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                                                                                                                                                                                                                                                                                 Length 13;
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                           Query Match

8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.48+02;
Matches 11; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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                       NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 245485
LENGTH: 13
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US-10-257-017B-245486/c
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Sequence 245006, Application US/10257017B

Sequence 245006, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Abrander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT PILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

NUMBER: OF SEQ ID NOS: 382046

SEQ ID NO 245006
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Defection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
                                              APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: B01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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; CTHER INFORMATION: Oligonucleotide for detection of SNP TSC0059825
US-10-257-017B-245005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0059825
US-10-257-017B-245006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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Pred. No. 8.4e+02;
0; Mismatches 1;
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8.0%; Score 10.4; DB 1;

Best Local Similarity 91.7%; Pred. No. 8.4e+02;

Matches 11; Conservative 0; Mismatches 1;
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Sequence 45485, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
                       Christian Piepenbrock
Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                  SEQ ID NO 245005
LENGTH: 13
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Sequence 246528, Application US/10257017B
Sequence 246528, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 245528
LENGTH: 13
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US-10-257-017B-250615/c
195-10-257-017B-250615/c
Sequence 250615, Application US/10257017B
Sequence 250615, Application US/10257017B
Sequence 250615, Application US/10257017B
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Current Berlin
TITLE OF INVENTION: methylations
FILE OF INVENTION: methylations
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 250615
LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
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US-10-257-017B-246528
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US-10-257-017B-250615
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91.7%; Pred. No. 8.4e+02;
tive 0; Mismatches 1;
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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Matches 11; Conservative
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US-10-257-017B-245490/c

Sequence 245490, Application US/10257017B

SEQUENCE APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/W0

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT PILING DATE: 2002-10-07

PRIOR PILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 245490

LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PLING DATE: 2002-10-07
PRIOR PAPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 246527
LENGTH: 13
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US-10-257-017B-246527
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ch 8.0%; Score 10.4; DB 1; Length 13; 1 Similarity 91.7%; Pred. No. 8.4e+02; 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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Pred. No. 8.4e+02;
0; Mismatches 1;
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US-10-257-017B-246527/c
F. Sequence 246527, Application US/10257017B
F. GRNERAL INFORMATION:
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Best Local Similarity 91.7%;
Matches 11; Conservative
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                               Local Similarity
       Query Match
Best Local S:
Matches 11,
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Sequence 253480

Sequence 253480

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian piepenbrock
APPLICANT: Christian of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILIE REFERENCE: 2002-10-07
CURRENT APPLICATION NUMBER: US/10/257,0178
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 253488
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICANTON NUMBER: US10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 253487
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                                                                              ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0061629
US-10-257-017B-252636
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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ORGANISM: Artificial Sequence
      TYPE: DNA ORGANISM: Artificial Sequence
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Sequence 252636, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER: OF SEQ ID NOS: 382046

SEQ ID NO 252636
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Sequence 25635, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 252635
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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; TITLE OF INVENTION: methylations; FILE REFERENCE: E01/1193/WO; CURRENT APPLICATION UNDER: US/10/257,0178; CTRRENT FILING DATE: 2002-10-07; PRIOR APPLICATION NUMBER: DE 10019173.8; NUMBER OF SEQ ID NOS: 382046; SEQ ID NO 250616; LENGTH: 13
                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/W0
CURRENT APPLICATION NUMBER: 0210/10257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 258853
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNFs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNFs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT PRILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US 10019173.8
PRIOR PLING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 8854
LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 8.4e+02; tive 0; Mismatches 1; Indels
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; Sequence 258884, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 11; Conservative
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: LD 1002-10-07
PRIOR PILING DATE: 2002-10-07
PRIOR PLING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 257658
                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations TITLE OF INVENTION: methylations CURRENT EDIALISM MOMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 257657
LENGTH: 13
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; CTHER INFORMATION: Oligonuclectide for detection of SNP TSC0062680 US-10-257-017B-257657
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Pred. No. 8.4e+02;
0; Mismatches 1;
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                                                                                                                                                                     US-10-257-017B-257657/c
; Sequence 257657, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
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US-10-257-017B-258853/c
; Sequence 258853, Application US/10257017B
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Best Local Similarity 91.7%;
Matches 11; Conservative
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ORGANISM: Artificial Sequence
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                   1365 CACGCATCACGA 1376
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Best Local Similarity
Matches 11; Conserva
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indel8
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                                                                       Score 10.4; DB 1; Length 13; Pred. No. 8.4e+02;
                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleon
TITLE OF INVENTION: Detection of single nucleon
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 108/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO SES970
                                                                                                                                                   0; Mismatches
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Sequence 259973, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Plepenbrock
APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-257-017B-259970/c; Sequence 259970, Application US/10257017B; GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 259973
LENGTH: 13
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ORGANISM: Artificial Sequence
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                                                                           Query Match
Best Local Similarity 91.7
Matches 11; Conservative
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       US-10-257-017B-25969
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Sequence 259006, Application US/10257017B
Sequence 259006, Application US/10257017B
Sequence 259006, Application
Sequence 259006, Application
Sequence 259006, Application
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methy
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Sequence 25959, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1191/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DS 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DS 10019173.8
PRIOR APPLICATION NUMBER: DS 10019173.8
PRIOR APPLICATION NUMBER: DS 10019173.8
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OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0063118
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US-10-257-017B-259006
                                                                                                                                                                                                                                                                        , OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0062939 US-10-257-0178-259005
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8.0%; Score 10.4; DB 1; Length 13;

Best Local Similarity 91.7%; Pred. No. 8.4e+02;

Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ 1D NOS: 382046
SRQ 1D NO 259005
LENCTH: 13
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LENGTH: 13
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TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations FILE REFERENCE: EDI/J193/MO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07
single nucleotide polymorhphisms (SNPs) and cytosine
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0063118
US-10-257-017B-259973
                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0063118
US-10-257-017B-259970
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
READ APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 260274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms of the cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT PRILING NATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 260273
LENGTH: 13
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OP INVENTION: methylations FILE REFERENCE: B01/1193/WO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR PILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 260034
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                                                                                                                                                                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0007828 US-10-257-017B-260034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0006237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.0%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 8.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 10.4; DB 1;
Pred. No. 8.4e+02;
0; Mismatches 1;
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
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                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Matches 11; Conserv
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US-10-257-017B-260273
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                                                              Sequence 259974, Application US/10257017B

Sequence 259974, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/W0

CURRENT PLLING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 259974

LENGTH: 13
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Sequence 260033, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 100/210-07
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 260033
LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0063118 US-10-257-017B-259974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0007828 US-10-257-017B-260033
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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8.0%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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; Sequence 260034, Application US/10257017B
; GENERAL INFORMATION:
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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US-10-257-017B-263360
US-10-257-017B-263360
US-10-257-017B-263360
SERVERAL INFORMATION:
SERVED INVENTION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Autr Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FITLE OF INVENTION: METHOD: METHOD IN TITLE OF INVENTION: METHOD IN TITLE OF INVENTION: METHOD IN TITLE OF INVENTION: DETECTION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
SERIOR APPLICATION NUMBER: DE 10019173.8
SEQ ID NO 263360
SEQ ID NO 263360
SERVET IN TITLE OF SEQ ID NOS: 382046
                                                                                                                                                                                                                                                                                   Sequence 263359, Application US/10257017B

| Sequence 263359, Application US/10257017B
| GENERAL INFORMATION:
| APPLICANT: Alexander Olek
| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Piepenbrock
| TITLE OF INVENTION: methylations
| TITLE OF INVENTION: methylations
| FILE REFERENCE: E01/1193/WO
| CURRENT FILING DATE: 2002-10-07
| PRIOR FILING DATE: 2002-10-07
| PRIOR FILING DATE: 2000-04-07
| NUMBER OF SEQ ID NOS: 382046
| SEQ ID NO 263359
| LENGTH: 13
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   Gaps
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US-10-257-017B-263359
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   IndelB
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Pred. No. 8.4e+02;
0; Mismatches 1;
   Mismatches
   0;
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Best Local Similarity 91.7%;
Matches 11; Conservative (
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ORGANISM: Artificial Sequence
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                                                                          1355 AAAATATTCCA 1366
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   Matches 11; Conservative
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US-10-257-017B-264565
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i Sequence 262883, Application US/10257017B

i Sequence 262883, Application US/10257017B

i Sequence 262883, Application US/10257017B

i SEQUENCE SEQUENCE CALL

i APPLICANT: Christian Piepenbrock

i APPLICANT: Christian Piepenbrock

i TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNP8] and cytosine

i TITLE OF INVENTION: methylations

i TITLE OF INVENTION: methylations

i TITLE OF INVENTION: methylations

i CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-77

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR PILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 262883

LENGTH: 13
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Sequence 262884 Application US/10257017B
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
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TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION [SNPs]
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US-10-257-017B-262884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0063773
US-10-257-017B-262883
                                                                                                                   FEATURE:
CTHER INFORMATION: Oligonuclectide for detection of SNP TSC0006237
US-10-257-017B-260274
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8.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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Pred. No. 8.4e+02;
0; Mismatches 1; Indels
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Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity
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                      LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 268506
LENGTH: 12
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US-10-257-017B-268506
                                                                                                                                                                                                                                         ; FRATURE:

; OTHER INFORMATION: Oligonuclectide primer for the detection of SNP TSC0000988

US-10-257-0178-268220
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7.7%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.2e+03;
ive 0; Mismatches 0; Indels
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: mothylations
TITLE OF INVENTION: mothylations
FILE OF INVENTION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 269609
LENGTH: 12
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; Sequence 268506, Application US/10257017B
; GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 268220
LENGTH: 12
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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US-10-257-017B-269609/c
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
SNDMER OF SEQ ID NOS: 382046
SEQ ID NO 264566
LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Rurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERRNCE: B01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
                                                    APPLICANT: Alexander Olek
APPLICANT: Christian Plepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PLING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 264565
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US-10-257-017B-264566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0064134 US-10-257-017B-264565
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; Sequence 264566, Application US/10257017B
; GENERAL INFORMATION:
APPLICANT: Alexander Olek
                           Sequence 264565, Application US/10257017B GENERAL INFORMATION:
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91.7%;
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity
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US-10-257-017B-268220/c
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GRENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Ciristian Piepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
FRIOR FILING DATE: 2000-04-07
SEQ ID NO 270350
LENGTH: 12
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US-10-257-017B-270638/c

US-10-257-017B-270638, Application US/10257017B

Sequence 270638, Application US/10257017B

Sequence 270638, Application US/10257017B

APPLICANT: Curistian Piepenbrock

APPLICANT: Curistian Piepenbrock

APPLICANT: Curistian Piepenbrock

APPLICANT: Curistian Piepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPS] and cytosine

FILE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPS] and cytosine

FILE REPERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257, 017B

CURRENT FILING DATE: 2002-10-07

PRIOR PILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 270638

LENGTH: 12
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US-10-257-0178-270638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002098 US-10-257-017B-270350
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP ISC0001822 US-10-257-017B-269609
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.7%; Score 10; DB 1; Length 12; 100.0%; Pred. No. 1.2e+03; tive 0; Mismatches 0; Indels
                                                                             Query Match 7.7%; Score 10; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 1.2e+03; Matches 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100."
Matches 10, Conservative
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1355 AAAAATATTC 1364

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WG-10-257-017B-272104

Sequence 272104, Application US/10257017B

Sequence 272104, Application US/10257017B

GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT ETLING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 272104
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GENERAL INFORMATION.
GENERAL INFORMATION.
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002711 US-10-257-017B-272104
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7.7%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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SEQ ID NO 272167
LENGTH: 12
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILS REFERENCE: E01/1193/WO
CURRENT PRILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR RILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 277777
LENGTH: 12
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UG-10-257-017B-276653, Application US/10257017B
Sequence 276653, Application US/10257017B
Sequence 276653, Application
Sequence 276653, Application
Sequence 276653, Application
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Muramiton Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT FILING DATE: 2002-10-07
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 276653
LENGTH: 12
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                                                              TYPE: DNA ORGANISM: Artificial Sequence PETURE: PEATURE: PRATURE: NPORMATION: Oligonucleotide primer for the detection of SNP TSC0004253 US-10-257-017B-276652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004253 US-10-257-0178-276653
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Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
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              SEQ ID NO 276652
LENGTH: 12
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR PLLING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 272991
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US-10-257-017B-276652/c

US-10-257-017B-276652, Application US/10257017B

Sequence 276652, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine; TITLE OF INVENTION: methylations
TITLE REFRENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046
APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosing

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 272927

LENGTH: 12
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US-10-257-017B-272991
                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
) OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002986
US-10-257-017B-272927
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100.0%; Pred. No. 1.2e+03;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.7%; Score 10; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 1.2e+03; Matches 10; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 10; Conservative
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US-10-257-077B-283348
US-10-257-077B-283348

Squence 283348, Application US/10257017B
Squence 283348, Application US/10257017B
Squence 283348, Application US/10257017B
Squence 283348, Application US/10257017B
Sprincant: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/MO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 283348
LENGTH: 12
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPREBNCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 280197
LENGTH ...
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Oligonuclectide primer for the detection of SNP TSC0011270
US-10-257-017B-283348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Oligonuclectide primer for the detection of SNP ISC0008335
US-10-257-017B-280197
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
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US-10-257-017B-284132
Sequence 284132, Application US/10257017B
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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US-10-257-017B-279418/c
Sequence 279418 Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin Piepenbrock
APPLICANT: Kurt Berlin Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: mechylations
TITLE OF INVENTION: mechylations
TITLE OF INVENTION NUMBER: US/10/257,017B
CURRENT APPLICANTON NUMBER: US/10-07
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
                                                                                                                                                                                                                                                                                                                             APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: 108/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 278342
LENGTH: 12
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US-10-257-017B-278342
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7.7%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.2e+03;
                                  Indels
       Best Local Similarity 100.0%; Pred. No. 1.2e+03; Matches 10; Conservative 0; Mismatches 0;
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; Sequence 278342, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                    1356 AAAATATTCC 1365
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LENGTH: 12
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RESULT 696

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US-10-257-017B-289718/C
US-10-257-017B-289718/C
Sequence 289718, Application US/10257017B
Sequence 289718, Application US/10257017B
Sequence 289718, Application US/10257017B
Sequence 289718, Applications
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Nurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FILE REPRENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 289718
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 289698, Application US/10257017B
| Sequence 289698, Application US/10257017B
| GENERAL INFORMATION:
| APPLICANT: Alexander Olek
| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Piepenbrock
| APPLICANT: Kurt Barlin
| TITLE OF INVENTION: methylations
| TITLE OF INVENTION: methylations
| FILE REFERENCE: E01/1193/W0
| CURRENT APPLICATION NUMBER: US/10/257,017B
| CURRENT APPLICATION NUMBER: DE 10019173.8
| PRIOR FILING DATE: 2002-04-07
| NUMBER OF SEQ ID NOS: 382046
| SEQ ID NO 289698
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, OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014062
US-10-257-017B-289718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014053
US-10-257-017B-289698
                      ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0013548 US-10-257-017B-288515
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                                                                                                        Query Match 7.7%; Score 10; DB 1; Le Best Local Similarity 100.0%; Pred. No. 1.2e+03; Matches 10; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 10; Conserv
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     FEATURE:
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US-10-257-017B-284167
Sequence 284167, Application US/10257017B
Sequence 284167, Application US/10257017B
Sequence 284167, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: ALexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: MORER: US/10/257,017B
CURRENT APPLICATION NUMBER: DS 10019173.8
PRIOR FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 284167
ILENGTH: 12
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Sequence 288515, Application US/10257017B
Sequence 288515, Application US/10257017B
Sequence 288515, Application US/10257017B
Sequence 288515, Application US/10257017B
Sequence 288515, Application Sequence
APPLICANT: Christian Plepenbrock
APPLICANT: Christian Plepenbrock
APPLICANT: Christian Plepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: SO1/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 288515
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                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0011676
US-10-257-017B-284132
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7.7%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                       Query Match 7.7%; Score 10; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 1.2e+03; Matches 10; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 284132 LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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US-10-257-017B-288515/c
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US-10-257-017B-296818, Application US/10257017B

Sequence 296818, Application US/10257017B

Sequence 296818, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Clek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
APPLICANT: Murt Berlin
APPLICANT: Murt Berlin
APPLICANT: Murt Berlin
APPLICANTON: Methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 295516, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Nutr Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
                     APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
SNDBER OF SEQ ID NOS: 382046
SEQ ID NO 294714
LENGTH: 12
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US-10-257-017B-295516
                                                                                                                                                                                                                                                                                                                                                                                                                           ), OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0016238
US-10-257-017B-294714
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7.7%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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7.7%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
Christian Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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APPLICANT:
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US-10-257-017B-291189

Sequence 291189, Application US/10257017B

SEQUENCE 291189, Application US/10257017B

SEQUENCE 291189, Application US/10257017B

SEQUENCE 201189, Application US/10257017B

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: Detection of Single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: DETECTION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 291189

LENGTH: 12

LENGTH: 12
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Sequence 292137, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR PRIOR PAPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
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; Sequence 294714, Application US/10257017B
; GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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SEQ ID NO 292137
JENGTH: 12
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11 AAAAATATTC
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Sequence 301021, Application US/10257017B

Sequence 301021, Application US/10257017B

Sequence 301021, Application US/10257017B

SEQUENCE 301021, Application US/10257017B

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

TITLE OF INVENTION UNMBER: US/10/257,017B

CURRENT PILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 301021

ILENGTH: 12
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10S-10-257-017B-299414

NS-10-257-017B-299414, Application US/10257017B

Sequence 299414, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REPERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT PILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018562 US-10-257-017B-299414
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1.2e+03;
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  DB 1; Length 12;
1.2e+03;
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Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 10; Conservative 0; Mismatches 0;
7.7%; Score 10; DB 100.0%; Pred. No. 1.2 ive 0; Mismatches
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100.0%; Pred. No.
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ORGANISM: Artificial Sequence
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SEQ ID NO 299414
LENGTH: 12
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Matches 10; Conservative
                             Best Local Similarity 100.
Matches 10; Conservative
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US-10-257-017B-301021
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     Query Match
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APPLICANT: Christian Pipenbrock
APPLICANT: Christian Pipenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 108/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
RUMBER OF SEQ ID NOS: 382046
SEQ ID NO 297809
LENGTH: 12
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO S: 382046
SEQ ID NO S: 29302
LENGTH: 12
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US-10-257-017B-299302
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                                                                                                                                                         ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0017285
US-10-257-017B-296818
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                                                                                                                                                                                                                                     7.7%; Score 10; DB 1; Length 12; 100.0%; Pred. No. 1.2e+03; tive 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
        NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 296818
LENGTH: 12
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Sequence 309268, Application US/10257017B
SEMERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
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US-10-257-017B-308711/C
US-10-257-017B-308711/C
Sequence 308711, Application US/10257017B
Sequence 308711, Application US/10257017B
Sequence 308711, Application US/10257017B
Sequence 308711, Application US/10257017B
SERVERANT: Christian Piepenbrock
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Murt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
CURRENT FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 308711
LENGTH: 12
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US-10-257-017B-305776
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FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 305776
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Best Local Similarity 1000
Matches 10; Conservative
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Matches 10; Conservative
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SEQ ID NO 309268
LENGTH: 12
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                                             Sequence 301047, Application US/10257017B

Sequence 301047, Application US/10257017B

SEQUENCEAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 301047
LENGTH: 12
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Curristian Piepenbrock
APPLICANT: What Berlin Piepenbrock
APPLICANT: What Berlin Piepenbrock
APPLICANT: What Berlin Piepenbrock
APPLICANT: What Berlin Piepenbrock
TITLE OF INVENTION: mechylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR FILING DAIE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.2e+03;
Live 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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nes 10; Conservative
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LENGTH: 12
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR RIPLING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 314317
LENGTH: 12
TYPE: DNA
ORGANIE: 12
TYPE: DNA
ORGANIE: Artificial Sequence
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPERENCE: 5002-10-07
CURRENT APPLICATION NUMBER: US/10/257,0178
CURRENT APPLICATION NUMBER: DE 10019173.8
FRICH APPLICATION NUMBER: DE 10019173.8
FRICH APPLICATION DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
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US-10-257-017B-314317
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CTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026652
US-10-257-017B-314959
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                 Sequence 314317, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
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Best Local Similarity 100.
Matches 10; Conservative
  1399 AGGTAAATT 1408
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                                                   10 AGGTAAATT 1
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US-10-257-017B-315150/c
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US-10-257-017B-314959
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US-10-257-017B-314317
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LENGTH: 12
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Sequence 312533, Application US/10257017B
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Sequence 312533, Application US/10257017B
Sequence 312533, Application US/10257017B
Sequence 312533, Application US/10257017B
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION UNMBER: DS/10/257,017B
CURRENT FILING DATE: 2000-04-07
RUMBER OF SEQ ID NOS: 382046
SEQ ID NO 312533
IENGTH: 12
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TILE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT APPLICATION WUMBER: DE 10019173.8
PRIOR PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 312688
LENGTH: 12
) ORGANISM: Artificial Sequence

FEATURE:

) OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0023447

US-10-257-017B-309268
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                                                                                                                             7.7%; Score 10; DB 1; Length 12; 100.0%; Pred. No. 1.2e+03; tive 0; Mismatches 0; Indels
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APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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                                                                                                                          Query Match
Best Local Similarity 100.
Matches 10; Conservative
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US-10-257-017B-312533
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"GENERAL INFORMATION:
Sequence 319241, Application US/10257017B
Sequence 319241, Application US/10257017B
Sequence 319241, Application US/10257017B
Sequence 319241, Application:
GENERAL INFORMATION:
GENERAL Expendence of Sequence of S
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Sequence 320308, Application US/10257017B
GENERAL INFORMATION:
Sequence 320308, Application of Sequence 320308, Application Sequence 320308, Applicant Applicant Applicant: Rurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
SEQ ID NO 320308
LENGTH: 12
                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: PEATURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0028863
US-10-257-0178-318767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0029130 US-10-257-017B-319241
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ORGANISM: Artificial Sequence
                                  NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 318767
LENGTH: 12
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Best Local Similarity 100.
Matches 10; Conservative
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PRIOR FILING DATE:
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US-10-257-017B-318767/c

Sequence 318767/c

Sequence 318767/c

Sequence 318767/c

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Plepenbrock

APPLICANT: Christian Plepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REPRENEUE: 8017,1937/00

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8
                                                                                                    TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations right Reference: methylations FILE REFERENCE: E01/1193/WO CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: US/10/257,017B PRIOR APPLICATION NUMBER: D10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NOS: 382046 LENGTH: 12
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: 801/1193/WO
CURRENT APPLICATION NUMBER: 2010/257,0178
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 315562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.7%; Score 10; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 1.2e+03; Matches 10; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                  Christian Piepenbrock
Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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APPLICANT: Alexander Olek
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Sequence 3.4567, Application US/10257017B

Sequence 3.24567, Application US/10257017B

SEQUENCE 3.24567, Application US/10257017B

SEQUENCE 3.24567, Application US/10257017B

SEQUENCE 3.24567, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Wurt Berlin

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT PILING DATE: 2002-10-07

PRIOR FILING DATE: 2002-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 324567
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 331234
LENGTH: 12
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US-10-257-017B-332249
; Sequence 332249, Application US/10257017B
; Sequence 332249, Application US/10257017B
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
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; Sequence 331234, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                   Sequence 321158
Sequence 321158, Application US/10257017B
Sequence 321158, Application US/10257017B
Sequence 321158, Application US/10257017B
Sequence 321158, Application US/10257017B
SEGUENCANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 321158
LENGTH: 12
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Sequence 322127, Application US/10257017B
Sequence 322127, Application US/10257017B
Sequence 322127, Application US/10257017B
SEQUENCEANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detaylations
FILE REFERENCE: B01/1193/WO
CURRENT PAPLICATION WUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 322127
LENGTH: 12
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US-10-257-017B-321158
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7.7%; Score 10; DB 1; Length 12;
100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
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                                                      0; Indels
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                         Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                1357 AAATATTCCA 1366
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  Query Match
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WS-10-257-017B-333613
Sequence 333613 Application US/10257017B
Sequence 333613 Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT PELLION UNMBER: US/10/257,017B
CURRENT PELLION DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
SEQ ID NOS: 382046
SEQ ID NOS: 382046
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1199/WO
CURRENT APPLICATION NUMBER: US/10/257,0178
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 334046
LENGTH: 12
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US-10-257-017B-334046
                           ORGANISM: Artificial Sequence
FRAUTURE:
OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0037578
US-10-257-0178-333508
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                                                                                                                                                       Query Match 7.7%; Score 10; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 1.2e+03; Matches 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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UG-10-257-017B-333508
UG-10-257-017B-333508
GROUPCE 333508, Application US/10257017B
GROUPCE 333508, Application US/10257017B
GROUPCE 333508, Application US/10257017B
GROUPCE 333508, Application US/10257017B
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPS] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-14-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 333508
LENGTH: 12
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kutt Berian
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: 2010/173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 333164
LENGTH: 12
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; OTHER INFORMATION: Oligonuclectide primer for the detection of SNP ISC0037394
US-10-257-017B-333164
                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0036792 US-10-257-017B-332249
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
; TITLE OF INVENTION: methylations;
FILE REFERENCE: E01/1193/WO;
CURRENT APPLICATION NUMBER: US/10/257,017B;
CURRENT FILING DATE: 2002-10-07;
PRICR APPLICATION WIMBER: DE 10019173.8
FRICR FILING DATE: 2000-04-07;
NUMBER OF SEQ ID NOS: 382046;
SEQ ID NO 332249
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; Sequence 333164, Application US/10257017B
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                                               FEATURE:
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US-10-257-017B-343946/C
US-10-257-017B-343946/C
Sequence 343946, Application US/10257017B
Sequence 343946, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Murt Berlin
APPLICANTON: methylations
FILE REFERENCE: E01/1193/WO
CURRENT PELING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
SEQ ID NO 343946
SEQ ID NO 343946
SEQ ID NO 343946
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosine
TITLE REPERENCE: E01/1193/wo
FILE REPERENCE: E01/1193/wo
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 02(10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 342344
LENGTH: 12
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US-10-257-017B-343946
                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042503
US-10-257-017B-342344
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                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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US-10-257-017B-344354
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APPLICANT: Christian Plepenbrock
APPLICANT: Christian Plepenbrock
APPLICANT: Christian Plepenbrock
APPLICANT: Christian Plepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 100-210-07
PRIOR APPLICATION NUMBER: E0 1019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 337711
LENGTH: 12
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: BOL/1193/MO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
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US-10-257-017B-340768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0040026
US-10-257-017B-337711
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7.7%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.2e+03;
Live 0; Mismatches 0; Indels
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                                                                                                                                                                                        US-10-257-017B-337711
; Sequence 337711, Application US/10257017B
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 340768
LENGTH: 12
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Matches 10; Conservative
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                            1437 ACATATACAT 1446
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                                                                                   12 ACATATACAT 3
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US-10-257-017B-340768/c
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US-10-257-017B-342344
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US-10-257-017B-346862/c
US-10-257-017B-346862/c
US-10-257-017B-346862/c
Sequence 34662. Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE REFERENCE: B01/1193/w0
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 346862
LENGTH: 12
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US-10-257-017B-344752/c
US-10-257-017B-344752/c
Sequence 344752, Application US/10257017B
Sequence 344752, Application US/10257017B
Sequence 344752, Application:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0005691
US-10-257-017B-344752
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                                                         7.7%; Score 10; DB 1; Length 12; 00.0%; Pred. No. 1.2e+03;
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                                                                        100.0%; Pred. ...
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                      Query Match
Best Local Similarity 100.
Matches 10; Conservative
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  US-10-257-017B-344643
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LENGTH: 12
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 344643
MINISTITE OF INDEX OF SEQ ID NOS: 382046
SEQ ID NO 344643
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DS 10019173.8
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
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US-10-257-017B-344578
                                                                                                                                                                                                 FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043503
US-10-257-017B-344354
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OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004577
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-257-017B-344643/c
; Sequence 344643, Application US/10257017B
; GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SRQ ID NO 344354
LENGTH: 12
                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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10 ATTGTTAATG

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Sequence 352091, Application US/10257017B
Sequence 352091, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kutt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPB] and cytosine
TITLE OF INVENTION: Methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
FILE REFERENCE: 2002-10-07
PRIOR FILING DATE: 2002-10-07
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 352091
LENGTH: 12
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION methylations
FILE REFERENCE: E01/1193/WO
CURRENT PAPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION OF SEQ ID NOS: 382046
SEQ ID NO 352518
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations FILE REPERENCE: E01/193/WO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 31979 LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0047604 US-10-257-017B-351979
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
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US-10-257-017B-351099

SEQUENCE 3151099, Application US/10257017B

SEQUENCE 3151099, Application US/10257017B

SEQUENCE 3151099, Application US/10257017B

SEQUENCE 3151099

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: US/10/257,017B

PRIOR FILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 351099
                                                                                                 Sequence 349496, Application US/10257017B

SENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 349496
SEQ ID NO 349496
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US-10-257-017B-351099
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Pred. No. 1.2e+03;
0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No.
Matches 10; Conservative 0; Mismatcl
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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US-10-257-017B-351979
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Sequence 357200, Application US/10257017B
Sequence 357200, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE DE INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FPLING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 357200
LENGTH: 12
                                                                                                                                                                                                                Sequence 357004, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-04-07
PRIOR FILING DATE: 2000-04-07
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US-10-257-017B-357004
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7.7%; Score 10; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 10; Conservative 0; Mismatches 0;
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SEQ ID NO 357004
LENGTH: 12
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Best Local Similarity 100.0
Matches 10, Conservative
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Matches 10; Conservative
                                              1397 GGAGGTAAAA 1406
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US-10-257-017B-357400/c
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APPLICANT: ALexander Olek
APPLICANT: ALexander Olek
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: MUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
WUMBER OF SEQ ID NOS: 382046
SEQ ID NO 354698
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i Sequence 353237, Application US/10257017B

i GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 353237

LENTH: 12
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; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0049232
US-10-257-017B-354698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048393
US-10-257-017B-353237
                                                    ORGANISM: Artificial Sequence
FRATURE:
CHARTURE:
OTHER OLIGONUCLECTION OLIGONUCLECTION OF SNP TSC0047931
US-10-257-017B-352518
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7.7%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
       LENGTH: 12
                            TYPE: DNA
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT EPLING NATE: 2002-10-07
PRIOR APPLICATION NUMBER: 0210-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 360354
LENGTH: 12
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, OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0052044
US-10-257-017B-360354
                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0051481 US-10-257-0178-359150
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleor
TITLE OF INVENTION: Detection of single nucleor
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 105/027,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 360593
LENGTH: 12
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
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; Sequence 360354, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                           CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
WIMBER OF SEQ ID NOS: 382046
SEQ ID NO 359150.
LENGTH: 12
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ORGANISM: Artificial Sequence
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Sequence 357400, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 357400
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: DETECTION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050647 US-10-257-017B-357488
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
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US-10-257-017B-357488

Sequence 357488, Application US/10257017B

GENERAL INFORMATION:
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; Sequence 359150, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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Sequence 365863, Application US/10257017B
Sequence 365863, Application US/10257017B
Sequence 365863, Application US/10257017B
Sequence 365863, Application US/10257017B
SEQUENCE OF INVENTION: Percention of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/W0
CURRENT PAPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 365863
LENGTH: 12
                                                                                    US-10-257-017B-365860
US-10-257-017B-365860, Application US/10257017B
Sequence 365860, Application US/10257017B
Sequence 365860, Application US/10257017B
Sequence 365860, Application US/10257017B
SETION Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US/10/257,017B
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 365860
LENGTH: 12
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US-10-257-017B-365863
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US-10-257-017B-365860
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
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Best Local Similarity 100.0
Matches 10, Conservative
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     11 AAAAATATTC 2
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US-10-257-017B-366148/c
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Sequence 365441, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 2002-10-07
PRIOR APPLICATION NUMBER: DE 2002-10-07
PRIOR APPLICATION NUMBER: DE 382046
SEQ ID NO 365441
LENGTH: 12

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Sequence 361638, Application US/10257017B

Sequence 361638, Application US/10257017B

Sequence 361638, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Kurt Berlin

APPLICANT: Kurt Berlin

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 361638
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US-10-257-017B-365441
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; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0052150 US-10-257-017B-360593
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7.7%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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10 AATTGTTAA 1
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OP INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OP INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 0210-07
PRIOR APPLICATION NUMBER: DE 1019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 368959
LENGTH: 12
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APPLICANT: Christian Piepenbrock
APPLICANT: Kutt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: 0210/1057,017B
CURRENT FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 366837
LENGTH: 12
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, OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0056010 US-10-257-017B-366837
                                                                                                                          ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0055712
US-10-257-017B-366389
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US-10-257-017B-368959
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                                                                                                                                                                                                   Query Match 7.7%; Score 10; DB 1; Le Best Local Similarity 100.0%; Pred. No. 1.2e+03; Matches 10; Conservative 0; Mismatches 0;
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; Sequence 368959, Application US/10257017B
; GENERAL INFORMATION:
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; Sequence 366837, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
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                                                 TYPE: DNA ORGANISM: Artificial Sequence
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SEQ ID NO 366389
LENGTH: 12
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Sequence 366149, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 1019173.8
PRIOR PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 366149
                  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations FILE REFERENCE: E01/193/WO FILE REFERENCE: E01/193/WO CURRENT APPLICATION WUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER: OF SEQ ID NOS: 382046 SEQ ID NOS: 382046 LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0055561
US-10-257-017B-366148
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US-10-257-017B-366149
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7.7%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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7.7%; Score 10; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 10; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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  Kurt Berlin
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     APPLICANT:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Plepenbrock
APPLICANT: Christian Plepenbrock
TITLE OF INVENTION:
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: DETECTION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR PLING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
SEQ ID NOS: 382046
SEQ ID NO 375300
LENGTH: 12
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine.
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
SQUENCE 373960, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1133/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: B1019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 373960
LENGTH: 12
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100.0%; Pred. No. 1.2e+03;
rive 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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Matches 10; Conservative
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US-10-257-017B-373960/c
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US-10-257-017B-370864/C
Sequence 370864, Application US/10257017B
Sequence 370864, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPRENCE: 801/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 370864
LENGTH: 12
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 370557
LENGTH: 12
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; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0058439US-10-257-017B-370864
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7.7%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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Pred. No. 1.2e+03; Mismatches 0; Indels
                                                                                                                                                                                                                       US-10-257-017B-370557; Sequence 370557, Application US/10257017B; GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 10; Conservative 0
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RESULT 769

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US-10-257-017B-379728/C
US-10-257-017B-379728, Application US/10257017B
Sequence 379728, Application US/10257017B
Sequence 379728, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
FRIOR APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 379728
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 1007
PRIOR APPLICATION NUMBER: DB 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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US-10-257-017B-379728
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0062251
US-10-257-017B-377296
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                                                                                                           Query Match
7.7%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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; Sequence 378745, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
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Best Local Similarity
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LENGTH: 12
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Sequence 377296, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Plepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 377296
SEQ ID NO 377296
BENCH FILE TELEBRATE SEQ ID NOS: 382046
SEQ ID NO 377296
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US-10-257-017B-375918

US-10-257-017B-375918

US-10-257-017B-375918

Sequence J75918, Application US/10257017B

Sequence J75918, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFRENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: D000-04-07

PRIOR APPLICATION NUMBER: D000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 375918
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US-10-257-0178-375918
                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0008682
US-10-257-017B-375753
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                           7.7%; Score 10; DB 1; Length 12; 100.0%; Pred. No. 1.2e+03; tive 0; Mismatches 0; Indels
        CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 375753 LENGTH: 12
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                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US110/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 2873
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nuclectide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-110-07
PRIOR FILING DATE: 2000-04-07
                 APPLICANT: Kurt Berlin Triangle nucleotide polymorhphisms (SNPs) and cytosine TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosine TITLE OF INVENTION: methylations FILE REPERBNCE: E0/1/193/WO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT APPLICATION NUMBER: US/10/257,017B PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 2872 LENGTH: 13
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001128
US-10-257-017B-2872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001128 US-10-257-017B-2873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.7%; Score 10; DB 1; Length 13; Best Local Similarity 83.3%; Pred. No. 1.1e+03; Matches 10; Conservative 1; Mismatches 1; Indels
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
Christian Piepenbrock
                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-257-017B-2874/c
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/Wo
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 379901
LENGTH: 12
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Sequence 2821, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: Methylations
TITLE OF INVENTION WUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PRILING DATE: 2002-10-07
PRIOR SPELIATION NUMBER: DE 10019173.8
PRIOR SEQ ID NOS: 382046
SEQ ID NOS: 382046
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US-10-257-017B-2871
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0; Indels
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; Sequence 2872, Application US/10257017B
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 10; Conservative
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                               12 AGAAAAATAT
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US-10-257-017B-5728/C

US-10-257-017B-5728/C

Sequence 5728, Application US/10257017B

Sequence 5728, Application US/10257017B

Sequence 5728, Application US/10257017B

Sequence 5728, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT FILING DATE: 2000-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR PLING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 5728

LINGTH: 13
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Murk Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/193/WO
CURRENT APPLICATION NUMBER: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 5727
LENGTH: 13
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US-10-257-0178-5727
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US-10-257-017B-5728
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  Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.7%; Score 10; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 10; Conservative 0; Mismatches 0; Indels
                                                       1; Indels
  Score 10; DB 1; I Pred, No. 1.1e+03;
                                                                                                                                                                                                                                                                                          Sequence 5727, Application US/10257017B GENERAL INFORMATION:
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Query Match 7.7%;
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                             1356 AAAATATTCCAC 1367
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Sequence 2984, Application US/10257017B

Sequence 2984, Application US/10257017B

SEQUENCANT: LINFORMATION:
APPLICANT: Christian Plepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 2984
LENGTH: 13
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Sequence 2983, Application US/10257017B
Sequence 2983, Application US/10257017B
Sequence 2983, Application US/10257017B
Sequence 2983, Application US/10257017B
Sequence 2983, Application Sequence
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: 2001/1193/W0
CURRENT FILING DATE: 2010-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 2983
LENGTH: 13
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US-10-257-017B-2984
                                                                                      ; TYPE: DNA
; ORGANIEM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0001128
US-10-257-017B-2874
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                                                                                                                                                                                                                                             Score 10; DB 1; Length 13;
Pred. No. 1.1e+03;
1; Mismatches 1; Indels
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83.3%; Pred. No. 1.1e+03;
ive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                             Query Match 7.7%;
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                       1397 GGAGGTAAATT 1408
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     NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 2874
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Matches
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Sequence 15956, Application US/10257017B

Sequence 15956, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Details US/10/257,017B
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Details US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2000-10-07
RHORE FILING DATE: 2000-10-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 15956
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
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US-10-257-017B-15956
                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003512
US-10-257-017B-15955
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                                                                                                                                                                                                                                                                                                                                                                                       Length 13
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83.3%; Pred. No. 1.1e+03;
iive 1; Mismatches 1;
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 15955
LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
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                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 83.33
Matches 10; Conservative
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Matches 10; Conservative
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US-10-257-017B-15956/c
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Sequence 15955, Application US/10257017B

Sequence 15955, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of Single nucleotide polymorhphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
RUMBER OF SEQ ID NOS: 382046
SEQ ID NO 15942
LENGTH: 13
                                                                                                                                                                                                 single nucleotide polymorhphisms [SNPs] and cytosine
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US-10-257-017B-15942
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US-10-257-017B-15941
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100.0%; Pred. No. 1.18+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 13;
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                                                                                                              GENERAL INVORMENTION:
GENERAL INVORMENTION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TUTLE OF INVENTION: Detection of single nucleo
TITLE OF INVENTION: DETECTION WUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
; SEQ ID NO 15941
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                                                           Sequence 15941, Application US/10257017B GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 10; Conserva'
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                                                US-10-257-017B-15941/c
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US-10-257-017B-15942
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Page 181

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Sequence 2031, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Curtistian Piepenbrock
APPLICANT: Curtistian Control of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
                                                                                                                                                                                                                                                APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kutt Berlin
TITLE OF INVENTION: Detection of single nuclectide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: BO1/1193/WO
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 16322
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0004157
US-10-257-017B-20311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003567 US-10-257-017B-16322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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US-10-257-017B-20312/c
; Sequence 20312, Application US/10257017B
; GENERAL INPORMATION:
                                                                                                                                                                            Sequence 16322, Application US/10257017B GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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1402 TAAAATTGTT 1411
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US-10-257-017B-16322/c
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LENGTH: 13
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US-10-257-017B-15960/c
Sequence 15960, Application US/10257017B
Sequence 15960, Application US/10257017B
Septingary INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Wart Berlin
TITLE OF INVENTION: methylations
FILTE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR RILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 15960
LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR PLING DATE: 2000-04-07
RUMBER OF SEQ ID NOS: 382046
SEQ ID NO 16321
LENGTH: 13
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                                                                                                                                                                                 Gaps
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US-10-257-017B-15960
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                                                   OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0003512
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Pred. No. 1.1e+03;
1; Mismatches 1; Indels
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100.0%; Pred. No. 1.1e+03;
tive 0; Mismatches 0; Indels
                                                                                                                             Query Match 7.7%; Score 10; DB 1; Length 13; Best Local Similarity 83.3%; Pred. No. 1.1e+03; Matches 10; Conservative 1; Mismatches 1; Indels
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.7%;
Best Local Similarity 83.3%;
Matches 10; Conservative
ORGANISM: Artificial Sequence
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US-10-257-017B-16321
                                                                               US-10-257-017B-15959
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Sequence 22561, Application US/10257017B

Sequence 22561, Application US/10257017B

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ALexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Mit Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 22561
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurk Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PLING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 22562
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                                                                                                                                                                                    FEATURE:
; CTHER INFORMATION: Oligonucleotide for detection of SNP TSC0004405
US-10-257-017B-22212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0004456
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                                                                                                                                                                                                                                                                                               Query Match 7.7%; Score 10; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 10; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                 PRIOR FILING DATE: 2000-04-07
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                                            NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 22212
LENGTH: 13
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Matches 10, Conservative
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US-10-257-017B-22561/c
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US-10-257-017B-22211/c
Sequence 22211, Application US/10257017B
Sequence 22211, Application US/10257017B
SEQUENCE 22211, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
CURRENT APPLICANTON: UNBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 22211
LENGTH: 13
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Sequence 22212, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: SO1/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 20312
LENGTH: 13
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) OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0004405
US-10-257-017B-22211
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
; CTHER INFORMATION: Oligonucleotide for detection of SNP TSC0004157 US-10-257-017B-20312
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Seguence
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Sequence 26637, Application US/10257017B
; Sequence 26637, Application US/10257017B
; Sequence 26637, Application US/10257017B
; GENERAL INFORMATION:
    APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
    TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
; TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/W0
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 26637
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kutt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosine
TITLE OF INVENTION: Detection of Single nucleotide polymorhphisms (SNPs) and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 0210/10-77
PRIOR PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 26638
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Oligonucleotide for detection of SNP ISC0007097
US-10-257-017B-26638
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7.7%; Score 10; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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US-10-257-017B-24121/C

Sequence 24121, Application US/10257017B

Sequence 24121, Application US/10257017B

Sequence 24121, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Alexander Olek

APPLICANT: Current Control of Single nucleotide polymorhphisms [SNPs] and cytosine

TILE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ 1D NOS: 382046

SSQ 1D NO 24121

LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: D8 10019173.8
PRIOR PLING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 24122
LENGTH: 13
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                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Artificial Sequence
; FRATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0005613
US-10-257-017B-24121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0005613
US-10-257-017B-24122
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  Length 13;
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7.7%; Score 10; DB 1; 1
83.3%; Pred. No. 1.1e+03;
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                                                1; Mismatches
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ORGANISM: Artificial Sequence
                                                                                                     1351 GAAGAAAATAT 1362
                                                     10; Conservative
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                                                                                                                                                     1 RAATAAAAATAT 12
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                  Best Local Similarity
Matches 10; Conserv
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US-10-257-017B-24122
     Query Match
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Sequence 48143, Application US/10257017B

Sequence 48143, Application US/10257017B

GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT PAPLICATION NUMBER: D2 10019173.8
FRIOR PILING DATE: 2002-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER: D2 10019173.8
SEQ ID NOS: 382046
SEQ ID NO 48143
                                                                                                                                                                                                                                                                                                                                                                              RESULT 806
US-10-257-017B-42008/C
US-10-257-017B
Sequence 42008, Application US/10257017B
Sequence 42008, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 4208
LENGTH: 13
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, OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0012567 US-10-257-017B-42008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0013757 US-10-257-017B-48143
                                                                             ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0012567
US-10-257-0178-42007
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                                                                                                                                                       7.7%; Score 10; DB 1; Length 13;
100.0%; Pred. No. 1.1e+03;
tive 0; Mismatches 0; Indels
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Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 10; Conservative 1; Mismatches 1;
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Matches 10; Conservative
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                                                                                                                                                          Query Match
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APPLICANT: Christian Plepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: LB 10019173.8
PRIOR FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 40988
ILENGTH: 13
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Sequence 42007, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILLE OF INVENTION: methylations
FILLE OF INVENTION: METHYLATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/757,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILLING DATE: 2000-04-07
PRIOR FILLING DATE: 2000-04-07
SEQ ID NO 42007
LENGTH: 13
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0012366
US-10-257-017B-40988
                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0012366 US-10-257-017B-40987
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                                                                                                                                                                                                                                                                                                                                                                                         Length 13;
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  ; TITLE OF INVENTION: methylations; FILE REFERENCE: E01/1193/WO; CURRENT APPLICATION NUMBER: U01/0/257,017B; CURRENT FILING DATE: 2002-10-07; PRIOR APPLICATION NUMBER: DE 10019173.8; NUMBER OF SEQ ID NOS: 382046; SEQ ID NO 40987; LENGTH: 13
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; Sequence 40988, Application US/10257017B
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Matches 10, Conservative
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Sequence 50663, Application US/10257017B

Sequence 50663, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DAIE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/193/M0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
                   APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: UNBER: US110/257,017B
FILE REFERENCE: E01/1193/WO
CURRENT PELLING DATE: 2000-04
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 48148
LENGTH: 13
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US-10-257-017B-50663
                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0013759 US-10-257-017B-48148
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                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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APPLICANT: Alexander Olek
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LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kutt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: BO1/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 48147
LENGTH: 13
                                                                                                                                             US-017B-48144

Sequence 48144, Application US/10257017B

Sequence 48144, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Plepenbrock

APPLICANT: Christian Plepenbrock

APPLICANT: Nurs Berlin

APPLICANT: Nurs Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: WOWBER: US/10/257,017B

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 48144
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0013757
US-10-257-017B-48144
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Pred. No. 1.18+03;
1; Mismatches 1; Indels
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83.3%; Pred. No. 1.1e+03;
tive 1; Mismatches 1; Indels
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US-10-257-017B-48148/c
; Sequence 48148, Application US/10257017B
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Best Local Similarity 83.3%;
Matches 10; Conservative
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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          1460 ATCAAGCAAATA 1471
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                                                      13 RTCAAACAATA 2
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US-10-257-017B-48147
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US-10-257-017B-53710/c
US-10-257-017B-53710/c
Squarez 53710, Application US/10257017B
; Sequence 53710, Application US/10257017B
; GENERAL INFORMATION:
APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Christian Piepenbrock
; APPLICANT: Christian Piepenbrock
; APPLICANT: Christian Piepenbrock
; TILLE OF INVENTION: methylations
; TILLE OF INVENTION: methylations
; FILLE OF INVENTION: methylations
; FILLE OF INVENTION: METHYLATION NUMBER: US/10/257,017B
; CURRENT APPLICATION NUMBER: DE 10019173.8
; PRIOR FILLING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 53710
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION WUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 53709
LENGTH: 13
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US-10-257-017B-53710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0014802
US-10-257-017B-53709
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100.0%; Pred. No. 1.1e+03;
tive 0; Mismatches 0; Indels
                                                Length 13;
                                                                                                 0; Indels
                                             7.7%; Score 10; DB 1; Le 100.0%; Pred. No. 1.1e+03; tive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10, Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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US-10-257-017B-53654
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Sequence 53664, Application US/10257017B
Sequence 53664, Application US/10257017B
SEQUENCE 53664, Application US/10257017B
SEQ IN SECURIARY Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 53654
LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-04-07
PRIOR FILING DATE: 2000-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0014796 US-10-257-017B-53653
                                                                                                                                                                                                          ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0014212
US-10-257-017B-50664
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100.0%; Pred. No. 1.1e+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                           Length 13;
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1.1e+03;
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PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 50664
LENGTH: 13
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine; TITLE OF INVENTION: methylations
TITLE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 54064
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US-10-257-017B-56067/c
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Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067, Squence 56067
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations FILE REFERENCE: E01/1193/WO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07
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                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0014864 US-10-257-017B-54063
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100.0%; Pred. No. 1.1e+03;
tive 0; Mismatches 0;
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; Sequence 54064, Application US/10257017B
; GENERAL INFORMATION:
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                                                                                                                                                       NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 54063
LENGTH: 13
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Best Local Similarity
Matches 10; Conserv
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                                               US-10-257-017B-53941/c
US-10-257-017B-53941/c
US-10-257-017B-53941/c
SEMENAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Murk Berlin
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US/10/257,017B
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 53941
LENGTH: 13
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US-10-257-017B-53942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Oligonucleotide for detection of SNP ISC0014838
US-10-257-017B-53941
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Pred. No. 1.1e+03;
1; Mismatches 1; Indels
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Kurt Berlin
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illarity 83.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.7%;
Best Local Similarity 83.3%;
Matches 10; Conservative
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APPLICANT: Christian Pier
APPLICANT: Kurt Berlin
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Gristian Piepenbrock
APPLICANT: Gristian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/MO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 59775
LIENGTH: 13
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US-10-257-017B-57846/c
Sequence 57846, Application US/10257017B
Sequence 57846, Application US/10257017B
Sequence 57846, Application US/10257017B
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FILE REPERRICE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
LENGTH: 13
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US-10-257-017B-59775
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US-10-257-017B-57846
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7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
  Indels
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Best Local Similarity 100.0
Matches 10, Conservative
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     Matches 10; Conservative
                                                        1375 GAGCGATCGT 1384
                                                                                                        3 GAGCGATCGT 12
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US-10-257-017B-59776
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; Sequence 57845, Application US/10257017B
; GENERAL INFORMATION:
    APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
: CURRENT FILING DATE: 2002-10-07
CURRENT FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
SEQ ID NOS: 382046
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Sequence 56068, Application US/10257017B

Sequence 56068, Application US/10257017B

Sequence 56068, Application US/10257017B

Sequence 56068, Application US/10257017B

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: methylations

TITLE REFERENCE: E01/193/WO

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 5608

LENGTH: 13
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US-10-257-017B-57845
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OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015245
US-10-257-017B-56068
                                                                                           ; FEATURE:
; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0015245
US-10-257-017B-56067
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Pred. No. 1.1e+03;
1; Mismatches 1; Indels
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.3%;
Matches 10; Conservative
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ORGANISM: Artificial Sequence
                                             TYPE: DNA ORGANISM: Artificial Sequence
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US-10-257-017B-56068
                  LENGTH: 13
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RESULT 829
US-10-257-017B-61279, Application US/10257017B
; Sequence 61279, Application US/10257017B
; Sequence 61279, Application US/10257017B
; GENERAL INPORMATION:
    APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
    TITLE OF INVENTION: methylations
; FILE OF INVENTION: methylations
; FILE REPERRICE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 61279
LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
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US-10-257-017B-61279
                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016082 US-10-257-017B-60200
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CURRENT FLING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 61280
LENGTH: 13
                       PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 60200
LENGTH: 13
2002-10-07
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ORGANISM: Artificial Sequence
FEATURE:
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CURRENT FILING DATE:
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US-10-257-017B-61280/c
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Sequence 60199, Application US/10257017B

Sequence 60199, Application US/10257017B

SEGNERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: meth
                                                                                         APPLICANT: Christian View Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
ITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
ITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 100-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 59776
LENGTH: 13
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1133/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
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US-10-257-017B-60199
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0015989
US-10-259-017B-59776
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; Sequence 60200, Application US/10257017B
; GENERAL INFORMATION:
APPLICANT: Alexander Olek
Sequence 59776, Application US/10257017B GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                             APPLICANT: Alexander Olek
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PELING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 63973
LENGTH: 13
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APPLICANT: Christian Plepenbrock
APPLICANT: Kurt Barlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
SEQ ID NOS: 392046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016888
US-10-257-017B-63973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 63974, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                              Sequence 63973, Application US/10257017B
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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  4 AAATATTCCA 13
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US-10-257-017B-63974/c
                                                                                                  US-10-257-017B-63973
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Sequence 62977, Application US/10257017B

Sequence 62977, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REFERENCE: BO1/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT PILING DATE: 2002-10-07

PRIOR PILING DATE: 2002-10-07

PRIOR PILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 62977

LENGTH: 13
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Sequence 62978, Application US/10257017B
Sequence 62978, Application US/10257017B
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 62978
MENTY: 13
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US-10-257-017B-62977
; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0016313
US-10-257-017B-61280
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100.0%; Pred. No. 1.1e+03;
ive 0; Mismatches 0; Indels
                                                                        Query Match

7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.10+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10, Conservative
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Matches 10; Conservative
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1357 AAATATTCCA 1366

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Sequence 73027, Application US/10257017B

SEQUENCE 73027, Application US/10257017B

SEQUENCE 73027, Application US/10257017B

SEQUENCE 73027, Application of SEQUENCE APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock
APPLICANT: Curt Berlin

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 73027

LENGTH: 13
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Sequence 66684, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: BO1/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR PAPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0017494
US-10-257-017B-66684
                                                                                                                                    ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0017494 US-10-257-017B-66683
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7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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7.7%; Score 10; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0;
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                                    LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
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        SEQ ID NO 66683
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 65110
LENGTH: 13
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Sequence 66683, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

APPLICANT: Kurt Berlin

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

TITLE OF INVENTION WOMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: US/10-07

PRIOR FILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

WUMBER OF SEQ ID NOS: 382046
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FITLE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
SEQ ID NO 65109
LENGTH: 13
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US-10-257-017B-65110
                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0017151
US-10-257-017B-65109
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7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 10; Conservative 1; Mismatches 1; Indels
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; Sequence 65110, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.33
Matches 10; Conservative
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 80365
LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
  Sequence 80072, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
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US-10-257-017B-80072
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7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 80072
LENGTH: 13
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Best Local Similarity 100.
Matches 10; Conservative
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US-10-257-017B-80366/c
US-10-257-017B-80072/c
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### Sequence 80071, Application US/10257017B
### Sequence 80071, Application US/10257017B
### Sequence 80071, Application US/10257017B
### APPLICANT: Christian Piepenbrock
### APPLICANT: Kurt Barlin
### TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosine
### TITLE OF INVENTION: methylations
### RICE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 80071

LENGTH: 13
                                                                                                                                                                                                                                                                                                          APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OP INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: LD 1007-10-07
PRIOR PILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 73028
LENGTH: 13
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US-10-257-017B-80071
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US-10-257-017B-73028
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     Best Local Similarity 100.0%; Pred. No. 1.10+03; Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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Matches 10; Conservative
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                                                                                  1403 AAAATTGTTA 1412
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US-10-257-017B-73028/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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RESULT 842

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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Diepenbrock
APPLICANT: Christian Diepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
RIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 82290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: BO1/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 82289
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0020785 US-10-257-017B-82290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0020785
US-10-257-017B-82289
                        ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0020728 US-10-257-017B-81968
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                                                                                                    Length 13;
                                                                                                                                                        1; Indels
                                                                                                 Query Match 7.7%; Score 10; DB 1; Best Local Similarity 83.3%; Pred. No. 1.1e+03; Matches 10; Conservative 1; Mismatches 1
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; Sequence 82290, Application US/10257017B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 82289, Application US/10257017B; GENERAL INFORMATION: APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                              1354 GAAAAATATTCC 1365
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Best Local Similarity
Matches 10; Conserv
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     FEATURE:
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Sequence 81967, Application US/10257017B

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ALexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNP8] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION UNMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 81967
LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 81968
LENGTH: 13
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US-10-257-017B-81967
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7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 80366 LENGTH: 13
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ORGANISM: Artificial Sequence
                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-257-017B-81968
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Matches
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Sequence 200707, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
MANDER OF STILING DATE: 2000-04-07
                    APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: BOJ/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 85949
LENGTH: 13
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US-10-257-017B-85950
                                                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0021601 US-10-257-017B-85949
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7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
Christian Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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SEQ ID NO 85950
LENGTH: 13
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APPLICANT:
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Sequence 85484 Application US/10257017B
Sequence 85484 Application
GENERAL INFORMATION:
APPLICANT: ALT Berlin
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANTON: Establish
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 85484
LENGTH: 13
                                                                                                                   APPLICANT: Alexander Olek
Sequence 85483, Application US/10257017B
Sequence 85483, Application US/10257017B
Sequence 85483, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Rutt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/MO
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 84883
LENGTH: 13
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US-10-257-017B-85484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Oligonucleotide for detection of SNP TSC0021482 US-10-257-017B-85483
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7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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; Sequence 85949, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1437 ACATATACAT 1446
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                                            11 AGAAAATAT 2
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US110/257,017B
CURRENT FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 92315
LENGTH: 13
                                                                                                                                                                                                                                                                                                            APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,0178
CURRENT PILING DATE: 2002-10-07
PRIOR PILING DATE: 2000-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0023077 US-10-257-017B-92315
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    DB 1; Length 13;
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7.7%; Score 10; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0;
                       1.1e+03;
                                            0; Mismatches
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7.7%; Score 10;
100.0%; Pred. No.
                                                                                                                                                                                                                                             Sequence 90354, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
                     100.08;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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SEQ ID NO 90354
LENGTH: 13
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Best Local Similarity 100.'
Matches 10; Conservative
                     Best Local Similarity 100.
Matches 10; Conservative
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US-10-257-017B-90354/c
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    Query Match
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US-10-257-017B-90353
Sequence 90353, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 90353
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2010 Application US/10257017B
Sequence 30108 Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPERENCE: B01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 86708
LENGTH: 13
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                                                                                                         FEATURE:
CTHER INFORMATION: Oligonuclectide for detection of SNP TSC0021791
US-10-257-017B-86707
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                                                                                                                                                                                                     Length 13;
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100.0%; Pred. No. 1.1e+03;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                               0; Indels
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7.7%; Score 10; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 86707
LENGTH: 13
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nes 10; Conserv
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US-10-257-017B-86708/c
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Matches
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Page 196

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Sequence 94173, Application US/10257017B

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 0210/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR PILING DATE: 2000-04-07
NUMBER: E000-04-07
SEQ ID NOS: 382046
SEQ ID NOS: 382046
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
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US-10-257-017B-93510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0023509
US-10-257-017B-94173
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100.0%; Pred. No. 1.1e+03;
tive 0; Mismatches 0; Indels
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        CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 93510
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                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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SEQ ID NO 94174
LENGTH: 13
TYPE: DNA
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Best Local Similarity 100.
Matches 10, Conservative
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US-10-257-017B-94173/c
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                                                                                                           APPLICANT: Christian Fiepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 108/1097, 017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SRQ ID NO 92316
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR RAPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 93509
LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
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US-10-257-017B-93509
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US-10-257-017B-92316; Application US/10257017B; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 93509, Application US/10257017B GENERAL INFORMATION:
APPLICANT: Alexander Olek
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MS-10-257-017B-95633/C
Sequence 95633, Application US/10257017B
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
APPLICANT: Methylations
FILE REFERENCE: E01/1193/WO
SCURRENT APPLICATION WHERE: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 95633
LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 96534
LENGTH: 13
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US-10-257-017B-95633
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US-10-257-017B-95634
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ORGANISM: Artificial Sequence
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               1355 AAAAATATTC 1364
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US-10-257-017B-95634
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GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Christian
APPLICANT: Chris
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Barlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: 2002-10-07
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR PRIJNG DATE: 2002-10-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 95060
LENGTH: 13
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; ORGANISM: Artificial Sequence
; FEATURE:
; CTHEN INFORMATION: Oligonucleotide for detection of SNP TSC0023509
US-10-257-017B-94174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0023684 US-10-257-017B-95059
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                                                                                                                                                                                   7.7%; Score 10; DB 1; Length 13;
83.3%; Pred. No. 1.1e+03;
tive 1; Mismatches 1; Indels
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; Sequence 95060, Application US/10257017B
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                    1361 ATTCCACGCATC 1372
                                                                                                                                                                               Query Match
Best Local Similarity 83.39
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                  1355 AAAAATATTC 1364
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US-10-257-017B-95059/c
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Sequence 102561, Application US/10257017B

Sequence 102561, Application US/10257017B

GENERAL INPORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: 801/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 102561
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: With Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: BO1/1193/WO
CURRENT APPLICATION NUMBER: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 100536
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                                                                                                                                                                                          ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0025011 US-10-257-017B-100535
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7.7%; Score 10; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0;
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                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 100535
LENGTH: 13
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US-10-257-017B-97056/C
US-10-257-017B-97056/C
Sequence 97056, Application US/10257017B
Sequence 197056, Application US/10257017B
Sequence 197056, Application Sequence 197056
APPLICANT: Christian Plepenbrock
APPLICANT: Christian Plepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPB] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPB] and cytosine
FILE REFERENCE: E01/1195/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 97056
                                                                     TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations FILE REPERBYCE: 801/1193/W0 CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: 02 100-10-07 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NOS: 382046 SEQ ID NOS: 382046
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024079
US-10-257-017B-97055
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                      Christian Piepenbrock
Kurt Berlin
                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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APPLICANT: Alexander Olek
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kutt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of Single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 0210-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 103208
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 103331
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0025853
US-10-257-0178-103331
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83.3%; Pred. No. 1.1e+03;
tive 1; Mismatches 1; Indels
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                                                             ; Sequence 103208, Application US/10257017B; GENERAL INFORMATION: APPLICANT: Alexander olek
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; Sequence 103331, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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Matches 10; Conservative
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                                 US-10-257-017B-103208/c
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US-10-25-017B-102562, Application US/10257017B
Sequence 102562, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPB] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR PLLING DATE: 2002-10-07
PRIOR PLLING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 102562
LENTH: 13
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US,10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 103207
LENGTH: 13
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0025589
US-10-257-0178-102562
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7.7%; Score 10; DB 1; Length 13; 100.0%; Pred. No. 1.1e+03; tive 0; Mismatches 0; Indels
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7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 10; Conservative 1; Mismatches 1; Indels
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ORGANISM: Artificial Seguence
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                                                           10; Conservative
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                            Best Local Similarity
Matches 10; Conserva
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US-10-257-017B-103207
        Query Match
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 107611
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 2010-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PRIOR DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 107612
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                                                                                        ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0026360 US-10-257-017B-105252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0026951
US-10-257-017B-107611
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US-10-257-017B-107612
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Pred. No. 1.1e+03;
1; Mismatches 1; Indels
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83.3%; Pred. No. 1.1e+03;
tive 1; Mismatches 1; Indels
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                                   ORGANISM: Artificial Sequence
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Best Local Similarity 83.3%;
Matches 10; Conservative
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.3
Matches 10; Conservative
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1 RAAAAAATAT 12
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                                                               FEATURE:
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Defection of single nuclectide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nuclectide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION WUMBER: us/10/257,017B
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 105251
LENGTH: 13
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Sequence 10525, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
FRIOR PILING DATE: 2002-10-07
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SRQ ID NO 105252
LENGTH: 13
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7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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Pred, No. 1.18+03;
1; Indels
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 103332
LENGTH: 13
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; Sequence 105251, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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Best Local Similarity 83.3%;
Matches 10; Conservative
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPS] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPERENCE: BOIL/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR PELICATION NUMBER: DE 10019173.8
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 107941
LENGTH: 13
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Sequence 107942, Application US/10257017B

Sequence 107942, Application US/10257017B

Sequence 107942, Application US/10257017B

Sequence 107942, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: US/10/257,017B

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 107942

LENGTH: 13
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US-10-257-017B-107941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027027
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Sequence 11351, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nuclee
TITLE OF INVENTION: methylations
FILE REPERENCE: E0/1193/WO
FULE REPERENCE: 2011193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
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ORGANISM: Artificial Sequence
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APPLICANT: Christian Plepenbrock
APPLICANT: Kurt Berlin lepenbrock
APPLICANT: Kurt Berlin lepenbrock
APPLICANT: Kurt Berlin lepenbrock
TITLE OF INVENTION: Defection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 107687
LENGTH: 13
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Abristian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US,10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
SEQ ID NO 107688
LENGTH: 13
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0026969
US-10-257-017B-107687
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CTHER INFORMATION: Oligonuclectide for detection of SNP TSC0026969

US-10-257-017B-107688
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7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 10; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                         US-10-257-017B-1076B7/c
; Sequence 1076B7, Application US/10257017B
; GENERAL INFORMATION:
A PPPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 883
US-10-257-017B-107941
; Sequence 107941, Application US/10257017B
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/W0
CURRENT APPLICATION NUMBER: 0200-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 115216
LENGTH: 13
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UG-10-227-017B-118837/c
UG-10-227-017B-118837/c
Sequence 118837, Application US/10257017B
Sequence 118837, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 118837
LENGTH: 13
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US-10-257-017B-115216
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                                                               Query Match 7.7%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 1.1 Matches 10; Conservative 0; Mismatches
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US-10-257-017B-115216/c
'Sequence 115216, Application US/10257017B
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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           US-10-257-017B-115215
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Sequence 115215, Application US/10257017B
Sequence 115215, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Abrander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-10-07
FRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 115215
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 113532
LENGTH: 13
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US-10-257-017B-113531
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US-10-257-017B-113532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 113532, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 113531
LENGTH: 13
                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 10, Conservative
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Sequence 123026, Application US/10257017B GENERAL INFORMATION: APPLICANT: Alexander Olek APPLICANT: Christian Piepenbrock APPLICANT: Kurt Berlin

APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNDs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 128463
LENGTH: 13 TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine ritle OF INVENTION: methylations FILE REFERENCE: E01/193/WO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT PILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 Sequence 128464, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT PAPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PRIOR BATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 128464 ö .. Gaps Gaps ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0030755 US-10-257-017B-123026 ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032178 US-10-257-017B-128463 0; .. ; DB 1; Lc.._ '^. 1.1e+03; Indels 7.7%; Score 10; DB 1; Length 13; 100.0%; Pred. No. 1.1e+03; tive 0; Mismatches 0; Indels Query Match 7.7%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 1.1 Matches 10; Conservative 0; Mismatches Sequence 128463, Application US/10257017B GENERAL INFORMATION: TYPE: DNA ORGANISM: Artificial Sequence TYPE: DNA ORGANISM: Artificial Sequence NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 123026 LENGTH: 13 Best_Local Similarity 100. Matches 10; Conservative 1448 GAAGATGGGT 1457 1357 AAATATTCCA 1366 m 12 GAAGATGGGT 13 AAATATTCCA US-10-257-017B-128463/c US-10-257-017B-128464 Query Match ò g ð g

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RESULT 897

UG-10-257-0178-131753/c

Sequence 131753, Application US/10257017B

Sequence 131753, Application US/10257017B

Sequence 131753, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/MO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: US/10/257,017B

PRIOR PILING DATE: 2002-10-07

PRIOR PILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 131753

LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Alexander Depenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: UNMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10-07
CURRENT FILING DATE: 2002-10-07
PRIOR PELICING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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     Mismatches
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ORGANISM: Artificial Sequence
  Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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                                                   1402 TAAAATTGTT 1411
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US-10-257-017B-132237/c
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LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT PRILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 129040
LENGTH: 13
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0032305
US-10-257-017B-129039
                                                                                            ; OTHER INFORMATION: Oligonuclectide for detection of SNP ISC0032178 US-10-257-017B-128464
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US-10-257-017B-129040
                                                                                                                                                                    7.7%; Score 10; DB 1; Length 13; 100.0%; Pred. No. 1.1e+03; tive 0; Mismatches 0; Indels
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; Sequence 129040, Application US/10257017B
; GENERAL INFORMATION:
                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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LENGTH: 13
LENGTH: 13
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Page 205

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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: 108/10/257,017B
FUND APPLICATION NUMBER: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR FILING DATE: 2000-04-07
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US-10-257-017B-132805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033117 US-10-257-017B-132806
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. 1.le+03;
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100.0%; Pred. No. 1.1
:ive 0; Mismatches
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
             CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
WIMBER OS ESQ ID NOS: 382046
SEQ ID NO 132805
LENGTH: 13
                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
PEATURE:
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SEQ ID NO 132806
LENGTH: 13
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SEQ ID NO 135433
LENGTH: 13
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Best Local Similarity 100.
Matches 10; Conservative
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Sequence 132237, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: LD 1002-10-07
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 132237
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kutt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPREMENCE: B01/1193/W0
CURRENT PPLING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 132238
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GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL OF INFORMATION:
APPLICANT:
TITLE OF INVENTION:
METHYLATION:
FILE REPERENCE: E01/1193/WO
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US-10-257-017B-132238
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7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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; Sequence 132238, Application US/10257017B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 10; Conserv
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US-10-257-017B-136312/C
US-102-257-017B-136312/Application US/10257017B
; Sequence 136312, Application US/10257017B
; Sequence 136312, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: methylations
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT PILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; CURRENT PILING DATE: 2000-04-07
; WUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 136312
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US-10-257-0178-140385

Sequence 140385, Application US/10257017B

Sequence 140385, Application US/10257017B

Sequence 140385, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Perentin

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT FILING DATE: 2002-10-07

PRIOR PILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 140385

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0035188 US-10-257-017B-140385
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; Sequence 140386, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: ALExander Olek
; APPLICANT: Christian Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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US-10-257-017B-135434/C

US-10-257-017B-135434 Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Curistian Piepenbrock

APPLICANT: Curistian Piepenbrock

APPLICANT: Curistian Piepenbrock

TITLE OF INVENTION: methylations

FILE REFERENCE: B01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR PILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 135434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Christian Pipenbrock
APPLICANT: Christian Pipenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: D002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 136311
LENGTH: 13
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0033799 US-10-257-017B-135433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Oligonuclectide for detection of SNP ISC0033799 US-10-257-017B-135434
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0034044
US-10-257-0178-136311
                                                                           Query Match 7.7%; Score 10; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.7%; Score 10; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 10; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Seguence
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% Sequence 14315, Application US/10257017B

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: NITE BETLIN
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/137/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
FRICR APPLICATION NUMBER: DE 10019173.8
FRICR APPLICATION NUMBER: DE 10019173.8
FRICR FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 443215
FRICRAMENT 12315
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Sequence 143216, Application US/10257017B
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 143216
LENGTH: 13
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                                                                                                                                                  OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0035679 US-10-257-017B-142324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0035935
US-10-257-017B-143215
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US-10-257-017B-143216
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                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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13 RATATTCCCGC 2
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Best Local Similarity
Matches 10; Conserva'
                 SEQ ID NO 142324
LENGTH: 13
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OP INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: LD 100/257,017B
FRIOR APPLICATION NUMBER: E0 100/257,017B
FRIOR APPLICATION NUMBER: E0 100/20173.8
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 140386
LENGTH: 13
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Sequence 142323, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 142323
MENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPERENCE: EQ1/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
NUMBER OF SEQ ID NOS: 382046
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OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0035188
US-10-257-017B-140386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0035679 US-10-257-017B-142323
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                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.7
Best Local Similarity 100.
Matches 10; Conservative
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US-10-257-017B-142323
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GENERAL INFORMATION:
APPLICANT: Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 147577
LIENGTH: 13
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Sequence 147578, Application US/10257017B
Sequence 147578, Application US/10257017B
Sequence 147578, Application US/10257017B
Sequence 147578, Application US/10257017B
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Murt Berlin
APPLICANT: Murt Berlin
APPLICANT: Murp Content Of Single nucleotide polymorhphisms [SNPS] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257, 017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 147578
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
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; CTHER INFORMATION: Oligonuclectide for detection of SNP TSC0037287
US-10-257-0178-147577
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US-10-257-017B-147578
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100.0%; Pred. No. 1.1e+03;
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7.7%; Score 10; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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Matches 10; Conservative
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          US-10-257-017B-147577
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US-10-257-017B-144232/c
Sequence 144232, Application US/10257017B
Sequence 144232, Application US/10257017B
Sequence 144232, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FITLE REPRENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 144232
LENGTH: 13
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APPLICANT: Christian Pipenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nuclectide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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; CTHER INFORMATION: Oligonuclectide for detection of SNP TSC0036260 US-10-257-017B-144231
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; CTHER INFORMATION: Oligonucleotide for detection of SNP TSC0036260
US-10-257-0178-144232
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7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
     Pred. No. 1.1e+03;
1; Mismatches 1; Indels
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
     83.3%;
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                             10; Conservative
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1 AAGATGGGTT 10
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Best Local Similarity
Matches 10; Conserv
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US-10-257-017B-144231
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 447880
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                                              ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037346 US-10-257-017B-147879
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0037461
US-10-257-017B-148407
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7.7%; Score 10; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Defection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PRIOR ELING DATE: 2000-04-07
NUMBER OF SOC ID NOS: 382046
SEQ ID NO 147658
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Pepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT PAPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: E01019173.8
PRIOR PAPLICATION NUMBER: E01019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 147879
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US-10-257-017B-147657
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100.0%; Pred. No. 1.1e+03;
ive 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/10/257,017B
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; Sequence 147658, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
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                            CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 147657
LENGTH: 13
                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 10; Conservative
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11 GGTAAAATTG 2
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US-10-257-017B-147879/c
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GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ALexander Olek
APPLICANT: ALexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PAPLICATION NUMBER: BI 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 154055
LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: D8 10019173.8
PRIOR FILING DATE: 2000-04-07
                       APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
FILE REPERBNCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 100/257,017B
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0000577
US-10-257-017B-154055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.7%; Score 10; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 10; Conservative 0; Mismatches 0; Indels
        Christian Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                        DEPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVERTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVERTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 148408
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 148707
LENGTH: 13
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CTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037542
US-10-257-017B-148707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037461
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US-10-257-017B-148708/c
; Sequence 148708, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                                                                                                                                          US-10-257-017B-148408/c; Sequence 148408, Application US/10257017B; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-257-017B-148707
; Sequence 148707, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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1 AAGAAAATA 10
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Matches 10; Conserva
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Sequence 15554, Application US/10257017B

SEQUENCE INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Rurt Berlin
APPLICANT: NUMBER: US/10/257,017B
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 155548
LENGTH: 13
                                                                                                                                                                                                                                                              Sequence 155547, Application US/10257017B
Sequence 155547, Application US/10257017B
GRNERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 155547
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          Length 13;
                                                         1; Indels
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7.7%; Score 10; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0;
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7.7%; Score 10; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0;
          Score 10; DB 1;
Pred. No. 1.1e+03;
                                                         1; Mismatches
     Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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ORGANISM: Artificial Sequence
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Sequence 154224, Application US/10257017B
Sequence 154224, Application US/10257017B
Sequence 154224, Application US/10257017B
Sequence 154224, Application US/10257017B
Sequence 154224, Application of Sequence 154224, Application of Sequence 154224, Application of Sequence 157122 OF INVENTION: Detection of Single nucleotide polymorhphisms (SNPs) and cytosine TILLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 154224
LENGTH: 13
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Sequence 15423, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kutt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 154223
IENGTH: 13
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                                                                                                                                          ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0000577 US-10-257-017B-154056
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US-10-257-0178-154223
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Pred. No. 1.1e+03;
1; Mismatches 1; Indels
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                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                   Query Match 7.7%;
Best Local Similarity 83.3%;
Matches 10; Conservative
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ORGANISM: Artificial Sequence
FEATURE:
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 154056
LENGTH: 13
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Best Local Similarity
Matches 10; Conserv
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US-10-257-017B-165853
; Sequence 165853, Application US/10257017B
; Sequence 165853, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; TITLE OF INVENTION: methylations
; TITLE OF INVENTION: methylations
; FILE REFRENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; FRIOR FILING DATE: 2000-04-07
; NUMBER OP SEQ ID NOS: 382046
; SEQ ID NO 165853
; LENGTH: 13
; TYPE: DNA
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of Single nucleotide polymorhphisms (SNPs) and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 164658
LENGTH: 13
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100.0%; Pred. No. 1.18+03;
cive 0; Mismatches 0; Indels
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                       CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 164657
LENGTH: 13
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; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
FILE REFERENCE: E01/1193/WO
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Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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US-10-257-017B-164658
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Methylations
TITLE OF INVENTION: Methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 100/2-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 161190
                                  Sequence 161189, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Plepenbrock
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/7
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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Sequence 164657, Application US/10257017B

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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US-10-257-017B-161190
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7.7%; Score 10; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 10; Conserv
                          US-10-257-017B-161189/c
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LENGTH: 13
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APPLICANT: ALGARDED OF APPLICANT: ALGARDED OF APPLICANT: Christian Piepenbrock APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO CURRENT EPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 168698
LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 0210-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 169517
LENGTH: 13
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US-10-257-017B-168698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042350 US-10-257-017B-169517
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100.0%; Pred. No. 1.1e+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                               ; Sequence 168698, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander olek
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; Sequence 169518, Application US/10257017B
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.4
Matches 10, Conservative
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Best Local Similarity 100.
Matches 10; Conservative
       1354 GAAAAATATT 1363
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US-10-257-017B-168698
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Sequence 168697, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 168697
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Christian Pipenbrock
APPLICANT: Christian Pipenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 105/10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 165854
LENGTH: 13
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; ORGANISM: Artificial Sequence
; FEATURE:
; CTHEN INFORMATION: Oligonucleotide for detection of SNP TSC0041592
US-10-257-017B-165853
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JOTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042182
US-10-257-017B-168697
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                                                                                                                         7.7%; Score 10; DB 1; Length 13; 100.0%; Pred. No. 1.1e+03; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 165854, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                Best Local Similarity 100.
Matches 10; Conservative
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US-10-257-017B-165854/c
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Sequence 171967. Application US/10257017B
Sequence 171967. Application US/10257017B
Sequence 171967. Application US/10257017B
Sequence 171967. Application US/10257017B
SEPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION WHABER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 171967
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Sequence 171568, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPS] and cytosine
TITLE OF INVENTION: methylations
FILE REFERRICE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
FILE APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
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US-10-257-017B-171968
                                                                                                                                                                                                            ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042725 US-10-257-017B-171406
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US-10-257-017B-171967
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ORGANISM: Artificial Sequence
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                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 171406
LENGTH: 13
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Best Local Similarity 100.
Matches 10; Conservative
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Sequence 171405, Application US/10257017B

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Alexander Olek

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR PLING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 171405

LENGTH: 13
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Sequence 171406, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Fiepenbrock
APPLICANT: Christian Fiepenbrock
APPLICANT: Christian Fiepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
FILE REFERENCE: E01/1193/WO
GURRENT APPLICATION NUMBER: US/10/257,017B
GURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
            APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPRENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: D10019173.8
PRIOR APPLICATION NUMBER: D2 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 169518
LENGTH: 13
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0042350 US-10-257-017B-169518
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7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10, Conservative
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      APPLICANT: Alexander Olek
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Sequence 173005, Application US/10257017B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms (SNPs) and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT PRILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 173006
LENGTH: 13
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Rurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
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US-10-257-017B-173005
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US-10-257-017B-173006
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
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SEQ ID NO 173005
LENGTH: 13
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Best Local Similarity 100.
Matches 10; Conservative
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1137/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 172185
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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        Length 13;
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     Score 10; DB 1; La
; Pred. No. 1.1e+03;
Query Match 7.7%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 1.1 Matches 10; Conservative 0; Mismatches
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US-10-257-017B-172185
; Sequence 172185, Application US/10257017B
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10, Conservative
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Matches 10; Conservative
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Sequence 189086, Application US/10257017B
Sequence 189086, Application US/10257017B
Sequence 189086, Application US/10257017B
SEQUENCEANT: NTGORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Mark Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT PAPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 189086
LENGTH: 13
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Sequence 189409, Application US/10257017B
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                                                                    FEATURE:
OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046541
US-10-257-017B-189085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046541 US-10-257-017B-189086
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; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0000731
US-10-257-017B-189409
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ORGANISM: Artificial Sequence
                                           ORGANISM: Artificial Sequence
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| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Poetection of Single nucleotide polymorhphisms [SNPs] and cytosine | TITLE OF INVENTION: methylations | TITLE OF INVENTION: methylations | FILE REFERENCE: E01/1193/WO | CURRENT APPLICATION NUMBER: US/10/257,017B | CURRENT APPLICATION NUMBER: DE 10019173.8 | PRIOR APPLICATION NUMBER: DE 10019173.8 | PRIOR FILING DATE: 2000-04-07 | NUMBER OF SEQ ID NOS: 382046 | SEQ ID NO
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GRNERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNP8] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: R01/1193/WO
CURRENT PAPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
RIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 189085
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; CTHER INFORMATION: Oligonucleotide for detection of SNP TSC0045258
US-10-257-017B-183308
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US-10-257-017B-183307
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; TITLE OF INVENTION: methylations; FILE REFERENCE: E01/1193/WO CURRENT APPLICATION WUMBER: US/10/257,017B; CHRENT FILING DATE: 2002-10-07; PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07; NUMBER OF SEQ ID NOS: 382046; SEQ ID NO 183307
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                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 10; Conserva
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Best Local Similarity
Matches 10; Conserv
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
CURRENT PELICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 189702
LENOTH: 13
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US-10-257-017B-194095/c
155-017B-194095, Application US/10257017B
Sequence 194095, Application US/10257017B
Sequence 194095, Application US/10257017B
Sequence 194095, Application US/10257017B
Sequence 194095, Application Sequence 194095, Triangle US/10-194095
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine CURRENT FILING DATE: 2002-10-07
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 194095
LENGTH: 13
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APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
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, OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0047730 US-10-257-017B-194095
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-257-017B-194096
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US-10-257-017B-189701/ Application US/10257017B
Sequence 189701, Application US/10257017B
Sequence 189701, Application US/10257017B
Sequence 189701, Application of single nucleotide polymorhphisms (SNPs) and cytosine TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPERENCE: B01/1193/W0
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 189701
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT APPLICATION WUMBER: De 10019173.8
PRIOR PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 189410
LENGTH: 13
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7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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83.3%; Pred. No. 1.1e+03;
tive 1; Mismatches 1; Indels
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US-10-257-017B-189702
; Sequence 189702, Application US/10257017B
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
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Best Local Similarity 83.33
Matches 10; Conservative
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US-10-257-017B-201792/c
US-10-257-017B-201792/c
Sequence 201792, Application US/10257017B
Sequence 201792, Application US/10257017B
Sequence 201792, Application US/10257017B
Sequence 201792, Application US/10257017B
Sequence 201792, Application Pleated Colek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Murt Berlin
TITLE OF INVENTION: methylations
FITLE OF INVENTION: methylations
FITLE OF INVENTION: MUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 201792
LENGTH: 13
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Rut Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OP INVENTION: methylations
FILE REFERENCE: BO1/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,0178
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 382046
SEQ ID NO 201791
LENGTH: 13
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                                                                                                      Gaps
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US-10-257-017B-201791
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                                                Length 13;
                                                Score 10; DB 1; I
Pred. No. 1.1e+03;
1; Mismatches 1;
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                                                   7.7%;
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Best Local Similarity 100.
Matches 10; Conservative
                                                Query Match 7.7
Best Local Similarity 83.3
Matches 10; Conservative
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US-10-257-017B-195784
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Sequence 195783 Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 195783
LENGTH: 13
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Sequence 195784, Application US/10257017B

Sequence 195784, Application US/10257017B

Sequence 195784, Application US/10257017B

Sequence 195784, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

APPLICANT: Muxt Berlin

APPLICANT: Muxt Berlin

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2000-01-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER: OF SEQ ID NOS: 382046

SEQ ID NO 195784

LENGTH: 13
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0047730 US-10-257-017B-194096
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US-10-257-017B-195783
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7.7%; Score 10; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 194096
LENGTH: 13
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 10; Conserv
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Sequence 207428, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
PRIOR SEQ ID NOS: 382046
SEQ ID NO 207428
LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations FILE REFERENCE: E01/193/WO CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT APPLICATION NUMBER: US/10/257,017B PRIOR PILING DATE: 2002-10-07 PRIOR PILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 207427 LENGTH: 13
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US-10-257-017B-207427
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1.1e+03;
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7.7%; Score 10; DB
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 10; Conservative 0; Mismatches
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Matches 10; Conserv
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 100/257,017B
FRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
SRIOR FILING DATE: 2000-04-07
SRIOR FILING DATE: 2001-04-07
SRIOR FILING DATE: 2001-04-07
SRIOR FILING DATE: 2001-04-07
SRIOR FILING DATE: 10019173.8
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US,10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 202318
LENGTH: 13
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Pred. No. 1.1e+03;
1; Mismatches 1; Indels
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                                                                                                              Sequence 202317, Application US/10257017B GENERAL INFORMATION:
APPLICANT: Alexander Olek
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.3%;
Matches 10; Conservative
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ORGANISM: Artificial Sequence
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US-10-257-017B-202317/c
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Sequence 209360, Application US/10257017B

GENERAL INFORMATION:
Sequence 209360, Application US/10257017B

GENERAL INFORMATION:
BAPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 209360
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/MO
CURRENT PRILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR RILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 211887
LENGTH: 13
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Pred. No. 1.1e+03;
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100.0%; Pred. No. 1.1e+03;
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
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Best Local Similarity 83.3%;
Matches 10; Conservative
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Matches 10; Conservative
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Matches 10; Conservative
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                                                                             13 RAAAAAAATAT 2
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                                                                                                                                                              US-10-257-017B-209360
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US-10-257-017B-211887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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APPLICANT: Kurt Barlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR PEDLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0005053
US-10-257-017B-208650
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                                                           ; FEATURE:
OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0005053
US-10-257-017B-208649
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Pred. No. 1.1e+03;
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                                                                                                                                         Score 10; DB 1; Length 13;
Pred. No. 1.1e+03;
                                                                                                                                    Query Match 7.7%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 1.1 Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                          Sequence 208650, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.7%;
                 TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity
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LENGTH: 13
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 217085
LENGTH: 13
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: MUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10-07
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0052741 US-10-257-017B-217002
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; Sequence 217086, Application US/10257017B
; GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 217002
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 217085, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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LENGTH: 13
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Sequence 217001, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Earlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
GURRENT APPLICATION NUMBER: 105/10/7
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 217001
                                                        APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION WHOBER: U01/0/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 211888
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Sequence 217002, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: B01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
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US-10-257-017B-217001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0051655 US-10-257-017B-211888
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100.0%; Pred. No. 1.1e+03;
ive 0; Mismatches 0; Indels
              Sequence 211888, Application US/10257017B GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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Sequence 212395, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REPREBENCE: E01/133/MO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
FRIOR APPLICATION NUMBER: DE 10019173.8
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ DID NOS: 382046
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; Sequence 222396, Application US/10257017B
; Sequence 222396, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: methylations
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/W0
; CURRENT FILING DATE: 2002-10-07
; CURRENT FILING DATE: 2000-04-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 22396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0054111
US-10-257-017B-222395
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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US-10-257-017B-223435
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US-10-257-017B-218419, Application US/10257017B
Sequence 218419, Application US/10257017B
Sequence 218419, Application US/20257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Murk Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT FILING DATE: 2002-10-07
CURRENT FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 218419
LENGTH: 13
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REFRENCE: E01/1193/MO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 100/257,017B
REACH APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
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; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0053101
US-10-257-017B-218420
; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0052768
US-10-257-017B-217086
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US-10-257-017B-218419
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                                                                                        Length 13;
                                                                                      Query Match 7.7%; Score 10; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 10; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserva
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1358 AATATTCCAC 1367

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Sequence 223704, Application US/10257017B

Sequence 223704, Application US/10257017B

Sequence 223704, Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1133/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT PILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 223704

LIBNGTH: 13
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Sequence 223829, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1133/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
RHORE RO FEQ ID NOS: 382046
SEQ ID NO 223829
LENGTH: 13
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                                                                                                                                         ) OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0054459 US-10-257-017B-223703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0054459 US-10-257-0178-223704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0054504 US-10-257-017B-223829
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7.7%; Score 10; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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13 GAAAATATT 4
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SEQ ID NO 223703
                              LENGTH: 13
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                                                                                                                 FEATURE:
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APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 100/20-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 223436
LENGTH: 13
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 100-2-10-07
PRIOR PRILOS APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
                  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine TITLE OF INVENTION: methylations TITLE OF INVENTION: methylations FILE REPERENCE: E01/1193/W0 CURRENT PAPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 223435 LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Oligonuclectide for detection of SNP TSC0054398 US-10-257-017B-223435
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7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Matches 10; Conservative
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Kurt Berlin
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: ALTE Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: DETECTION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: US 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
                                                    APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICANION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 223908
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Sequence 225650, Application US/10257017B

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
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OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055004
US-10-257-017B-225649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0054543 US-10-257-017B-223908
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                  Sequence 223908, Application US/10257017B GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Matches 10; Conservative
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US-10-257-017B-225649
US-10-257-017B-223908
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LENGTH: 13
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GRANEAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANTON: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
FILER REFERENCE: 2000-10-07
PRIOR PILING DATE: 2000-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 223907
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosing
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT PAPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 223830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Oligonuclectide for detection of SNP TSC0054504-US-10-257-017B-223830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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                              Indels
   Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 10; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                    US-10-257-017B-223830/c
; Sequence 223830, Application US/10257017B
; GENERAL INFORMATION;
APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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RESULT 988

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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
CURRENT ELER REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NOS: 382046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Christian Dispenbrock
APPLICANT: Christian Dispenbrock
APPLICANT: Kutt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 228869
LENGTH: 13
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US-10-257-017B-228869
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US-10-257-017B-228870
                         ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC00551111 US-10-257-017B-226100
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7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                         Query Match 7.7%; Score 10; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 10; Conservative 0; Mismatches 0; Indels
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; Sequence 228870, Application US/10257017B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 228869, Application US/10257017B
GENERAL INFORMATION:
APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
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Best Local Similarity
Matches 10; Conserva
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GENERAL INFORMATION:

APPLICANT: Alexander olek

APPLICANT: Alexander olek

APPLICANT: Alexander olek

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

TITLE OF INVENTION: methylations

FILE REFERENCE: B01/1193/W0

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 222099

LENGTH: 13
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: METHYLATION
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT PILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 226100
IENGTH: 13
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US-10-257-017B-226099
                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055004 US-10-257-017B-225650
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7.7%; Score 10; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 10; Conservative 1; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/10/257,017B CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: DE 10019173.8 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 382046 SEQ ID NO 225650 LENGTH: 13
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ORGANISM: Artificial Sequence
FRATURE:
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Sequence 235997, Application US/10257017B
Sequence 235997, Application US/10257017B
Sequence 235997, Application US/10257017B
Sequence 235997, Application of APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 2010/10-07
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Christian Dispendencek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nuclectide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US/10/257,017B
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 234088
LENGTH: 13
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TILLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 234087
LENGTH: 13
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US-10-257-017B-234088
                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0057126 US-10-257-017B-234087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.7%; Score 10; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 10; Conservative 0; Mismatches 0; Indels
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APPLICANT: Alexander Olek
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ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Plepenbrock
APPLICANT: Christian Plepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
FILE OF INVENTION: methylations
FILE OF INVENTION: WHERE: US/10/257,017B
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2002-10-07
PRIOR FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 232898
LENGTH: 13
                                                                                                                                                                                                      APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: 105/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 232897
LENGTH: 13
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US-10-257-017B-232898
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Pred. No. 1.1e+03;
1; Mismatches 1; Indels
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GENERAL INFORMATION:
APPLICANT: Alexander Olek
                                                                                                                         RESULT 995
US-10-257-017B-232897/c
Sequence 232897, Application US/10257017B
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.33
Matches 10; Conservative
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11 AGGTAAAATT
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US-10-257-017B-234087
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RESULT 1000

WS-10-257-017B-235998/c

WS-10-257-017B-235998/c

Sequence 235998. Application US/10257017B

Sequence 235998. Application US/10257017B

Sequence 235998. Application US/10257017B

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: Methylations

FILE REFERENCE: B01/1193/WO

CURRENT APPLICATION NUMBER: US/10/257,017B

CURRENT FILING DATE: 2002-10-07

PRIOR PILING DATE: 2000-04-07

WHERE OF SEQ ID NOS: 382046

SEQ ID NO 235998

TOTAL OF THE OFFICE OFF
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CHER INFORMATION: Oligonucleotide for detection of SNP TSC0057608
US-10-257-017B-235998
                                                                                                                                                                          TYPE: DNA
) ORGANISM: Artificial Sequence
) PEATURE:
) CTHER INFORMATION: Oligonuclectide for detection of SNP ISC0057608
US-10-257-017B-235997
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Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.18+03;
Matches 10; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 235997
LENGTH: 13
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Search completed: April 7, 2004, 07:12:42 Job time : 8 secs

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1352 AAGAAAAATA 1361

12 AAGAAAATA 3

Search completed: April 7, 2004, 07:15:00 Job time: 0.001 secs

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(db xref="catal:185760"

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ABF1--05-A03 gl ABF3-overexpressing transgenic rice lambda phage cDNA library (ABF1) Oryza sativa cDNA clone ABF1--05-A03, mRNA
                                                                                                                                                                   herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,J.
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae, Oryzaee; Oryza.
1 (bases 1 to 11)
Kim,J.S., Jun,Km., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta. [bases 1 to 13]
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/organism="Beta vulgaris"
/mol type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
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12472698
Contact: Weisehaar B
ADIS DNA core facility at MPIZ
ADIS DNA core facility at MPIZ
ADIS DNA core facility at MPIZ
Carl-von-linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissha@mpiz-koeln.mpg.de
Insert Length: 13 Std Error: 0.00
Plate: 11 row: K column: 22
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
Location/Qualifiers
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1 (Dases 1 to 11)
S Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 2 handwareh; Comes Andrewship, Montaling Comes Andrewship, MyongJi Liliophy
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7LEAF--04-A13.gl Rice leaf plasmid cDNa library II (7LEAF) Oryza sativa cDNa clone 7LEAF--04-A13, mRNA sequence.
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                        Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Location/Qualifiers
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vative 0; Mismatches
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Gaps .. gchultz911-3.rst

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Contact: Weisshaar B
                                 Query Match
Best Local Similarity 100.
Matches 8; Conservative
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BQ595495/c
LOCUS
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1 (bases 1 to 10)

1 (kim,J.S., Jun,K., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

YongIn, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, KyeongGi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Location/Qualifiers
                                                                                                                                                                                                                                   Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      'organism="Oryza sativa"
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'cultivar="Nackdong"
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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Binbeck, Germany, contact:
b.schulz@kwB.de; cloning sites Sal1-Not1, primer sites and
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SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Not1-T7; Note:
SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Not1-T7;
Sequencing granted in the context of the GABI-Beet
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                        11 bp mRNA linear EST 06-DEC-2002
E012691-024-022-014-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
cDNA clone 024-022-014 5-PRIME, mRNA sequence.
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota, Viridiplantae; Streptophyta; Eucliocts;

Spermatophyta; Magnoliophyta; euclioctyledons; core eucliocts;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 11)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,

Prungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

Construction of a 'unigene' cDNA clone set by oligonucleotide

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)
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Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                            0; Indels
Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: weisshaadmpiz-koeln.mpg.de
Insert Length: 11 Std Brror: 0.00
Plate: 22 row: 0 column: 14
Seg primer: SP6; CATACGATTTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | db xref="GABI:191359"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.2%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches
6.2%; Score 8; DB 1;
100.0%; Pred. No. 6.2;
tive 0; Mismatches
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EST.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

April 7, 2004, 07:15:00 ; Search time 0.001 Seconds (without alignments) 27.300 Million cell updates/sec Run on:

Title: Perfect score:

us-10-006-911-3 130 1 tcaggggaagaaaaatattc.....ggttgatcaagcaaatagga 130 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 0.5 Scoring table:

9 seqs, 105 residues Searched:

18 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 8 Maximum DB seq length: 50

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 9 summaries

rst.seg:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		ACTROSTON: DOLLOS	ACCESSION: DOOR 2000	ACCESCE MOTERATOR	ACCEPTION: DESCRIPTION OF STREET	ACCESSION: DESCRIPTION	ACCESSION: DESCRIPTION	ACCESSION: CF302914	ACCESSION: BQ595495
ID	BO594229	BO587288	BO587706	BO582939	CF299850	BO587101	CF304450	CF302914	BQ595495
DB	7	Н	Н	-	Н	~	ч	П	1
% Query Match Length DB	12	12	12	13	11	13	11	10	11
% Query Match	8.0	7.7	7.7	7.7	7.2	7.2	6.5	6.2	6.2
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ALIGNMENTS

Plant J. 3 22362189 22362189 Contact: YADIS DNA Max-Planck Carl-von-I Fax: 00493 Email: well Insert Len Plate: 25 Seq primez	/ the property of the content of the content of the condition of the content of t	Similari 1, Cons GGGGAAG GGGGAAA	BQ587288 E012340w-024-010-G19-SP6 MPIZ-ADIS-024-leaf Beta vulgaris E012340w-024-010-G19 -SPRIME, mRNA sequence. E0587288 E0587288 I G1:26116870 EST. Beta vulgaris Beta vulgaris Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach	Caryophylales: Amaranthac Laryophylales: Amaranthac 1 (bases 1 to 12) Hervig.K., Schulz,B., Weis Drungowski,M., Stahl,D., W and Radelof,U. Construction of a 'unigene Cingerprinting allows acce plant J. 32 (5), 845-857 (2285189) 1247269 Contact: Weisshaar B ADIS DNA core facility at Max-Planck-Institute for P Carl-von-Linne Weg 10, 508 Fax: 00492215062851 Emmäl: weisshaa@mpiz-koeln Insert Length: 12 Std Er
JOURNAL MEDLINE PUBMED COMMENT FEATURES SOURCE		Query Match Best Local (Matches I: Qy 1348	RESULT 2 BQ587288/c LOCUS DEFINITION ACCESSION VERSION VERYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED COMMENT

Gaps

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/note="Vector: pCMVSPORT6; Site_1: Sall; Site_2: Not1; Contains 1: Soll; Site_2: Not1; Contains 1: Soll library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, Contact: b.schulz@kws.de; cloning sites Sall-Not1, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Endicotyledons; Coré eudicots; Caryophylales; Amaranthaceae; Beta.

1 (Dass 1 to 13)

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1 (Dass 2 to 13)

1 (Dass 3 to 13)

1 (Dass 3 to 13)

1 (Dass 4 to 13)

1 (Dass 5 to 13)

1 (Dass 6 to 13)

1 (Dass 6 to 13)

2 (Dass 7 to 13)
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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQS82939
S015369-024-006-K21-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris
cDNA clone 024-006-K21 5-PRIME, mRNA sequence.
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SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
                                                                                                                                                                                                                                                                  Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Ratharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"
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ADIS DNA core facility at MPIZ
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Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
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Flate: 6 row: K column: 21
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Location/Qualifiers
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; Pred. No. 1.8;
0; Mismatches 0; Indels
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1 [bases 1 to 12]
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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CDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saarzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-Notl, primer sites and
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                                                                                                                                 /mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
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Insert Length: 12 Std Error: 0.00
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
Location/Qualifiers
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100.0%; Pred. No. 1.8;
cive 0; Mismatches 0; Indels
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Location/Qualifiers
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